



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 172533

TO: Ruixiang Li
Art Unit: 1646
Location: rem/4D75/4C70
Serial Number: 10/712615

Monday, December 12, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

Published Applications Database - November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).



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STIC-Biotech/ChemLib

172533

me

From: CR
Sent: FE
To:
Subject: Li, Ruixiang
Sunday, November 27, 2005 12:02 PM
STIC-Biotech/ChemLib
Sequence search of Application No. 10/712,615

Please do a standard search on:

(i).SEQ ID NOS: 2 and 103 against both commercial and interference amino acid databases;

(ii). SEQ ID NO: 1 and 2 against both commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
REM 4D75
Mail Box 4C70
(571) 272-0875

2 aa 508
103aa 372
17aa 1527

me

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed: _____
Searcher: Beverly e 2528
Terminal time: _____
Elapsed time: _____
CPU time: _____
Total time: _____
Number of Searches: _____
Number of Databases: _____

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
_____ Other CBN

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:00 ; Search time 155.286 Seconds

(without alignments)
1437.373 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644

Sequence: 1 MTSTCTNSTRSNSHTCMP.....GTEGTEGKIYPSYDSTAFP 508

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2644	100.0	508	5	ABR75712 G-protein
2	2644	100.0	508	5	AA015503 Human G-P
3	2644	100.0	508	5	AAE25236 Human HGB
4	2644	100.0	508	6	ABR98721 Human G-P
5	2644	100.0	508	6	ABR57432 Human NOV
6	2644	100.0	508	7	ABR42865 Human G-P
7	2644	100.0	508	9	AEA33200 Human GPC
8	2644	100.0	508	9	AEA33070 Human G-P
9	2644	100.0	746	7	ADP70508 Oryz
10	2641	99.9	508	4	AAAB6428 Human bra
11	2641	99.9	508	4	AAU25605 Human G-P
12	2641	99.9	508	4	AAU25605 Human G-P
13	2641	99.9	508	4	AAU25605 Human G-P
14	2641	99.9	508	5	AAU04369 Human G-P
15	2641	99.9	508	5	AAU1764 Human G-P
16	2641	99.9	508	5	AAU1764 Human G-P
17	2641	99.9	508	5	AAU1764 Human G-P
18	2641	99.9	508	5	AAU1764 Human G-P
19	2641	99.9	508	6	ABR82501 Human TGR
20	2641	99.9	508	7	ABR82501 Human TGR
21	2641	99.9	508	7	ADL96462 Human G-P
22	2641	99.9	508	8	ADL96462 Human G-P
23	2641	99.9	508	8	ADL96462 Human G-P
24	2641	99.9	508	9	AEA33109 Human GPC

25	2641	99.9	508	9	ABR20819	Aeb20819 Human RUP
26	2641	99.9	926	4	AAU04387	Adi04387 GPCR-Gs F
27	2641	99.9	926	7	ADL96550	Adi96550 G protein
28	2641	99.9	926	9	ADW44723	Adw44723 Human RUP
29	2641	99.9	926	9	ABR20907	Aeb20907 Human RUP
30	2637	99.7	508	4	ABR61982	Aab61982 Human G-P
31	2637	99.7	508	6	ABR81704	Abp81704 Human G-P
32	2637	99.7	508	6	AEA33111	Aea33111 Human GPC
33	2636	99.7	508	4	AAU04384	AAU04384 Human G-P
34	2636	99.7	508	7	ADL96538	Adl96538 Human mut
35	2636	99.7	508	9	ADW44711	Adw44711 Human RUP
36	2636	99.7	508	9	ADW44799	Adw44799 Human RUP
37	2636	99.7	508	9	AEA33110	Aea33110 Human GPC
38	2636	99.7	508	9	ABR20895	Aeb20895 Human RUP
39	2629	99.4	508	6	ABR57433	Abi57433 Human NOV
40	2628	99.4	508	5	AAE25245	AAE25245 Human GPC
41	2628	99.4	508	9	AEA33117	Aea33117 Human GPC
42	2619	99.1	508	5	ABR07985	ABR07985 Human sev
43	2551	96.5	580	7	ADW08310	Adw08310 Novel pro
44	2518	95.2	485	5	AAE15642	Aae15642 Human G-P
45	2518	95.2	485	7	ADC86473	Adc86473 Human GPC

ALIGNMENTS

RESULT 1	ABR75712	standard, protein, 508 AA.
ID	ABR75712	
XX	ABR75712;	
AC	ABR75712;	
XX	ABR75712;	
XX	ABR75712;	
DT	24-JUN-2002	(first entry)
XX	24-JUN-2002	
DE	G-protein coupled receptor AXOR69.	
XX	G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;	
XX	antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; anabolic;	
KW	antimicrobial; antiparkinsonian; cardiant; cerebroprotective;	
KW	hypotensive; hypertensive; antidiabetic; antiallergic;	
KW	antileptic; tranquilizer; neuroleptic; nootropic; anticonvulsant;	
KW	vaccine.	
OS	Homo sapiens.	
XX	Homo sapiens.	
XX	GB2367295-A.	
PN	GB2367295-A.	
PD	03-APR-2002.	
XX	03-APR-2002.	
XX	12-JUN-2001; 2001GB-00014287.	
PF	12-JUN-2001; 2000US-00596400.	
XX	16-JUN-2000; 2000US-00596400.	
PR	(SMK) SMITHKLINE BEECHAM CORP.	
PA	(SMK) SMITHKLINE BEECHAM PLC.	
PA	(SMK) SMITHKLINE BEECHAM PLC.	
XX	(SMK) SMITHKLINE BEECHAM PLC.	
XX	Elshourbagy N, Gattu M, Shabon U;	
PI	WPI; 2002-294789/34.	
XX	WPI; 2002-294789/34.	
DR	N-PSDB; ABL53719.	
XX	N-PSDB; ABL53719.	
PT	An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,	
XX	for treating diseases such as obesity, stroke and anxiety.	
XX	Claim 1; Page 27; 34pp; English.	
XX	The present sequence is that of human AXOR69, a G-protein coupled	
CC	receptor (GPCR) that shows homology to other members of the GPCR family,	
CC	such as human adrenergic alpha-1a receptor. The invention provides AXOR69	
CC	polypeptides and polynucleotides, and methods for producing such	
CC	polypeptides by recombinant techniques. Also provided are methods for	
CC	using the AXOR69 polypeptides and polynucleotides to screen for compounds	

Yes, discloses SEQ ID NO: 1 and 2

CC that stimulate or inhibit AXOR69 levels or activity. The polypeptides,
CC polynucleotides, agonists and antagonists are used to treat conditions
CC associated with AXOR69 imbalance, including bacterial, fungal, protozoan
CC and viral infections, particularly HIV-1 and HIV-2 infections, pain,
CC cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, stroke,
CC ulcers, asthma, allergies, benign prostatic hypertrophy, migraine,
CC vomiting, psychotic and neurological disorders, including anxiety,
CC schizophrenia, manic depression, depression, delirium, dementia and
CC severe mental retardation, and dyskinesias such as Huntington's disease
CC and Gilles de la Tourette syndrome. AXOR69 polypeptides are also useful
CC in vaccines, and for raising specific antibodies

XX Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIRNLVTDLQISLVAPWVAVTSVPLFPLNSHFCALVSLTHLPFASVN 120
DB 61 QLLQVTRNFIRNLVTDLQISLVAPWVAVTSVPLFPLNSHFCALVSLTHLPFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSYPSKMTORRGYLLYGTVIAVLIQSTPPLVGMGOAFADERNA 180
DB 121 TIVLVSVDRLYSIIHPLSYPSKMTORRGYLLYGTVIAVLIQSTPPLVGMGOAFADERNA 180
QY 181 LCSMIMGASPSYTIISVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLVLRVYD 240
DB 181 LCSMIMGASPSYTIISVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLVLRVYD 240
QY 241 CVENEDDEGAKKEKFEFODESEFRROHGEVYAKGSRMEAKGSLAKKSGTSTSSVEA 300
DB 241 CVENEDDEGAKKEKFEFODESEFRROHGEVYAKGSRMEAKGSLAKKSGTSTSSVEA 300
QY 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
DB 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
QY 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCAAXVFIIFSVYLSLGPYCFPLAV 420
DB 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCAAXVFIIFSVYLSLGPYCFPLAV 420
QY 421 LAVWVDVETQVPOWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQDMLKKFCKEKPXK 480
DB 421 LAVWVDVETQVPOWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQDMLKKFCKEKPXK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 2

AA015503
ID AA015503 standard; protein; 508 AA.

XX AA015503;

XX 24-OCT-2002 (first entry)

XX Human G-protein coupled receptor protein #1.

XX Human; G-protein coupled receptor protein; TGR34;
XX central nervous system disease; Alzheimer's disease; metabolic disease;
XX diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;
XX inflammatory disease; arthritis; respiratory disease; bronchitis;
XX digestive disease; stomach ulcer; immune disorder; autoimmune disease;
XX infection; AIDS.

XX Homo sapiens.
OS
XX WO200259304-A1.
PN
XX 01-AUG-2002.
PD
XX 22-JAN-2002; 2002WO-JP000405.
PF
XX 23-JAN-2001; 2001JP-00015050.
PR
XX 30-MAR-2001; 2001JP-00102560.
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX Miwa M, Ito T, Shintani Y, Miyajima N;
PI
XX WPI: 2002-557949/59.
DR
XX N-PSDB; AAL44179.
DR
XX
XX Human G-protein coupled receptor protein and DNA encoding it for design
XX of drugs and reagents for treatment and diagnosis of cancer or
XX respiratory and metabolic diseases.
XX
XX Claim 1; Page 94-96; 109pp; Japanese.
XX
XX The invention comprises the amino acid and coding sequences of two human
XX G-protein coupled receptor proteins (TGR34). The DNA and protein
XX sequences of: central nervous system diseases (e.g. Alzheimer's disease);
XX metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
XX circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
XX arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
XX (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
XX infections (e.g. AIDS). The present amino acid sequence represents a
XX human G-protein coupled receptor protein

SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIRNLVTDLQISLVAPWVAVTSVPLFPLNSHFCALVSLTHLPFASVN 120
DB 61 QLLQVTRNFIRNLVTDLQISLVAPWVAVTSVPLFPLNSHFCALVSLTHLPFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSYPSKMTORRGYLLYGTVIAVLIQSTPPLVGMGOAFADERNA 180
DB 121 TIVLVSVDRLYSIIHPLSYPSKMTORRGYLLYGTVIAVLIQSTPPLVGMGOAFADERNA 180
QY 181 LCSMIMGASPSYTIISVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLVLRVYD 240
DB 181 LCSMIMGASPSYTIISVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLVLRVYD 240
QY 241 CVENEDDEGAKKEKFEFODESEFRROHGEVYAKGSRMEAKGSLAKKSGTSTSSVEA 300
DB 241 CVENEDDEGAKKEKFEFODESEFRROHGEVYAKGSRMEAKGSLAKKSGTSTSSVEA 300
QY 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
DB 301 RGSEEVRESSSTVVASGMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEEDMERGEDDI 360
QY 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCAAXVFIIFSVYLSLGPYCFPLAV 420
DB 361 NFESEDDVEAVNIPESLPSRRNSNSNPPLPRCYOCCAAXVFIIFSVYLSLGPYCFPLAV 420
QY 421 LAVWVDVETQVPOWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQDMLKKFCKEKPXK 480
DB 421 LAVWVDVETQVPOWVITIIIMLFLOCCIHPRVYGYMKTIKKEIQDMLKKFCKEKPXK 480

OY 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508
 |||||
 DB 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508

RESULT 3

AAE25236
 ID AAE25236 standard; protein; 508 AA.
 AC AAE25236;
 DT 30-OCT-2002 (first entry)
 XX
 DE Human HGPBMY8 protein #1.
 XX
 KW Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
 KW neurological disorder; brain; immunological; cell growth; cytostatic;
 KW neoplastic disease; CAMP; signalling pathway; immune disorder; cancer;
 KW gene therapy; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 124
 FT nucleotide="Leu at this position changes to Val due to single
 FT Misc-difference 352
 FT nucleotide polymorphism"
 FT /note="Asp at this position changes to Gly due to single
 FT Misc-difference 398
 FT nucleotide polymorphism"
 FT /note="Ala at this position changes to Asp due to single
 FT nucleotide polymorphism"
 FT Misc-difference 398
 FT /note="Ala at this position changes to Thr due to single
 FT nucleotide polymorphism"
 XX
 PN MO200240670-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 14-NOV-2001; 2001WC-US043909.
 XX
 PR 14-NOV-2000; 2000US-0248285P.
 PR 14-FEB-2001; 2001US-0268581P.
 PR 27-JUL-2001; 2001US-0308285P.
 PR 04-SEP-2001; 2001US-0317166P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Batteglino P, Feder J, Mintier G, Nelson T, Ramanathan C;
 PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
 XX
 DR WPI; 2002-519383/55.
 DR N-PSDB; AAD41159.
 PT A substantially purified human G-protein coupled receptor polypeptide,
 PT termed HGPBMY8, useful for treating a neurological disorder or brain
 PT disorder in a mammal.
 XX
 PS Claim 4; Page 161-163; 223pp; English.

CC diseases or disorders related to the brain, e.g., neurological disorders.
 CC HGPBMY8 DNA and protein are useful for modulating intracellular CAMP
 CC associated signalling pathways. An expression vector containing HGPBMY8
 CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
 CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
 CC in gene therapy. The present sequence is human HGPBMY8 protein
 XX
 SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 5; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1,le-233;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLVIFPAASFGNIVLALVQRKP 60
 |||||
 DB 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLVIFPAASFGNIVLALVQRKP 60
 OY 61 QLLQVYTNRIFFMLVTDLLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTLFAPASVN 120
 |||||
 DB 61 QLLQVYTNRIFFMLVTDLLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTLFAPASVN 120
 OY 121 TIVLVSVDRYLSIHPSTPSKMTORRGYLLXGTWIVAILLOSTPPLVGMGAARDERNA 180
 |||||
 DB 121 TIVLVSVDRYLSIHPSTPSKMTORRGYLLXGTWIVAILLOSTPPLVGMGAARDERNA 180
 OY 181 LGSMTWGAASPSYTIISVSVFIVPIVMACYSVFCARROHALLVNVKRSLEVRVND 240
 |||||
 DB 181 LGSMTWGAASPSYTIISVSVFIVPIVMACYSVFCARROHALLVNVKRSLEVRVND 240
 OY 241 CVENBDEBGAKEKEEFODESEFRROHGEFVKAKEGMEAKDGLAKKEGSTGTSSSVEA 300
 |||||
 DB 241 CVENBDEBGAKEKEEFODESEFRROHGEFVKAKEGMEAKDGLAKKEGSTGTSSSVEA 300
 OY 241 CVENBDEBGAKEKEEFODESEFRROHGEFVKAKEGMEAKDGLAKKEGSTGTSSSVEA 300
 |||||
 DB 241 CVENBDEBGAKEKEEFODESEFRROHGEFVKAKEGMEAKDGLAKKEGSTGTSSSVEA 300
 OY 301 RGSSEYRESSTVYASDGSNMGKSGSTKYVENSMAKDKGRVENVQCSIDLGEDMEFGEEDI 360
 |||||
 DB 301 RGSSEYRESSTVYASDGSNMGKSGSTKYVENSMAKDKGRVENVQCSIDLGEDMEFGEEDI 360
 OY 361 NFSEDDVEAVNTPESLPSPRRNSNSNPPLPRCQCKAAVYFIIFSYLSDGPYFLAV 420
 |||||
 DB 361 NFSEDDVEAVNTPESLPSPRRNSNSNPPLPRCQCKAAVYFIIFSYLSDGPYFLAV 420
 OY 421 LAVWVDETQVPOWVYTIITIMLFLQCCIHPPVYGYMAKTIKKEIQDMLKKEFCCKEPPK 480
 |||||
 DB 421 LAVWVDETQVPOWVYTIITIMLFLQCCIHPPVYGYMAKTIKKEIQDMLKKEFCCKEPPK 480
 OY 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508
 |||||
 DB 481 EDSDPDLPTGEGTGGKIVPSYDSATFP 508

RESULT 4

ABB98721
 ID ABB98721 standard; protein; 508 AA.
 XX
 AC ABB98721;
 DT 17-JUN-2003 (first entry)
 XX
 DE Human G protein coupled receptor, 50879.
 XX
 KW G protein coupled receptor; receptor; anorectic; antiparkinsonian;
 KW hypotensive; hypertensive; tranquilizer; neuroleptic; antidepressant;
 KW nootropic; anticonvulsant; antimigraine; human; 50879; hippocampus;
 KW hypothalamus; brain; obesity; bulimia; anorexia; Parkinson's disease;
 KW hypotension; hypertension; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; manic depression; delirium; dementia; epilepsy;
 KW migraine; insomnia; circadian rhythm disorder; cognitive function.
 XX
 OS Homo sapiens.
 XX
 PN FR2822844-A1.
 XX
 PD 04-OCT-2002.

XX 27-MAR-2001; 2001FR-00004074.
 XX 27-MAR-2001; 2001FR-00004074.
 XX (SERV-) LES LAB SERVER SA.
 PA Galizzi JP, Coge F, Rique H, Boutin JA;
 DR WPI; 2003-021471/02.
 DR N-PSDB; ABV74517.
 XX New nucleic acid encoding human G protein coupled receptors, useful for
 PT creating e.g. obesity, also derived polypeptides, antibodies and
 PT modulators.
 XX
 XX Claim 15; Page 27-29; 44pp; French.
 XX
 XX The present sequence is the protein sequence for human G protein-coupled
 CC receptor, 50879. The receptor and its coding sequence can be used for
 CC creating diseases associated with abnormal expression of the receptor,
 CC particularly diseases involving the hippocampus or hypothalamus,
 CC particularly obesity, bulimia, anorexia, Parkinson's disease, hypo- or
 CC hypercortisolemia, and psychotic or neurological disorders such as anxiety,
 CC schizophrenia, manic depression, delirium, dementia, epilepsy, migraine,
 CC insomnia, circadian rhythm disorders and loss of cognitive function. The
 CC G protein-coupled receptor coding sequence was isolated from human brain
 CC tissue

XX Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 6; Length 508;
 Beft Local Similarity 100.0%; Pred. No. 1.1e-233;
 Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSCTNSTRNSGHTCMPLSKMPLSLAHGIRSTVLFVFLAASFVGNIVLALVLRKP 60
 DB 1 MTSCTNSTRNSGHTCMPLSKMPLSLAHGIRSTVLFVFLAASFVGNIVLALVLRKP 60
 QY 61 QLVNTRNFNLVTDLQISLVAPVWVATVPLFVFWPLNSHFCALVSLTLFPAFASV 120
 DB 61 QLVNTRNFNLVTDLQISLVAPVWVATVPLFVFWPLNSHFCALVSLTLFPAFASV 120
 QY 121 TIVAVSVDRYLSIHPISYPSKMTORRGVLLYGTWIVALLQSTPPLYGWGOAFDERNA 180
 DB 121 TIVAVSVDRYLSIHPISYPSKMTORRGVLLYGTWIVALLQSTPPLYGWGOAFDERNA 180
 QY 181 LCMWIMGASPSYTLISVSVFIVPLIWMACSVFCAARHALLVYKRSLEVRKYD 240
 DB 181 LCMWIMGASPSYTLISVSVFIVPLIWMACSVFCAARHALLVYKRSLEVRKYD 240
 QY 241 CVENEDDEGAKEKEFEFODESEFRROHEGEVKAKEGMEAKDGLAKEGSTGTSSEVEA 300
 DB 241 CVENEDDEGAKEKEFEFODESEFRROHEGEVKAKEGMEAKDGLAKEGSTGTSSEVEA 300
 QY 301 RGSSEVRSSSTVASDGSMEGKSGTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
 DB 301 RGSSEVRSSSTVASDGSMEGKSGTKVEENSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
 QY 361 NFESEDDVAANVPELSPRSRNSNSNPPLPRCYCKAAKVFITITFSVYLSIGPCFLAV 420
 DB 361 NFESEDDVAANVPELSPRSRNSNSNPPLPRCYCKAAKVFITITFSVYLSIGPCFLAV 420
 QY 421 LAVWVDETOVPOWVITITIMLFLOCCIHPRVYVYGMHTIKKEIDMLKKFCEKBPX 480
 DB 421 LAVWVDETOVPOWVITITIMLFLOCCIHPRVYVYGMHTIKKEIDMLKKFCEKBPX 480
 QY 481 EDSHPDLPGTSGTEGKIIVPSYDSATFP 508
 DB 481 EDSHPDLPGTSGTEGKIIVPSYDSATFP 508

RESULT 5

ABR57432
 ID ABR57432 standard; protein; 508 AA.
 AC ABR57432;
 XX 15-SEP-2003 (first entry)
 DT Human NOV14a protein SEQ ID NO:42.
 DE
 XX Human; NOVX; cytosolic; cardiac; antiinflammatory; immunosuppressive;
 KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
 KW anorectic; antiaesthetic; nephroprotective; antiarthritic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; vitricide; antiparkinsonian;
 KW relaxant; anticonvulsant; hypotensive; vasotropic; vaccine; cancer;
 KW vulnerability; angiogenic; antilipogenic; gene therapy; vaccine; cancer;
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
 KW muscular dystrophy; epilepsy; wasting disorder; chromosome X.
 OS Homo sapiens.
 PN WO200294870-A2.
 XX 28-NOV-2002.
 PD
 XX 02-NOV-2001; 2001WO-US051580.
 PF
 XX 02-NOV-2000; 2000US-0245291P.
 PR 02-NOV-2000; 2000US-0245317P.
 PR 07-NOV-2000; 2000US-0245622P.
 PR 08-NOV-2000; 2000US-0246871P.
 PR 26-JAN-2001; 2001US-0254389P.
 PR 26-JAN-2001; 2001US-0254423P.
 PR 29-JAN-2001; 2001US-0264799P.
 XX (CURA-) CURAGEN CORP.
 PA
 XX Grose WM, Macdougall JR, Smithson G, Miller J, Stone DJ;
 PI Gunther EA, Ellerman K, Alsobrook JP, Lepley DM, Burgess CE;
 PI Spytek KA, Edinger SR, Gangoli EA, Gorman L, Taulier RO, Li L;
 PI Guo X, Fernandez ER, Verret CAM, Tchervet VT, Caeman SJ, Shenoy S;
 PI Mishra V, Furtak K, Baumgartner JC, Colman SD;
 XX WPI; 2003-140359/13.
 DR N-PSDB; ACF03567.
 DR
 XX New NOVX polypeptide useful for preventing or treating NOVX-associated
 PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
 PT in chromosome mapping, tissue typing or pharmacogenomics.
 XX Claim 1; Page 130; 346pp; English.
 PS
 XX ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
 CC to ABR57435. (I) have cytostatic, cardiac, antiinflammatory, nootropic,
 CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
 CC antiarteriosclerotic, anorectic, antiaesthetic, nephroprotective, vitricide,
 CC antiarthritic, hepatotropic, neuroprotective, antibacterial, relaxant,
 CC antiparkinsonian, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
 CC vulnerability, angiogenic and antilipogenic activities, and can be used in
 CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
 CC be used to determine the presence or absence of (I) in a sample. The NOVX
 CC polypeptides, polynucleotides encoding them, and antibodies against them,
 CC are useful in manufacturing a medicament for treating or preventing a
 CC syndrome associated with a NOVX-associated disorder such as hypertension,
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
 CC autoimmune disorders, allergies, blood disorders, obesity, infection,
 CC immunodeficiency syndrome (AIDS), immunoglobulin (IgA) nephropathy,
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX

Yes, SEQ ID NO:2 is present

CC sequence, which are used in an example from the present invention
SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MTSTCTNSTRSSNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRSSNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVYTRNRIENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
DB 61 QLLQVYTRNRIENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMQRGVLLYGTMVIAIIOSTPPLVGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMQRGVLLYGTMVIAIIOSTPPLVGMGAAPDERNA 180
QY 181 LCSMIMGASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
DB 181 LCSMIMGASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
QY 241 CVENEDDEGAERKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGAERKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
QY 301 RSESEVRESSTVASDGSMEGKSTGVENSMAKDGRTVENQCSIDLCEDDMERGEDDI 360
DB 301 RSESEVRESSTVASDGSMEGKSTGVENSMAKDGRTVENQCSIDLCEDDMERGEDDI 360
QY 361 NSESDDEVAVNIPESLPSPSRNSNSNPPLRCYQCKAAVYFIIFISYVLSIGPYCEFLAV 420
DB 361 NSESDDEVAVNIPESLPSPSRNSNSNPPLRCYQCKAAVYFIIFISYVLSIGPYCEFLAV 420
QY 421 LAWVVDVETQVQWVITIIIMLFELQCCIHPPYVGYMHTIKKEIDMLKKEFCCKEPPK 480
DB 421 LAWVVDVETQVQWVITIIIMLFELQCCIHPPYVGYMHTIKKEIDMLKKEFCCKEPPK 480
QY 481 EDSHPDLPTGEGTEKIVPSYDSATFP 508
DB 481 EDSHPDLPTGEGTEKIVPSYDSATFP 508

RESULT 6
ABR42865
ID ABR42865 standard; protein; 508 AA.
XX
AC ABR42865;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human G-protein coupled receptor OM_10.
XX
KW G-protein coupled receptor; GPCR; OM_10; human; receptor; cardiant;
KW hypertensive; hypotensive; antidiagonal; cytosolic; antiporiatic;
KW anaesthetic; gynaecological; antidepressant; antistimatic; osteocytic;
KW neuroleptic; cranulilizer; nephrotoxic; antidiacer; antiallergic;
KW neurotoxic; anticonvulsant; neuroprotective; antiparkinsonian;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 34..49
FT /note= "predicted transmembrane domain"
FT 86..90
FT /note= "predicted transmembrane domain"
FT 109..118
FT /note= "predicted transmembrane domain"
FT 155..162
FT /note= "predicted transmembrane domain"
FT Domain

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FT Domain 188..214
FT /note= "predicted transmembrane domain"
FT Domain 403..418
FT /note= "predicted transmembrane domain"
FT Domain 437..446
FT /note= "predicted transmembrane domain"
XX
XX WO2003044162-A2.
XX
XX 30-MAY-2003.
XX
XX 12-NOV-2002; 2002WO-US036204.
XX
XX 16-NOV-2001; 2001US-0332110P.
XX
XX (AMBP ) WYETH.
XX
XX Blatcher M, Paulsen JE, Bates BG,
XX
XX WPI; 2003-449811/42.
XX
XX N-PSDB; ACC42865.
XX
PT New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
PT UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
PT Parkinson's disease, acute heart failure, hypertension, cancer or
PT osteoporosis.
XX
XX
PS Claim 27; Page 178-180; 190pp; English.
XX
XX The present sequence is the protein sequence of a novel human G-protein
XX coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
XX from a genome database search using the human 5-HT6 receptor sequence.
XX Identified regions of genomic DNA were used to predict full-length genes,
XX and these gene predictions were used to design probes and primers for the
XX isolation of a cDNA clone containing the predicted OM_10 open reading
XX frame. OM_10 is expressed predominantly in the putamen and caudate
XX nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists and
XX antagonists of the invention are useful in drug screening assays.
XX CC pharmacogenomics, monitoring of effects during clinical trial, or for
XX CC diagnosing, preventing and treating diseases associated with enhanced or
XX CC inhibited GPCR activity, e.g. acute heart failure, hypertension,
XX CC hypertension, angina pectoris, myocardial infarction, hyperproliferative
XX CC diseases such as cancers and psoriasis, apoplectic diseases, pain,
XX CC endometriosis, anorexia, bulimia, asthma, osteoporosis, schizophrenia,
XX CC delirium, depression, anxiety, urinary retention, ulcers, allergies,
XX CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
XX CC syndrome, Alzheimer's disease, or Parkinson's disease
XX
XX
SQ Sequence 508 AA;
XX
XX
Query Match 100.0%; Score 2644; DB 7; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRSSNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRSSNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVYTRNRIENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
DB 61 QLLQVYTRNRIENLVLTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMQRGVLLYGTMVIAIIOSTPPLVGMGAAPDERNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMQRGVLLYGTMVIAIIOSTPPLVGMGAAPDERNA 180
QY 181 LCSMIMGASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
DB 181 LCSMIMGASPSYTIISVSVFIVPLIWMIACTSVVFCARROHALLVYKRSLEVRVD 240
QY 241 CVENEDDEGAERKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300
DB 241 CVENEDDEGAERKEEFQDESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVYA 300

```

QY 301 RGSEVERESTVASDGSMEGEGSTKVEENSKADKGTENVQCSIDLGEEDMERGEDDI 360
 DB 301 RGSEVERESTVASDGSMEGEGSTKVEENSKADKGTENVQCSIDLGEEDMERGEDDI 360
 QY 361 NFSEDDVAVANIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISVLSLGPYCFILAV 420
 DB 361 NFSEDDVAVANIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISVLSLGPYCFILAV 420
 QY 421 LAWVVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKPFCKEKRPK 480
 DB 421 LAWVVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKPFCKEKRPK 480
 QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
 DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 7
 AEA33200
 ID AEA33200 standard; protein; 508 AA.
 XX

AC AEA33200;

DT 11-AUG-2005 (first entry)

DE Human GPCR HGRPMY8-related RAI-3 protein SegID134.

XX protein purification; cytosolic; neuroprotective; antiparkinsonian;
 KW tranquilizer; hypotension; anti-HIV; virocid; osteopathic; cancer;
 KW asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
 KW anxiety disorder; hypertension; neurological disease; RAI-3.

XX Homo sapiens.

XX WO2005048951-A2.

XX 02-JUN-2005.

XX 12-NOV-2004; 2004WO-US038387.

XX 13-NOV-2003; 2003US-00712615.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Battaglin P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;

PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;

DR WPI; 2005-395945/40.

XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
 PT polynucleotide, useful for diagnosing or treating cancer, asthma,
 PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
 PT diseases.

XX Example 18; SEQ ID NO 134; 261pp; English.

XX This invention relates to a novel isolated human G-protein and the DNA
 CC sequence which encodes it. The invention may be useful for the
 CC development of compounds with a cytosolic, neuroprotective,
 CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virocid or
 CC osteopathic activity acting as G-protein antagonists. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the human G-protein coupled receptor,
 CC HGRPMY8, such as cancer, asthma, allergies, HIV infections,
 CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
 CC diseases. The present sequence is that of the human RAI-3 protein which
 CC was used in the exemplification of the invention.

XX Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 9; Length 508;

Best Local Similarity 100.0%; Pred. No. 1,1e-233; Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHQIIRSTVLVIFLAASFVGNIVLALVLRKP 60
 DB 1 MTSTCTNSTRESNSHTCMPLSKMPLSLAHQIIRSTVLVIFLAASFVGNIVLALVLRKP 60
 QY 61 QLLQVNFIFNLVLTDLQISLVAWVAVTSVPLFMPPLNSHFTALVSLTHLFAFASVN 120
 DB 61 QLLQVNFIFNLVLTDLQISLVAWVAVTSVPLFMPPLNSHFTALVSLTHLFAFASVN 120
 QY 121 TIVVSVDRYVLSIHPLSYPSKMTQRGTYLLVGTWVAIIQSTPPLXGMOAAFDERNA 180
 DB 121 TIVVSVDRYVLSIHPLSYPSKMTQRGTYLLVGTWVAIIQSTPPLXGMOAAFDERNA 180
 QY 181 LCSMTWGSFSTYLLSVSFIVIPLIWIAICYVFCARQHLLVYVKHSLFVRVXD 240
 DB 181 LCSMTWGSFSTYLLSVSFIVIPLIWIAICYVFCARQHLLVYVKHSLFVRVXD 240
 QY 241 CVENDEBGAKEKEFODESEFFRRQHEGEVAKEGMEAKDGLKAKEGSTGTSESSVYA 300
 DB 241 CVENDEBGAKEKEFODESEFFRRQHEGEVAKEGMEAKDGLKAKEGSTGTSESSVYA 300
 QY 301 RGSEVERESTVASDGSMEGEGSTKVEENSKADKGTENVQCSIDLGEEDMERGEDDI 360
 DB 301 RGSEVERESTVASDGSMEGEGSTKVEENSKADKGTENVQCSIDLGEEDMERGEDDI 360
 QY 361 NFSEDDVAVANIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISVLSLGPYCFILAV 420
 DB 361 NFSEDDVAVANIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISVLSLGPYCFILAV 420
 QY 421 LAWVVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKPFCKEKRPK 480
 DB 421 LAWVVDVETQVPQWVITIIIMLFLOCCIHPRVYVGYMKTIKKEIQDMLKKPFCKEKRPK 480
 QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
 DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 8

AEA33070
 ID AEA33070 standard; protein; 508 AA.

AC AEA33070;

DT 11-AUG-2005 (first entry)

DE Human G-protein coupled receptor HGRPMY8 protein SegID2.

XX protein purification; cytosolic; neuroprotective; antiparkinsonian;
 KW tranquilizer; hypotension; anti-HIV; virocid; osteopathic; cancer;
 KW asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
 KW anxiety disorder; hypertension; neurological disease; HGRPMY8;
 KW G protein coupled receptor.

XX Homo sapiens.

XX WO2005048951-A2.

XX 02-JUN-2005.

XX 12-NOV-2004; 2004WO-US038387.

XX 13-NOV-2003; 2003US-00712615.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Battaglin P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;

PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;

DR WPI; 2005-395945/40.

DR N-PSDB; AEA33069.

XX New isolated human G-protein coupled receptor, HGPBMY8, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
PS Claim 4; SEQ ID NO 2; 261pp; English.
XX
CC This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytostatic, neuroprotective,
CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGPBMY8, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human HGPBMY8 protein of
CC the invention.
XX
SQ Sequence 508 AA;

Query Match 100.0%; Score 2644; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.1e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTLVIFLAASFGVNIATLVQORP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTLVIFLAASFGVNIATLVQORP 60
QY 61 QLLQVYTNRFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASV 120
DB 61 QLLQVYTNRFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASV 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMTQORGLLYGTWIVAILQSTPPLVGMGAADFEDNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMTQORGLLYGTWIVAILQSTPPLVGMGAADFEDNA 180
QY 181 LCSMTWGASPSYTIISVSVFIPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
DB 181 LCSMTWGASPSYTIISVSVFIPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEBGAEBKKEFODESEFRROHGEVYKAKEGMEAKDQSLKAKGSTGTSSESVYA 300
DB 241 CVENDEBGAEBKKEFODESEFRROHGEVYKAKEGMEAKDQSLKAKGSTGTSSESVYA 300
QY 301 RGSEEVRESSTVAVSDGSMGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RGSEEVRESSTVAVSDGSMGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYLSLGPYCFYLA 420
DB 361 NSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYLSLGPYCFYLA 420
QY 421 LAWVVDVETQVQWVYTIIFLFLQCCIHPPYVGYGMHKTIKKEIDQMLKFFCCKEPPX 480
DB 421 LAWVVDVETQVQWVYTIIFLFLQCCIHPPYVGYGMHKTIKKEIDQMLKFFCCKEPPX 480
QY 481 EDSHDPDLPETEGGTGKIVPSYDSATFP 508
DB 481 EDSHDPDLPETEGGTGKIVPSYDSATFP 508

RESULT 9
ADP70508
ID ADP70508 standard; protein; 746 AA.
XX
AC ADP70508;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SegID131.

XX ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
PI
DR MPI: 2003-697654/66.
DR N-PSDB; ADP70610.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 131; 594pp; Japanese.

Query Match 100.0%; Score 2644; DB 7; Length 746;
Best Local Similarity 100.0%; Pred. No. 1.9e-233;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTLVIFLAASFGVNIATLVQORP 60
DB 1 MTSTCTNSTRESNSSHTCMPISLKHGIIRSTLVIFLAASFGVNIATLVQORP 60
QY 61 QLLQVYTNRFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASV 120
DB 61 QLLQVYTNRFIFNLVTDLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASV 120
QY 121 TIVLVSVDRYLSIIHPLSPSKMTQORGLLYGTWIVAILQSTPPLVGMGAADFEDNA 180
DB 121 TIVLVSVDRYLSIIHPLSPSKMTQORGLLYGTWIVAILQSTPPLVGMGAADFEDNA 180
QY 181 LCSMTWGASPSYTIISVSVFIPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
DB 181 LCSMTWGASPSYTIISVSVFIPLIWMACYSVFCARROHALLYNKRHSLEVRVD 240
QY 241 CVENDEBGAEBKKEFODESEFRROHGEVYKAKEGMEAKDQSLKAKGSTGTSSESVYA 300
DB 241 CVENDEBGAEBKKEFODESEFRROHGEVYKAKEGMEAKDQSLKAKGSTGTSSESVYA 300
QY 301 RGSEEVRESSTVAVSDGSMGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RGSEEVRESSTVAVSDGSMGKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYLSLGPYCFYLA 420
DB 361 NSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYVFIIFSYLSLGPYCFYLA 420

QY 421 LAVWVDVETQVPQWVITIIILWLFLLQCCIHPPYVGYMKTIIKKEIQDMLKKFCEKEXPPK 480
 DB 421 LAVWVDVETQVPQWVITIIILWLFLLQCCIHPPYVGYMKTIIKKEIQDMLKKFCEKEXPPK 480
 QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
 DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 10

AAB86428
 ID AAB86428 standard; protein, 508 AA.

XX AAB86428;

DT 19-OCT-2001 (first entry)

DE Human brain SERALPHA protein.

XX SERALPHA; human; brain; G protein receptor; medicine.

XX Homo sapiens.

XX DE10004930-A1.

XX 09-AUG-2001.

PF 04-FEB-2000; 2000DE-01004930.

PR 04-FEB-2000; 2000DE-01004930.

XX (BRUE/) BRUES M.

PA (BOEN/) BOENISCH H.

XX Brues M, Boenisch H;

XX WPI; 2001-489887/54.

DR N-PSDB; AAH48673.

XX Gene encoding a protein of the G protein receptor super family, having

PT homology to neurotransmitter receptors is useful to develop new

PT medications.

XX Disclosure; Page 4; 8pp; German.

CC This invention describes a novel human brain-derived G protein receptor

CC gene and its encoding protein, designated SERALPHA. The receptor or cells

CC expressing the receptor are used to develop new medicines, chemicals and

CC technologies, and to devalueate existing medicines and technologies

XX Sequence 508 AA;

QY Query Match 99.9%; Score 2641; DB 4; Length 508;

DB Best Local Similarity 99.8%; Pred. No. 2,1e-233;

DB Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSSTRESNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFGNIVLALVQRKP 60

DB 1 MTSTCTNSSTRESNSHTCMPLSKMPSISLAHGIIIRSTVLVIFLAASFGNIVLALVQRKP 60

QY 61 QLLQVTNRFIFNLVTDLQISLVA PWVATSVPLFWPLNSHFCALVSLTHLFAFASVN 120

DB 61 QLLQVTNRFIFNLVTDLQISLVA PWVATSVPLFWPLNSHFCALVSLTHLFAFASVN 120

QY 121 TIVVSVVRYSIIPSLSPSKMQRGVLVYGTWIVAILDSTPLVYGMGAADDERNA 180

DB 121 TIVVSVVRYSIIPSLSPSKMQRGVLVYGTWIVAILDSTPLVYGMGAADDERNA 180

QY 181 LCSMTWGAASPSYTIISVSVFIVIPVIMACYSVFCAARHALLVYKHSLEVRVD 240

DB 181 LCSMTWGAASPSYTIISVSVFIVIPVIMACYSVFCAARHALLVYKHSLEVRVD 240

QY 241 CVENEDERGAKEKEFODESEFFRQHGCEVYAKGEMBAKGSIAKXEGSTGTSSESVYA 300
 DB 241 CVENEDERGAKEKEFODESEFFRQHGCEVYAKGEMBAKGSIAKXEGSTGTSSESVYA 300
 QY 301 RGESEVRSSSTVVASDGSMEGKEGSTKVBNEMKADKRTVEYNQCSIDLGEEDMERGEDDI 360
 DB 301 RGESEVRSSSTVVASDGSMEGKEGSTKVBNEMKADKRTVEYNQCSIDLGEEDMERGEDDI 360
 QY 361 NFESEDDVEAVNIPESLPSRSRNSNSNPPLPRCYQCKAKAVIIFIIISVLSLGPYCFILAV 420
 DB 361 NFESEDDVEAVNIPESLPSRSRNSNSNPPLPRCYQCKAKAVIIFIIISVLSLGPYCFILAV 420
 QY 421 LAVWVDVETQVPQWVITIIILWLFLLQCCIHPPYVGYMKTIIKKEIQDMLKKFCEKEXPPK 480
 DB 421 LAVWVDVETQVPQWVITIIILWLFLLQCCIHPPYVGYMKTIIKKEIQDMLKKFCEKEXPPK 480
 QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
 DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 11

AU25605
 ID AU25605 standard; protein, 508 AA.

XX AU25605;

DT 18-DEC-2001 (first entry)

DE Human G Protein-coupled Receptor (GPCR) polypeptide #52.

XX Human; G-protein coupled receptor; GPCR; mental disorder; schizophrenia;

XX attention deficit disorder; anxiety; depression; bipolar disorder;

XX neurological disorder; Huntington's disease; dementia; obesity; anorexia;

XX metabolic disorder; Parkinson's disease; Tourette's syndrome; thrombosis;

XX type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;

XX cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;

XX viral infection; immunostimulant; neuroleptic; nootropic; tranquiliser;

XX antidepressant; anorectic; gene therapy.

XX Homo sapiens.

XX WO200162797-A2.

XX 30-AUG-2001.

PF 23-FEB-2001; 2001WO-US005676.

XX 23-FEB-2000; 2000US-0184247P.

PR 23-FEB-2000; 2000US-0184303P.

PR 23-FEB-2000; 2000US-0184304P.

PR 23-FEB-2000; 2000US-0184305P.

PR 23-FEB-2000; 2000US-0184397P.

PR 02-MAR-2000; 2000US-0186457P.

PR 03-MAR-2000; 2000US-0186810P.

PR 09-MAR-2000; 2000US-0188064P.

PR 13-MAR-2000; 2000US-0194344P.

PR 23-JUN-2000; 2000US-0213861P.

PR 11-JUL-2000; 2000US-0217365P.

PR 14-JUL-2000; 2000US-0218337P.

PR 20-JUL-2000; 2000US-0218492P.

PA (PHAA) PHARMACIA & UPJOHN CO.

XX Vogel I G, Wood LS, Parodi LA, Lind P;

PI WPI; 2001-570628/64.

DR N-PSDB; AAS42857.

XX New isolated nucleic acid encoding a new G-protein coupled receptor

PT polypeptide for detecting receptor modulators that can treat mental

PT disorders, such as schizophrenia, anxiety, depression, or obesity.
PS Claim 35; Page 90; 279pp; English.
XX
XX
CC Sequences AAU2554-AAU25616 represent human G-protein coupled receptor
CC (GPCR) polypeptides of the invention. The proteins and their associated
CC DNA sequences can be used to identify compounds which bind to GPCR
CC polypeptides and in screening for compounds that modulate GPCR activity.
CC By screening a human subject for the presence of mutations in GPCR DNA, a
CC GPCR-related disorder or a genetic predisposition can be diagnosed. The
CC sequences can also be used for treatment and prevention of mental
CC disorders such as schizophrenia, attention deficit disorder, anxiety,
CC depression, dementia and bipolar disorder, neurological disorders such as
CC Huntington's disease, Parkinson's disease and Tourette's syndrome,
CC metabolic disorders such as obesity, anorexia and type 2 diabetes,
CC cardiovascular disorders such as thrombosis, myocardial infarction,
CC cardiomyopathy and atherosclerosis, viral infections caused by HIV and
CC cancers
XX
XX
SQ Sequence 508 AA;

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLYFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLYFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIFMLVTDLLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIFMLVTDLLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVN 120
QY 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILLOSTPPLXGMOAAPDERNA 180
DB 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILLOSTPPLXGMOAAPDERNA 180
QY 181 LCSMWGASPSYTIISVVSFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVD 240
DB 181 LCSMWGASPSYTIISVVSFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVD 240
QY 241 CVENDEBGAKEKEEFODESEFRROHEGVKAKEGMEAKDGLAKEGSTGTSSSVBA 300
DB 241 CVENDEBGAKEKEEFODESEFRROHEGVKAKEGMEAKDGLAKEGSTGTSSSVBA 300
QY 301 RSESEVRRESSTVASDGSMEKSGSTKVENSMKADKGRTEVNQCSIDLGEDDMEFGEEDI 360
DB 301 RSESEVRRESSTVASDGSMEKSGSTKVENSMKADKGRTEVNQCSIDLGEDDMEFGEEDI 360
QY 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYIFIIIFSYYLSLGPYCFLLAV 420
DB 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYIFIIIFSYYLSLGPYCFLLAV 420
QY 421 LAVVWVDETVQVPMVITIIIMLFLOCCIHPIYVYGTMHTIKKEIDMLKKFCEKPKPX 480
DB 421 LAVVWVDETVQVPMVITIIIMLFLOCCIHPIYVYGTMHTIKKEIDMLKKFCEKPKPX 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSTAFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSTAFP 508
RESULT 12
AAG64126 standard; protein; 508 AA.
ID AAG64126;
XX AAG64126;
AC AAG64126;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human G protein-coupled receptor GPRV72.
XX
KW Human; guanosine triphosphate binding protein-coupled receptor;

KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytosolic; hepatotropic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy.
XX
XX
OS Homo sapiens.
OS
PN WO200148188-A1.
PN
XX
XX
PD 05-JUL-2001.
XX
XX
PF 28-DEC-2000; 2000MO-JP009408.
XX
XX
PR 28-DEC-1999; 99JP-00375152.
PR 31-MAR-2000; 2000JP-00103339.
XX
XX
PA (HELI-) HELIX RES INST.
XX
XX
PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
XX
XX
DR WPI; 2001-425662/45.
DR N-PSDB; AAH73517.
XX
XX

New DNA encoding guanosine triphosphate binding protein coupled receptors
PT and their expression products for screening potential anticancer and
nootropic drugs and in diagnosis of these diseases.

Claim 1; Page 135-138; 170pp; Japanese.

The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes
CC encoding them. These genes and proteins and antibodies against the
CC protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The
CC present sequence is a G protein-coupled receptor of the invention
XX
XX

SQ Sequence 508 AA;

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLYFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCMPLSKMPLSLAHGIIRSTVLYFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIFMLVTDLLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIFMLVTDLLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVN 120
QY 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILLOSTPPLXGMOAAPDERNA 180
DB 121 TLVLSVDRYLSIIHPLSPSKTORRGYLLXGTMIVAILLOSTPPLXGMOAAPDERNA 180
QY 181 LCSMWGASPSYTIISVVSFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVD 240
DB 181 LCSMWGASPSYTIISVVSFIYPLIWMACYSVFCARROHALLYNKRSHLEVRVD 240
QY 241 CVENDEBGAKEKEEFODESEFRROHEGVKAKEGMEAKDGLAKEGSTGTSSSVBA 300
DB 241 CVENDEBGAKEKEEFODESEFRROHEGVKAKEGMEAKDGLAKEGSTGTSSSVBA 300
QY 301 RSESEVRRESSTVASDGSMEKSGSTKVENSMKADKGRTEVNQCSIDLGEDDMEFGEEDI 360
DB 301 RSESEVRRESSTVASDGSMEKSGSTKVENSMKADKGRTEVNQCSIDLGEDDMEFGEEDI 360
QY 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYIFIIIFSYYLSLGPYCFLLAV 420
DB 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYOCCAAYIFIIIFSYYLSLGPYCFLLAV 420

QY 421 LAWVAVDTQVPOWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
DB 421 LAWVAVDTQVPOWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 13
AAU04369
ID AAU04369 standard; protein; 508 AA.
AC AAU04369;
XX 23-OCT-2001 (first entry)
DE Human G-protein coupled receptor, hRUP15.
KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;
XX inverse agonist; lung cancer.
OS Homo sapiens.
XX WO200136471-A2.
XX 25-MAY-2001.
XX 16-NOV-2000; 2000MO-US031509.
XX 17-NOV-1999; 99US-0166086P.
XX 17-NOV-1999; 99US-0166099P.
XX 17-NOV-1999; 99US-0166369P.
XX 23-DEC-1999; 99US-0171900P.
XX 23-DEC-1999; 99US-0171901P.
XX 23-DEC-1999; 99US-0171902P.
XX 11-FEB-2000; 2000US-0181749P.
XX 14-MAR-2000; 2000US-0189258P.
XX 14-MAR-2000; 2000US-0189259P.
XX 10-APR-2000; 2000US-0195898P.
XX 10-APR-2000; 2000US-0195899P.
XX 10-APR-2000; 2000US-0195899P.
XX 28-APR-2000; 2000US-0200419P.
XX 12-MAY-2000; 2000US-0203630P.
XX 12-JUN-2000; 2000US-0210741P.
XX 12-JUN-2000; 2000US-0210982P.
XX 21-AUG-2000; 2000US-0226760P.
XX 26-SEP-2000; 2000US-0235418P.
XX 26-SEP-2000; 2000US-0235799P.
XX 20-OCT-2000; 2000US-0242332P.
XX 20-OCT-2000; 2000US-0242343P.
XX 24-OCT-2000; 2000US-0243019P.
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Chen R, Dang HT, Lowitz KP;
XX
XX MPI; 2001-355616/37.
XX N-PSDB; AMS07942.
XX
XX Endogenous and non-endogenous versions of human G-protein coupled
XX receptors for direct identification of candidate compounds as agonists,
XX inverse agonists or partial agonists for use as therapeutic agents.
XX
XX Claim 29; Page 102-104; 160pp; English.
XX
XX The sequence represents a human G-protein coupled receptor (GPCR),
XX hRUP15. The endogenous and non-endogenous, constitutively activated
XX versions of human G-protein coupled receptors (GPCR), are useful for
XX direct identification of candidate compounds as receptor agonists,
XX inverse agonists or partial agonists having applicability as therapeutic
XX agents for treating diseases related to GPCR, e.g. lung cancer. Non-
XX endogenous version of human GPCRs are also utilized in research settings

CC and in vitro and in vivo system, incorporating GPCRs can be utilized to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased
XX
XX Sequence 508 AA;
QY Query Match 99.9%; Score 2641; DB 4; Length 508;
DB Beat Local Similarity 99.8%; Pred. No. 2,1e-233;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLASFVGNIVLALVQKRP 60
DB 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLASFVGNIVLALVQKRP 60
QY 61 QLLQVTRNFIFNLVTDLLQISLVAWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
DB 61 QLLQVTRNFIFNLVTDLLQISLVAWVAVTSVPLFWPLNSHFCALVSLTHLPAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRCGYLLLYGTWIVALLQSTPPLYGWQQAFFDERNA 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRCGYLLLYGTWIVALLQSTPPLYGWQQAFFDERNA 180
QY 181 LCSMTWGAPESTYITISVSFIVIPLIWIACTSVFCAARQHALLVNKHSLSEVRXKD 240
DB 181 LCSMTWGAPESTYITISVSFIVIPLIWIACTSVFCAARQHALLVNKHSLSEVRXKD 240
QY 241 CVENEDDEGAARKEEFODESEFRROHEGEVAKGEMAKDGLAKGEGTGTSESSVEA 300
DB 241 CVENEDDEGAARKEEFODESEFRROHEGEVAKGEMAKDGLAKGEGTGTSESSVEA 300
QY 301 RGSEVERESTVYASDGSMEGKEGSTKYENSMKADKGTENVQCSIDLGEDDMERGEDDI 360
DB 301 RGSEVERESTVYASDGSMEGKEGSTKYENSMKADKGTENVQCSIDLGEDDMERGEDDI 360
QY 361 NFSEDDVAVNIPESLPSRNRNSNPPRPGCYCKAKAVFIIFISVYLSIGPCFLAV 420
DB 361 NFSEDDVAVNIPESLPSRNRNSNPPRPGCYCKAKAVFIIFISVYLSIGPCFLAV 420
QY 421 LAWVAVDTQVPOWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
DB 421 LAWVAVDTQVPOWVITITIIIMLFLOCCIHPIYVGYMKTIKKEIDMLKKFCEKRPK 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 14
AAU11764
ID AAU11764 standard; protein; 508 AA.
AC AAU11764;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human alpha adrenergic receptor-like GPCR.
XX
XX Human; alpha adrenergic receptor; G-protein-coupled receptor; GPCR;
XX peripheral nervous system disease; central nervous system disease;
XX urinary incontinence; benign prostatic hypertrophy; infection;
XX HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
XX bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
XX hypotension; hypertension; urinary retention; osteoporosis;
XX angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
XX neurological disorder; anxiety; schizophrenia; manic depression;
XX delirium; dementia; severe mental retardation; dyskinesia;
XX Huntington's disease; Tourette's syndrome.
XX
XX Homo sapiens.
XX
XX WO200188126-A2.
XX 22-NOV-2001.

XX 11-MAY-2001; 2001WO-EP005383.
 PF
 XX 15-MAY-2000; 2000US-020414SP.
 PR
 PR 04-DEC-2000; 2000US-0250505P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Ramakrishnan S;
 XX
 DR WPI: 2002-106124/14.
 DR N-PSDB; AAS18898, AAS18899.
 XX
 PT New polynucleotide, useful for treating pain, cancer, Parkinson's
 PT diseases, obesity, hypertension, asthma, schizophrenia, encodes an alpha
 PT (1a) adrenergic receptor-like G-protein coupled receptor (GPCR).
 XX
 PS Claim 25; Fig 3; 123pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding an alpha
 CC adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
 CC the encoded polypeptide, fragments, derivatives and allelic variants.
 CC Also include are an expression vector comprising the polynucleotide, a
 CC host cell containing the vector, screening for therapeutic agents which
 CC decrease or increase the activity of the receptor by binding a test agent
 CC to the protein and determining whether the activity is decreased or
 CC increased. A modulator of the receptor is useful for treating alpha
 CC adrenergic receptor-like GPCR disorder such as peripheral or central
 CC nervous system disease, urinary incontinence or benign prostatic
 CC hypertrophy. The receptor, polynucleotide or modulator is useful for
 CC treating disorders such as bacterial, fungal, protozoan, and viral
 CC infections, particularly those caused by HIV (human immunodeficiency
 CC virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
 CC obesity, acute heart failure, hypertension, hypertension, urinary
 CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
 CC allergy, benign prostatic hypertrophy, and psychotic and neurological
 CC disorders, including anxiety, schizophrenia, manic depression, delirium,
 CC dementia, severe mental retardation, and dyskinesias, such as
 CC Huntington's disease and Tourette's syndrome. The polynucleotide is
 CC useful in diagnostic assays for detecting diseases and abnormalities or
 CC susceptibility to disease and abnormalities related to the presence of
 CC mutations in the gene. The protein is useful to identify test compounds
 CC which may act as agonists or antagonists, and for raising antibodies
 CC which can block the receptor and effectively prevent ligand binding. The
 CC present sequence is the alpha adrenergic receptor-like GPCR
 XX
 XX Sequence 508 AA;
 SQ
 Query Match 99.9%; Score 2641; DB 5; Length 508;
 Best Local Similarity 99.8%; Pred. No. 2,1e-233;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTCTNSTRESNNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
 DB 1 MSTCTNSTRESNNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
 QY 61 QILOQVNRIRIFNLVTDLLQISLVAPWVAVATSVPLFWPANSRCTLVSLTHFAPASVND 120
 DB 61 QILOQVNRIRIFNLVTDLLQISLVAPWVAVATSVPLFWPANSRCTLVSLTHFAPASVND 120
 QY 121 TLVAVSVDRYLIIHPLSPYKMTORGVLVLTGTIVAILLOSTPLPYMGQAAPFERNA 180
 DB 121 TLVAVSVDRYLIIHPLSPYKMTORGVLVLTGTIVAILLOSTPLPYMGQAAPFERNA 180
 QY 121 TLVAVSVDRYLIIHPLSPYKMTORGVLVLTGTIVAILLOSTPLPYMGQAAPFERNA 180
 DB 121 TLVAVSVDRYLIIHPLSPYKMTORGVLVLTGTIVAILLOSTPLPYMGQAAPFERNA 180
 QY 181 LGSMTWASPSYTIISVSPFIVPLIWMIAQSVVFCARROHALLVNRKSLFVRVND 240
 DB 181 LGSMTWASPSYTIISVSPFIVPLIWMIAQSVVFCARROHALLVNRKSLFVRVND 240
 QY 241 CTENEBEBAKKEEFODSEPRROHEGEVAKAGEKMEAKDGLKAKESGTGSESSVVA 300
 DB 241 CTENEBEBAKKEEFODSEPRROHEGEVAKAGEKMEAKDGLKAKESGTGSESSVVA 300
 QY 301 RSESEVRSSSTVAASDGSMEGKSGTVENSMKADKGRTEVNOCSIDLGEDDMEFEDDI 360

DB 301 RSESEVRSSSTVAASDGSMEGKSGTVENSMKADKGRTEVNOCSIDLGEDDMEFEDDI 360
 QY 361 NFSEDDVAVNIPESLPPSRNSNPNPLPCYOCKAKAVFIITFSVYLSGPPCPLAV 420
 DB 361 NFSEDDVAVNIPESLPPSRNSNPNPLPCYOCKAKAVFIITFSVYLSGPPCPLAV 420
 QY 421 LAVWVDETOVPOWVITITIMLFPOCCIHPPVYVGMHTIKKEIQDMLKPFCKEKP 480
 DB 421 LAVWVDETOVPOWVITITIMLFPOCCIHPPVYVGMHTIKKEIQDMLKPFCKEKP 480
 QY 481 EDSDPDLPGTEGTEGKIIVPSYDSATFP 508
 DB 481 EDSDPDLPGTEGTEGKIIVPSYDSATFP 508
 RESULT 15
 AAO15504
 ID AAO15504 standard; protein; 508 AA.
 XX
 AC AAO15504;
 XX
 DT 24-OCT-2002 (first entry)
 XX
 DE Human G-protein coupled receptor protein #2.
 XX
 KW Human; G-protein coupled receptor protein; TGR34;
 KW central nervous system disease; Alzheimer's disease; metabolic disease;
 KW diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;
 KW inflammatory disease; arthritis; respiratory disease; bronchitis;
 KW digestive disease; stomach ulcer; immune disorder; autoimmune disease;
 KW infection; AIDS.
 XX
 OS Homo sapiens.
 XX
 PN WO200259304-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-JP000405.
 XX
 PR 23-JAN-2001; 2001JP-00015050.
 XX
 PR 30-MAR-2001; 2001JP-00102560.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Miwa M, Ito T, Shintani Y, Miyajima N;
 XX
 DR WPI: 2002-557949/59.
 DR N-PSDB; AAL44180.
 XX
 PT Human G-protein coupled receptor protein and DNA encoding it for design
 PT of drugs and reagents for treatment and diagnosis of cancer or
 PT respiratory and metabolic diseases.
 XX
 PS Claim 2; Page 97-99; 109pp; Japanese.
 XX
 CC The invention comprises the amino acid and coding sequences of two human
 CC G-protein coupled receptor proteins (TGR34). The DNA and protein
 CC sequences of the invention are useful for the treatment, prevention and
 CC diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
 CC metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
 CC circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
 CC arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
 CC (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
 CC infections (e.g. AIDS). The present amino acid sequence represents a
 CC human G-protein coupled receptor protein
 XX
 SQ Sequence 508 AA;
 Query Match 99.9%; Score 2641; DB 5; Length 508;
 Best Local Similarity 99.8%; Pred. No. 2,1e-233;
 Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRP 60
 Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLQRP 60
 QY 61 OLLQVNTNFIINLVLTDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
 Db 61 OLLQVNTNFIINLVLTDLQISLVAPWVATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
 QY 121 TIVLVSVDRYLSIIHPLSYPSKMTQRGVLILYGTWIVAILQSTPPLYGMCQAFAFERNNA 180
 Db 121 TIVLVSVDRYLSIIHPLSYPSKMTQRGVLILYGTWIVAILQSTPPLYGMCQAFAFERNNA 180
 QY 181 LCSMIMGASPSYTIISVVSFIVIPLIIVMIACYSVVFCARQHALLYNVKHSLEVRVD 240
 Db 181 LCSMIMGASPSYTIISVVSFIVIPLIIVMIACYSVVFCARQHALLYNVKHSLEVRVD 240
 QY 241 CVENDEDEGAEEKEEFODESEFRROHEGEVAKKEGRMEAKDGLKAKEGSTGTSSSVEA 300
 Db 241 CVENDEDEGAEEKEEFODESEFRROHEGEVAKKEGRMEAKDGLKAKEGSTGTSSSVEA 300
 QY 301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360
 Db 301 RGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI 360
 QY 361 NFESEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAkvIPIIIFSYYLSIGPYCFLAV 420
 Db 361 NFESEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAkvIPIIIFSYYLSIGPYCFLAV 420
 QY 421 LAVWVDVETQVPOWVITIIILWLFLOCCIHPRVYGYMHKTIKKEIQDMLKFFCKEKPPK 480
 Db 421 LAVWVDVETQVPOWVITIIILWLFLOCCIHPRVYGYMHKTIKKEIQDMLKFFCKEKPPK 480
 QY 481 EDSHEDLPCTEGTEGKIIVPSYDSATFP 508
 Db 481 EDSHEDLPCTEGTEGKIIVPSYDSATFP 508

Search completed: December 3, 2005, 06:30:43
 Job time : 160.286 secs

PD 01-AUG-2002.
PF 22-JAN-2002; 2002MO-JP000405.
XX 23-JAN-2001; 2001JP-00015050.
PR 30-MAR-2001; 2001JP-00102560.
XX
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
XX
PI Miwa M, Ito T, Shintani Y, Miyajima N;
XX
DR WPI: 2002-557949/59.
DR P-PSDB; AAO15503.
XX
XX
PT Human G-protein coupled receptor protein and DNA encoding it for design
PT of drugs and reagents for treatment and diagnosis of cancer or
PT respiratory and metabolic diseases.
XX
XX
XX
PS Claim 7; Page 99-100; 1099p; Japanese.
XX
XX
CC The invention comprises the amino acid and coding sequences of two human
CC G-protein coupled receptor proteins (TGR34). The DNA and protein
CC sequences of the invention are useful for the treatment, prevention and
CC diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
CC metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
CC circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
CC arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
CC (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
CC infections (e.g. AIDS). The present DNA sequence encodes a human G-
CC protein coupled receptor protein

Db 1201 ATCTTCATCATCATTTTCTCCATATGCTATCCCTGGGGCCCTACTGCTTTTACGACTC 1260
Qy 421 LeuAlaValITPValAspValGIuThxGlnValProGlnITRPValIleThrIleIleIle 440
Db 1261 CTGGCCGATGGGTGGATGTGAAACCCAGATACCCAGTGGGTATATACCATTAATCATTC 1320
Qy 441 TTPLeuPhePheLeuGlnCyAcValIleHISProIYValTYrGLYTYrMechIAsyThr 460
Db 1321 TGGCTTTTCTTCCTGACAGTGCATCCACCCCTATGTCTATAGCTATACATGACAAAGACC 1380
Qy 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1361 ATTAAGAGGAAATCCAGACATGCTGAAGAGATTCTTCTGCAAGGAAAGCCCGGAAA 1440
Qy 481 GluAspSerHISProAspLeuProGlyThxGluGlyThxGluGlyLysIleValPro 500
Db 1441 GAAGATACCAACCCAGACTGCCCCGAAACAGAGGTGGAGACTGAAGGCAAGATTCTCCT 1500
Qy 501 SerTYrAspSerAlaThrPhePro 508
Db 1501 TCCTACGATTCTGCTACTTTCTCT 1524
RESULT 3
ID ABL53719 standard; cDNA, 1527 BP.
XX ABL53719;
AC
XX 24-JUN-2002 (first entry)
DT
XX
DE G-protein coupled receptor AXOR69 cDNA.
KW G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;
KW antimicrobial; analgesic; cytostatic; antidiabetic; anorectic; anabolic;
KW antiasmatic; antiparkinsonian; cardiac; cerebroprotective;
KW hypotensive; hypertensive; antidiabetic; antiasmatic; antiallergic;
KW antileptic; tranquilizer; neuroleptic; nootropic; anticonvulsant;
KW vaccine; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1527
FT /*tag= a
FT /product= "AXOR69"
XX
PN GB2367295-A.
XX
PD 03-APR-2002.
XX
PE 12-JUN-2001; 2001GB-00014287.
XX
PF 16-JUN-2000; 2000US-00596400.
XX
PR
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PI Elahourbagy N, Gattu M, Shabon U;
XX
XX WPI: 2002-294789/34.
DR P-PSDB; ABB75712.
XX
XX An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide,
PT for treating diseases such as obesity, stroke and anxiety.
XX
XX Claim 2; Page 27; 34pp; English.
XX
PS The present sequence is that of cDNA encoding a human G-protein coupled
CC receptor, termed AXOR69 (see ABB75712). AXOR69 shows homology to other
CC members of the G-protein coupled receptor family, such as the human
CC adrenergic alpha-1a receptor. The invention provides AXOR69 polypeptides
CC and polynucleotides, and methods for producing such polypeptides by

CC recombinant techniques. Also provided are methods for using the AXOR69
CC polypeptides and polynucleotides to screen for compounds that stimulate
CC or inhibit AXOR69 levels or activity. The polypeptides, polynucleotides,
CC agonists and antagonists are used to treat conditions associated with
CC AXOR69 imbalance, including bacterial, fungal, protozoan and viral
CC infections, particularly HIV-1 and HIV-2 infections, pain, cancer,
CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute
CC heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
CC psychotic and neurological disorders, including anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia and severe mental
CC retardation, and dyskinesias such as Huntington's disease and Gilles de
CC La Tourette syndrome. The polynucleotides can also be used for diagnosing
CC mutations, in chromosome localisation studies, in pharmacogenomics, and
CC to construct transgenic animals. The polypeptides and polynucleotides are
XX also useful as vaccines
SQ Sequence 1527 BP, 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9,15e-244 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x ABL53719 (1-1527)
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Db 1 ATGAGTCCACCTGACCCACCAACGACGCGGACAGATACACAGACACACCGTGCATGCC 60
Qy 21 LeuSerLysMetProIleSerLeuAlaHISGlyIleIleArgSerThrValIleValIle 40
Db 61 CTCTCAAAAGTCCCATAGCGCTGAGCCCAAGGACATATCCCTCAACCGTCTGGTATATC 120
Qy 41 PheLeuAlaAlaSerPheValIGlyAsnIleValIleValIleValIleGlnArgHyPro 60
Db 121 TTCCTCGCGCGCTCTTCTGTCGCAACATAGTCTGGCGGTTCAGCGCAAGCCG 180
Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
Db 181 CAGCTGCTGACAGGTGACCAACCGTTTATCTTAACTCTCGTACCGACCTGTCAG 240
Qy 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
Db 241 ATTGCTGTCGTGCCCCCTGAGTGTGCGACCTGTGTCTCTTCTTGCCCTTCAAC 300
Qy 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTCTGACGCGCCCTGTAGCTTCAACCACTGTTGCTTGCCAGCGCTCAAC 360
Qy 121 ThrIleValIleValSerValAspArgTYrLeuSerIleIleHISProLeuSerTYrPro 140
Db 361 ACCATTGCTGTGGTGTGAGTGTGATGCTATGTCATCATCAACCTCTCTCTACCGG 420
Qy 141 SerLysMetThrGlnArgArgGlyTYrLeuLeuLeuTYrGlyThrTrpIleValAlaIle 160
Db 421 TCCAAAGTAGACCAAGCGCGCGGTACCTGTCTCTTATGACCTGTGATTTGTGCCATTC 480
Qy 161 LeuGlnSerThrProProLeuTYrGLYTrpGlyGlnAlaIlePheAspGlyArgAsnAla 180
Db 481 CTGACAGACATCTCTCCACTTACGCGCTGGGAGCCAGGTGCTTGTAGAGCGCAATCT 540
Qy 181 LeuCysSerMetIleTrpGlyAlaSerProSerTYrThrIleLeuSerValIleSerPhe 200
Db 541 CTCTGCTCAATGATCTGGGGGGCCAGCCCAAGTACATTAATTCAGAGGTGTGTCCTTC 600
Qy 201 IleValIleProLeuIleValIleMetIleAlaCysTYrSerValValPheCysAlaIleArg 220
Db 601 ATCGCATTCACATGATGTGATGATTCCTGCTACTCCGTGAGTGTCTGTGACGCCGG 660

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QY 221 ArgGlnHisAlaLeuLeuTyrTrpValLysArgHisSerLeuGluValArgValLysAsp 240
DB 661 AGGCAAGCATGCTCTGCTGACAAATGTCAGAGACACAGCTTGAGTGGAGTCAAGAC 720
QY 241 CysValGluAsnGluAspGluGluGluValArgLysLysGluGluGluGluGluGlu 260
DB 721 TGTGTGGAATATGAGATGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 GluPheArgArgGlnHisGluGluGluValLysAlaLysGluGluValArgMetGluAlaLys 280
DB 781 GAGTTTCGCGCCGACGATGAGGTGAGGTCAAGGCCAAGAGGCGCAATGGAGCCAG 840
QY 281 AspGlySerLeuLysAlaLysGluGluGluSerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGGGAGCCTGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluValArgLysSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGluSerThrLysValGluGluAsnSerMetLysAlaAspLysGluArgThrGlu 340
DB 961 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCysSerLysAspLeuGluGluAspAspMetGluPheGlyLysAspAspIle 360
DB 1021 GTCAACGAGTGACAGATTGACTTGGGTGAGATGATGATGATGATGATGATGATGATG 1080
QY 361 AsnPheSerGluAspAspValGluValAlaMetLysProGluSerLeuProSerArg 380
DB 1081 AATTTCAGTGAGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 381 ArgAsnSerAsnSerAsnProLeuProArgCysTyrGlyCysLysValAlaLysVal 400
DB 1141 CGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 401 IlePheIleIleIlePheSerTyrValLysSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTTCTCTATATGCTATCCCTGGGCGCTTATAGCATC 1260
QY 421 LeuAlaValTyrValAspValGluThrGlnValProGlnTyrValIleThrIleIle 440
DB 1261 CTGGCGGTGTGGGTGATGATGCAAAACCAAGTACCCAGTGGGTGATCAACATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGAGTGTGATCCACCCCTATGTATGTATGCTATGACACAGACC 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLeuGluLysPProPolys 480
DB 1381 ATTTAAGAGAGAAATCCAGACATGCTGAAGAACTTTTTCAGAGAGAAAGCCCCGAGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyTyrGluGlyLysIleValPro 500
DB 1441 GAAGATAGACCACTGACCGGAGACAGAGGGTGGAGATGAGAGAGCAAGATTGCTCT 1500
QY 501 SerTyrAspSerLysThrPhePro 508
DB 1501 TCTTACGATTCGCTACTTTTCT 1524

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KW neoplastic disease; CAMP, signalling pathway; immune disorder; cancer;
KM gene therapy; tumour; gene; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1527
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FT FT /product= "Human HGPBMY8 protein"
FT FT replace(370, G)
FT FT /*tag= b
FT FT /standard_name= "Single nucleotide polymorphism"
FT FT replace(1055, G)
FT FT /*tag= c
FT FT /standard_name= "Single nucleotide polymorphism"
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FT FT /*tag= d
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FT FT /standard_name= "Single nucleotide polymorphism"
XX MO200240670-A2.
XX PD 23-MAY-2002.
XX PF 14-NOV-2001; 2001WO-US043909.
XX PR 14-NOV-2000; 2000US-0248285P.
XX PR 14-FEB-2001; 2001US-0268581P.
XX PR 27-JUL-2001; 2001US-0308285P.
XX PR 04-SEP-2001; 2001US-0317166P.
XX PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX PI Battaglinio P, Feder J, Mantler G, Nelson T, Ramanathan C;
XX PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
XX DR WPI; 2002-519383/55.
XX DR P-PSDB; AAE25236.
XX PT A substantially purified human G-protein coupled receptor polypeptide,
XX PT termed HGPBMY8, useful for treating a neurological disorder or brain
XX PT disorder in a mammal.
XX PS Claim 1; Page 160-161; 223pp; English.
XX CC The invention relates to human G-protein coupled receptor (GPCR), termed
XX CC HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
XX CC screening for candidate compounds which are small molecules, biological
XX CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
XX CC treating a neurological disorder or a disease, a disorder or condition
XX CC related to the brain in a mammal. It is used for treating or preventing
XX CC neurological disorders, conditions or diseases and for inducing an
XX CC immunological response in a mammal. HGPBMY8 DNA, protein and its
XX CC antibody are useful in the diagnosis, treatment or prevention of
XX CC disorders associated with aberrant or uncontrolled cellular growth and/
XX CC or function, such as neoplastic diseases e.g., cancers and tumours and
XX CC diseases or disorders related to the brain, e.g., neurological disorders.
XX CC HGPBMY8 DNA and protein are useful for modulating intracellular CAMP
XX CC associated signalling pathways. An expression vector containing HGPBMY8
XX CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
XX CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
XX CC in gene therapy. The present sequence is human HGPBMY8 cDNA
XX SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Alignment Scores: 9,15e-244 Length: 1527
Pred. No.: 2644.00 Matches: 508
Score:

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RESULT 4
 AAD41159
 ID AAD41159 standard; cDNA; 1527 BP.
 XX AAD41159;
 AC AAD41159;
 XX
 DT 30-OCT-2002 (first entry)
 DE Human HGPBMY8 cDNA.
 XX
 KW Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
 neuro; neurological disorder; brain; immunological; cell growth; cycostatic;

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 6
 Gaps: 0

US-10-712-615-2 (1-508) x AAD41159 (1-1527)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
 DB 1 ATGAGGTCCACCTGCACCAACAGCAGCGCGAGAGTAACAGACAGCACACGTCATGCC 60
 QY 21 LeuSerLysMetProGluSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
 DB 61 CTCCTCAAAATGCCATCAGCTGGCGCCACGGCATCATCCGCTCAACCTGTGTGGTTATC 120
 QY 41 PheLeuAlaAlaSerPheValGlyValenIleValLeuAlaLeuValLeuGlnArgLysPro 60
 DB 121 TTCCTCGCGCGCTCTTTGCTGGCAACATAGTGTGGCTTGGCTTGGCAGCGCAAGCCG 180
 QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
 DB 181 CAGCTGTGACAGGTACCAACGTTTATCTTAACTCTCTGTCACCGACTGCTGAG 240
 QY 81 ILeSerLeuValAlaProTrrPValAlaThrSerValProLeuPheTrrProLeuAsn 100
 DB 241 ATTGGCTCGTGGCCCCCTGGGTGGTGGCCACTGTGTGCTCTCTTCTGGGCCCTCAAC 300
 QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
 DB 301 AGCCACTTTCGACCGGCGCTGTAGCTTACCTCACCCACTTGTGCTTGGCCAGCTCAAC 360
 QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
 DB 361 ACCATTGCTTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 141 SerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrrIleValAlaIle 160
 DB 421 TCCAGATGACCCAGCGCGCGGTTACCTGCTCTTAAGGACCTGGAATTTGGCCAAC 480
 QY 161 LeuGlnSerThrProProLeuTyrGlyTrrGlyGlnAlaAlaPheAspGluArgAsnAla 180
 DB 481 CTGCAAGACACTCTCCACTCTACGCGCTGGGCCAGGCTGCTTGGATGAGCGCATGCT 540
 QY 181 LeuCysSerMetIleTrrPValAspSerProSerTyrThrIleLeuSerValIleSerPhe 200
 DB 541 CTCTGCTCATGATCTGGGGGGCCAGCCCACTACATATTCTCAGCGTGTGCTTCT 600
 QY 201 ILeValIleProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaAlaIArg 220
 DB 601 ATCGTCATTTCCACTGATTTGTCATGATTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
 QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValAspArgHisSerLeuGlnValIleArgValIleAsp 240
 DB 661 AGCGACATGCTCTCTCTGTCATGATCAAGACACACAGTGTGAAGTGGAGCTCAAGGAC 720
 QY 241 CysValGluAsnGluAspGluGluGlyAlaGluLysLysGluGluPheGlnAspGluSer 260
 DB 721 TGTGTGAAGATGAAGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
 QY 261 GluPheArgArgGlnHisGluGlyGlyValIleValIleValIleValIleValIleValIle 280
 DB 781 GAGTTTCCCGCCACATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
 QY 281 AspGlySerLeuLeuValAlaValGluGlySerThrGlyThrSerGluSerSerValGluVal 300
 DB 841 GACGCGACGCTTAAGGCGCAAGAGAGAGACACGGGACCACTGAAGATGATTAAGGCGC 900
 QY 301 ArgGlySerGluGluValAlaArgLysSerThrValAlaSerAspGlySerMetGluGly 320
 DB 901 AGGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
 QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyValArgThrGlu 340

DB 961 AAGGAGCGACAGCAACAAAGTTGAGGAGACACGATGAAGGACACAGGCTCCACAGAG 1020
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 DB 1021 GTCACACAGTGAGATTTGACTTGGTGAAATGACATGAGATTGCGTAAGAGACACATC 1080
 QY 361 AsnPheSerGluAspAspValGluAlaValenIleProGluSerLeuProProSerArg 380
 DB 1081 AATTTCAGTGAAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1140
 QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysValAlaAlaIleVal 400
 DB 1141 GCTAACACACAGCAACCTCTCTGCGCAGGTCTACAGTGCACAAAGCTGCTTAAGTG 1200
 QY 401 ILePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
 DB 1201 ATCTTCATCATCATTTTCTCTCATGTGTATTCCTGGGGGCTTACTGCTTTTACAGATC 1260
 QY 421 LeuAlaValTrrPValAspValGluThrGlnValProGlnTrrPValIleThrIleIleIle 440
 DB 1261 CTGGCCGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 441 TrrLeuPhePheLeuGlnCysCysIleHisProTyrValIleGlyTyrMetHisLysThr 460
 DB 1321 TGGCTTTTCTTCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAATG 1380
 QY 461 ILeLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
 DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAAAGTTCTTCTGCAAGAAAGGCCCCGAAA 1440
 QY 481 GluAspSerHisProAspLeuProGlyTyrGluGlyGlyThrGluGlyLysIleValPro 500
 DB 1441 GAAGATACCCACCCAGACTCTCCCGAACAAGGGTGGAGTGAAGGCAAGATTGTCCCT 1500
 QY 501 SerTyrAspSerAlaThrPhePro 508
 DB 1501 TCTTACGATTCGTACTTTTCT 1524

RESULT 5
 ABV74517
 ID ABV74517 standard; cDNA, 1527 BP.
 XX
 AC ABV74517;
 XX
 DT 17-JAN-2003 (first entry)
 XX
 DE Human G protein coupled receptor, S0879, coding sequence.
 XX
 KW G protein coupled receptor; receptor; anorectic; antiparkinsonian; gene;
 KW hypotensive; hypertensive; tranquilizer; neuroleptic; antidepressant;
 KW nootropic; anticonvulsant; antimigraine; human; S0879; hippocampus;
 KW hypothalamus; brain; obesity; bulimia; anorexia; Parkinson's disease;
 KW hypertension; psychotic disorder; neurological disorder;
 KW anxiety; schizophrenia; manic depression; delirium; dementia; epilepsy;
 KW migraine; insomnia; circadian rhythm disorder; cognitive function; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1527
 FT /*tag= a
 FT /product= "G protein coupled receptor"
 XX
 PN FR2822844-A1.
 XX
 PD 04-OCT-2002.
 XX
 PF 27-MAR-2001; 2001FR-00004074.
 XX
 PR 27-MAR-2001; 2001FR-00004074.
 XX
 PA (SERV-) LBS LAB SERVIER SA.
 XX

PI Galizzi JP, Coge F, Rigue H, Boutin JA;
XX MPI; 2003-021471/02.
DR P-PSDB; ABB98721.
XX

PT New nucleic acid encoding human G protein coupled receptors, useful for
PT treating e.g. obesity, also derived polypeptides, antibodies and
PT modulators.

XX
XX
PS Claim 1: Page 23-24; 44pp; French.

XX
XX
CC The present sequence is the coding sequence for human G protein-coupled
CC receptor, 50879. The receptor and its coding sequence can be used for
CC creating diseases associated with abnormal expression of the receptor,
CC particularly diseases involving the hippocampus or hypothalamus,
CC particularly obesity, bulimia, anorexia, Parkinson's disease, hypo- or
CC hyperphagia, and psychomotor or neurological disorders such as anxiety,
CC schizophrenia, manic depression, delirium, dementia, epilepsy, migraine,
CC insomnia, circadian rhythm disorders and loss of cognitive function. The
CC G protein-coupled receptor coding sequence was isolated from human brain
CC tissue

XX
SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 9, 15e-244 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-712-615-2 (1-508) x ABV74517 (1-1527)

QY 1 MetThrSerThrCysThrAnserThrArgGluSerAnserSerHisThrCysMetPro 20
DB 1 ATGACCTCCACCTGCGACCAAGCAGCGCGAGATGAACAGCAGCAGCTGCATGCC 60
QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATGCGCCATGACCTGCGCCACGGCATATCGCTCCAAACCGTGTGTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 121 TTCCTGCGCGCTTTGCTGCGCAATAGTCTGCGCTAGTGTGCGACGCCAAGCGG 180
QY 61 GlnLeuLeuGlnValThrAnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTAACTCTCGTCAACGACCTGCTGCAG 240
QY 81 IleSerLeuValAlaProThrValAlaIleThrSerValProLeuPheThrProLeuAn 100
DB 241 ATTTGCTGCTGCGCCCTGCGGTGGTGGCACCTCTGCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAn 120
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DB 481 CTGCAAGACACTCTCTCACTCAAGGCTGGGCGCAAGGCTGCTTTATAGCCCATGT 540
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValAlaSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGCGCAAGCCGACCTAATATTCTCAGCGGTGTCTTCT 600

QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 601 ATCTGATTTCCACTGATTTGTCAATGATGCTGCTCTACTCCGTGGTGTCTGTGACGCCG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAnValLysArgHisSerLeuGlnValArgValLysAsp 240
DB 661 AGCGACATGCTCTGCTGACATGTCAGAGACACACAGCTTGGAAGTGCAGTCAAGAC 720
QY 241 CysValGluAsnGluAspGluGluValArgIleLysGluGluPheGlnAspGluSer 260
DB 721 TGTGTGAAATGAGATGTAAGAGGAGCAGAAAGAAAGAGAGATTCCAGATGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGluGluValLysAlaLysGluGlyArgMetGluAlaLys 280
DB 781 GAGTTTGGCCGCGCAGCATTAAGGTAGGTCAAGGCCAAGAGGCGCAAGTGAAGCCAA 840
QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGGCAGCTTAAGGCCAAGAGGACACCGGGACCACTGAGATGTGTAGAGGCC 900
QY 301 ArgGlySerGluGluValArgIleSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGGCGAGAGAGGTCAAGAGAGCAGCAGCGTGGCCAGCGCATGAGAGGT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
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DB 1021 GTCAACCAATGACAGATTGACTTGGGTGAAGATGACATGAGATTGGTGAAGCGACATC 1080
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DB 1201 ATCTTCATCATATTTTCTCTATGTCATGCTGCGGCGCTTACGCTTTTATGACAGTC 1260
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DB 1261 CTGGCCGTGTGGTGTATGCAAAACCCAGTAAACCCAGTGGGTGATCAACATAATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGAGTGTGATCCACCCCTATGTATAGGTACATGCAAGACCC 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
DB 1381 ATTTAAGAAGAATCCAGACATGCTGAAGAAGTTCTTGTGCAAGAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB 1441 GAAGATAGCACCCAGACCTGCGGACAGAGGGGTGAGCATGAAGGCAAGATTGTCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTCTGTACTTTTCTT 1524

RESULT 6
AEA33069
ID AEA33069 standard; DNA; 1527 BP.
XX AEA33069;
AC
XX
DT 11-AUG-2005 (first entry)
XX

DE Human G-protein coupled receptor HGRPMY8 gene SeqID1.
XX
XX protein purification; cytostatic; neuroprotective; antiparkinsonian;
KM tiranquillizer; hypotension; anti-HIV; virucide; osteoporosis; cancer;
KM asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
KM anxiety disorder; hypertension; neurological disease; gene; ds; HGRPMY8;
KM G protein coupled receptor.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FT CDS 1..1527
FT /tag= a
FT /product= "Human G-protein coupled receptor HGRPMY8
FT protein"
XX
XX MO2005048951-A2.
XX
XX 02-JUN-2005.
XX
XX 12-NOV-2004; 2004MO-US038387.
XX
XX 13-NOV-2003; 2003US-00712615.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Bactagline P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
PI Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX
XX WPI; 2005-395945/40.
XX
XX P-PSDB; AEA33070.
XX
XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
PT polynucleotide, useful for diagnosing or treating cancer, asthma,
PT allergies, HIV, osteoporosis, anxiety, hypertension and neurological
PT diseases.
XX
XX
XX Claim 1; SEQ ID NO 1; 261bp; English.
XX
XX This invention relates to a novel isolated human G-protein and the DNA
CC sequence which encodes it. The invention may be useful for the
CC development of compounds with a cytostatic, neuroprotective,
CC antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
CC osteopathic activity acting as G-protein antagonists. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of the human G-protein coupled receptor,
CC HGRPMY8, such as cancer, asthma, allergies, HIV infections,
CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
CC diseases. The present sequence is that of the human HGRPMY8 gene of the
CC invention.
XX
XX
SQ Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 9,156-244 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-712-615-2 (1-506) x AEA33069 (1-1527)

DB 121 TTCTCGCCGCGCTTTCTGTCGCAACATAGTGTGGCTGAGTGTCCAGCGCAAGCCG 180
QY 61 GlnleuLeuGlnVal1ThAsnArgPhe1IlePheAsnleuVal1ThAspLeuGln 80
DB 181 CAGCTGCGCAGGTAACCAACCGTTTATCTTTAACTTCCTGCGTACCCAGCTGTGAG 240
QY 81 IleserleuVal1AProTrpVal1Val1A1aThSerVal1ProleuPheTrpProleuAsn 100
DB 241 ATTTCGCTCGTGGCCCGCTGGGTGGTGGCCACTCTGCTCTTCTTGCGCCCTCAAC 300
QY 101 SerHisPheCystrAlaLeuVal1SerleuThrHisleuPheAlaPheAlaSerVal1Asn 120
DB 301 AGCCACTTCTCAGCGCCCTGTTAGCTTCAACCACTGTTGCGCTTGGCCAGCTCAAC 360
QY 121 ThrIleVal1leuVal1SerVal1AspArgThyIleuSerIle1IleHisProleuSerTyPro 140
DB 361 ACCATTGCTTGAGTGCAGTGAATGCTTACTTGTTCATCATCATCACTCTCTCTTACCCG 420
QY 141 SerIysMetTrpGlnArgArgGlyTyIleuLeuLeuTyrglyThTrpIleVal1A1a1le 160
DB 421 TCCAAGATGACCCAGCGCGCGGTTACTGCTCCCTATAGGCACTGGATTGTGGCCATC 480
QY 161 LeuGlnSerThrProProleuTyrglyTyrglyGlnAla1a1aPheAspGluArgAsnAla 180
DB 481 CTGCAGACACTCTCCCACTTACGCGCTGCGGCCAGCGCTGCTTGGATGAGCGCAATGCT 540
QY 181 LeuCySerMetIleTrpGlyAlaSerProSerTyThrIleleuSerVal1SerPhe 200
DB 541 CTGCTCTCATGATCTGGGGGGCCAGCCCAAGCTCACTATTTCTCAGGTGGTGTCTTC 600
QY 201 IleVal1leProleuIleVal1IleVal1IleVal1A1aCyTrsSerVal1PheCyAla1aArg 220
DB 601 ATTCGATTCATCATGATTTGTATGATGATTCCTGCTACTCGTGGTGTGGAGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyArgAsnVal1IyArgHisSerleuGlnVal1ArgVal1IyAsp 240
DB 661 AGGCAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGAAGTCCGAGTCAAGGAC 720
QY 241 CysVal1GluAsnGluVal1ArgGluGluGluVal1GluVal1IyVal1IyAspGluSer 260
DB 721 TGTGTGGAAATGAGATGAAAGAGAGACAGACAGAAAGAGAGAGTTCAGAGATGAGGT 780
QY 261 GluPheArgArgGlnHisGluGlyGluVal1IyVal1IyAspGluTyArgMetGluAlaIyAs 280
DB 781 GAGTTTCCCGCCCGCAGCAAGAGTGAAGTCAAGGCCAAGAGGCGAGATGAACCAAG 840
QY 281 AspGlySerleuVal1AlaIyGluGlySerThrGlyThrSerGluSerSerVal1GluAla 300
DB 841 GACGCGACCTGMAAGGCCAAGAGAGAGCAAGCGGAGCAAGTGAAGTGAAGAGGCC 900
QY 301 ArgGlySerGluGluVal1ArgGluSerSerThrVal1AlaSerAspGlySerMetGluGly 320
DB 901 AGGGCAGCAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 960
QY 321 LysGluGlySerThrIyVal1GluGluAsnSerMetClyAlaAspIyGlyArgThrGlu 340
DB 961 AAGGAGAGCAGACCAAAAGTTGAGAGAAACAGCATGAAGGAGAGCAAGAGTGCACAG 1020
QY 341 Val1AsnGlnCySerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACAGATGACAGATGATGCTGGGTGAATGACATGAGAGTGTGGAAGAGACATC 1080
QY 361 AsnPheSerGluAspAspVal1GluAlaVal1AsnIleProGluSerleuProProSerArg 380
DB 1081 AATTTCAGTGGAGATGAGTGAAGAGAGTGAACATCCCGAGAGAGCTCCACCCAGTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProleuProArgCyTrGlnCyVal1Ala1aIyVal1 400
DB 1141 GGTAAACAGACAGAGACCTCTCTTCCAGAGTCTTCCAGTGCAGAGCTGCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyVal1leuSerleuGlyProTyCyPheleuAlaVal1 420

DB 1201 ATCTCATCATCTTTTCTTCATATGCTATCCCTGGGCGCTTCTTTAGCAGTC 1260
QY 421 LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle 440
DB 1261 CTGGCGGTGGTGGATGTCGAACCCAGTACCCAGGGGTGATCACCATTATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisIleVal 460
DB 1321 TGGCTTTCTTCTCTGAGTGTCTCATATCCCTATGTCTATAGCTATGACAGAC 1380
QY 461 IleIleValGluIleGlnAspMetLeuValPhePheCysValGlySerProIleVal 480
DB 1381 ATTAAAGAGAAATCCAGACATGCTGAAGAAAGTTCTTCTGCAAGAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValPro 500
DB 1441 GAAAGATAGCCACCAAGCTGCGCCGAAACAGAGGGTGGACTGAAGCAAGATTTCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTACGATTCTGCTACTTTTCT 1524
RESULT 7
ID AAD41170 standard; DNA; 1580 BP.
XX AAD41170;
AC AAD41170;
XX 30-OCT-2002 (first entry)
DT Human HGPBMY8 DNA #1.
DE Human HGPBMY8 DNA #1.
XX Human; G-protein coupled receptor; GPCR; HGPBMY8; drug screening;
KM neurological disorder; brain; immunological; cell growth; cytostatic;
KM neoplastic disease; cAMP; signalling pathway; immune disorder; cancer;
KM gene therapy; tumour; gene; ds.
XX Homo sapiens.
OS WO200240670-A2.
XX 23-MAY-2002.
PD 14-NOV-2001; 2001WO-US043909.
PF 14-NOV-2000; 2000US-0248285P.
PR 14-FEB-2001; 2001US-0268581P.
PR 27-JUL-2001; 2001US-0308285P.
PR 04-SEP-2001; 2001US-0317166P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
PA Bactagilino P, Feder J, Mintier G, Nelson T, Ramanathan C;
PI Westphal R, Cacace A, Barber L, Hawken D, Kornacker M;
XX WPI; 2002-519383/55.
PT A substantially purified human G-protein coupled receptor polypeptide,
PT termed HGPBMY8, useful for treating a neurological disorder or brain
PT disorder in a mammal.
XX Disclosure; Page 207; 223pp; English.
PS The invention relates to human G-protein coupled receptor (GPCR), termed
XX HGPBMY8 and its corresponding nucleic acid. HGPBMY8 DNA is useful for
CC screening for candidate compounds which are small molecules, biological
CC agents, therapeutics or drugs. HGPBMY8 or its homologue is useful for
CC treating a neurological disorder or a disease, a disorder or condition
CC related to the brain in a mammal. It is used for treating or preventing
CC neurological disorders, conditions or diseases and for inducing an
CC immunological response in a mammal. HGPBMY8 DNA, protein and its
CC antibody are useful in the diagnosis, treatment or prevention of
CC disorders associated with aberrant or uncontrolled cellular growth and/

CC or function, such as neoplastic diseases e.g., cancers and tumours and
CC diseases or disorders related to the brain, e.g., neurological disorders.
CC HGPBMY8 DNA and protein are useful for modulating intracellular cAMP
CC associated signalling pathways. An expression vector containing HGPBMY8
CC DNA is useful to treat or prevent neoplastic disorders such as cancer or
CC tumours, immune disorders or neurological disorders. HGPBMY8 DNA is used
CC in gene therapy. The present sequence is human HGPBMY8 DNA
XX
SQ Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 9, 62e-244 Length: 1580
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x AAD41170 (1-1580)
QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 32 ATGACGTCACCTGCACCAACAGACAGCGCGGAGATGAACAGACAGCAGTCATGCC 91
QY 21 LeuSerTyrMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 92 CTCTCCAAATGCGCATCAGCTGCGCCCAAGCATATCCGTCACCGCGTGGTTATC 151
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgPro 60
DB 152 TTCCTGCGCGCCCTTCCTGCGCAATAGTGTGCGCTGATGTGAGCGCAAGCCG 211
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 212 CAGCTCTCAGGTGACCAACGTTTATCTTAACTCTCTGTCACCACTGCTGCAG 271
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 272 ATTTGCTGTGGCCCCCTGGGTGGGACACTGTGCTCTTCTGGGCCCTCAAC 331
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 332 AGCCACTTGTGACGCGCCCTGTTAGCTACACCACCTGTGCGCTTCCGCAAGCTCAAC 391
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 392 ACCATTGCTGTGGTGCAGTGCATGCTTGTCCATATCCACCTCTCTCAACCG 451
QY 141 SerTyrMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 452 TCCAAAGTACCCAGGCGCGGTTTCTGTCTCTTAAGCACCCTGGATTGGGCCATC 511
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 512 CTGCAGAGACATCTCTCACTTACGCTGAGGCGAGGCTGCTTATGAGCGCAATGCT 571
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 572 CTCTGTGCATATGATCTGGGGGCGCACCCAGCTACATATCTTCAGCGTGGTCTTCT 631
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 632 ATCGTATTCACATGATTTGTCAATGCTGCTCTACTCCGTGGTGTCTGTGACGCCGG 691
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleArgHisSerLeuGlnValArgValIleAsp 240
DB 692 AGGACAGACATGCTGCTGTGAACAATGCAAGACACACAGCTTGGAGTGGAGTCAAGAC 751
QY 241 CysValGluAsnGluAspGluGluGlyValArgIleValGluGluPheGlnAspGluSer 260
DB 752 TGTGTGAATAATGAGATGAAGAGGAGACAGAAAGAGAGAGTTCCAGAGTGAAGAG 811
QY 261 GluPheArgArgGlnHisGluGlyGluValIleValAlaValGluIleArgMetGluAlaVal 280

Db	812	GAGTTTCCGCCGACGCTAAAGTGAAGTCAAGAGCCAGAAATGAAAGCCAAAG	871
Qy	281	AapglYserLeuAlaLysGluGlySerThrGlyYThrSerGlySerSerValGluAla	300
Db	872	GACGCGACGCTGAAGGCCAAGGAAGAAACACGAGGAAACCACTGAGATGTGAAGGCCC	931
Qy	301	ArgGlySerSerGluGluValArgGluSerSerThrValAlaSerAapglYserMetGluGly	320
Db	932	AGGGGACAGGAGAGAGTCCAGAGAGACACACAGGTGGCCAGGACCGCAGCATGGAGGGT	991
Qy	321	LysGluGlySerThrLysValGluGluAaSerMetLysAlaAapLysGlyValThrGlu	340
Db	992	AAAGAAAGCAGACACAAAGTTAGAGGAACAGACAGATGAAGGACAAAGGCTGCACAGAG	1051
Qy	341	ValAaenGlyCysSerLeuAapLeuGlyGluAaAapMetGluPheGlyGluAaAapPile	360
Db	1052	GTCAACACAGTGCAGCATTTGACTCTGGGTGAAGATGACATGAGATTGGTGAACACACATC	1111
Qy	361	AaPheSerGluAaAapValGluAlaValAaenIleProGluSerLeuProSerArg	380
Db	1112	AATTTCAGTGAAGATGACCTGCAGGACAGTGAACATCCCGAAGAGCTCCACCCAGTGGT	1171
Qy	381	ArgAaSerAaPheSerAaPheProLeuProArgCysTyGlnCysLysValAlaLysVal	400
Db	1172	GCTAACAGCAACAGCAACCTCTCTGCCCCAGGTGCTACAGTGCAAAGCTCTAAAGTG	1231
Qy	401	IlePheIleIleIlePheSerTyValLeuSerLeuGlyProTyCysPheLeuAlaVal	420
Db	1232	ATCTTCATCATCATATTTTCTCCATATGTGCTATCCCTGGGSCCTACAGCTTTTATGACATC	1291
Qy	421	LeuAlaValTTPValAaPValGluThrGlnValProGlnTTPValIleThrIleIleIle	440
Db	1292	CTGGCGCGTGTGGTGGATGTCCAAACCACAGTAAACCCAGTGGGTGATCACCATATCATTC	1351
Qy	441	TTPLeuPhePheLeuGlnCysCysIleIleHisProTyValTytyGlyTyMetHisLysThr	460
Db	1352	TGGCTTTTCTTCTCTGCAGTGCATCCACCCCTATGTATTAAGCTACATGACAAAGAC	1411
Qy	461	IleLysLysGluIleGlnAaPheLeuLysLysPheCysLysGluLysProPheProLys	480
Db	1412	ATTAAAGAAAGAAATCCAGACATGCTGAAGAAAGTTCTTCTGCAGAGAAAGACCCCGAGA	1471
Qy	481	GluAaSerHisPheAaPheLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro	500
Db	1472	GAAATAGACCAACCAAGCCTGCCCGGAACAGAGGGTGGGACTGAAGGCAAATGTGCCCT	1531
Qy	501	SerTyraAaPheAlaThrPhePro 508	
Db	1532	TCCTACGATTCGTCTACTTTTCT 1555	
RESULT 8			
AEA33115			
ID	AEA33115 standard; DNA; 1580 BP.		
AC	AEA33115;		
XX			
DT	11-AUG--2005 (first entry)		
XX			
DE	Human GPCR HGRPRMW8 gene region SegId47.		
XX			
KW	protein purification; cytosolic; neuroprotective; antiparkinsonian;		
KW	tranquillizer; hypotension; anti-HIV; vincristine; osteoporosis; cancer;		
KW	asthma; allergy; HIV infection; osteoporosis; Parkinsons disease;		
KW	anxiety disorder; hypertension; neurological disease; gene; ds; HGRPRMW8;		
XX	G protein coupled receptor.		
OS	Homo sapiens.		
XX			
PN	WO2005048951-A2.		
XX			
PD	02-JUN--2005.		
XX			

12-NOV-2004; 2004MO-US038387.
 13-NOV-2003; 2003US-00712615.
 (BRIM) BRISTOL-MYERS SQUIBB CO.
 Battaglino P, Feder JN, Mintler G, Nelson TC, Ramanathan CS,
 Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
 WPI; 2005-395945/40.
 New isolated human G-protein coupled receptor, HGPBMY8, and encoding
 polynucleotide, useful for diagnosing or treating cancer, asthma,
 allergies, HIV, osteoporosis, anxiety, hypertension and neurological
 diseases.
 Disclosure; SEQ ID NO 47; 261pp; English.

Alignment Scores:

Pred. No.:	9.62e-244	Length:	1580
Score:	264.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	14	Gaps:	0

QY	1	MetThSerThrcYerhrrhanserThrrArgUserAansrSerThrrThrcYMePPro	20
Db	32	ATAGCGCCACCTGGACCAACAGACGGCGGAGATTAACACAGCCACACCTGCATGCC	91
QY	21	LeuSerIyMePProIleSerLeuIahIagIyIleIeArGserThrrValIeuValIle	40
Db	92	CTCTCCAAAATGGCCATCAAGCTGGGCCACGGCATCATCTGCTCAACCGTCTGTATC	151
QY	41	PheLeuIahIaSerPheValGIyAnuIleValIeuAlaIeuValIeuGlnArgLyPPro	60
Db	152	TTCTCGCCGCCCTCTTTTCCTGGCAACATAGTCGGGGCTAGTCTTGACCGCMAACCG	211
QY	61	GlnLeuLeuGlnValThrrAnaIrrPheIlePheAnLeuLeuValThrrAspLeuLeuGln	80
Db	212	CAGCTGTGAGGTGACCAACCGTTTATCTTTAACTCCTCGTACCGACCTGCTGAG	271
QY	81	IleSerIeuValIahProTrpValValAlaThrrSerValProLeuPheTrpProLeuAsn	100
Db	272	ATTTCGCTCGTGGCCCCCTGGGTGGTGCCACTGTGCTCTCTTCTGGCCCCCTCAAC	331
QY	101	SerThIaphcYerhrrhIaleuValSerIeuThrrhIaleuPheAlaPheAlaSerValAsn	120
Db	332	AGGCACCTTCGACGGCCCTGTGTAGCCCTCAACCCACTGTGGCTTCGCCAGGGTCAAC	391
QY	121	ThrIleValIeuValSerValAspArgTrpIleUserIleIleIleAspProLeuSerTyPPro	140
Db	392	ACCATTTGCTTGTCAGTGAAGTGAAGCTACTTGTCCATCAACACCCCTCTCTTACCG	451
QY	141	SerIyMePProGlnArgArgLyIrrLeuLeuLeuTyArgIlyThrrTrpIleValAlaIle	160

Db	452	TCGAAGATGACCCACGCGCGGGATTACCTGCTCCCTAATGACACCTGATTTGGCCATC	511
Oy	161	LeuGlnSerThrProProLeuThrArgLYTPGVLGlnAlaAlaPheAspGluAspGlnAla	180
Db	512	CTGCAGACACACTCTCCACTCTACCGCTGGGGCCAGGCTGCTTTATGAGCCCAATGCT	571
Oy	181	LeuCySermEIIeTrpGlyAlaSerProSerTYThrIleuSerValValaSerPhe	200
Db	572	CTCTCTCATATCTGGGGGGGCCACCCCAAGTACATAATTTACAGCGTGGTCTTC	611
Oy	201	IleValIleProLeuIleValMetIleaaCySTySerValValaPheCysAlaAlaArg	220
Db	632	ATCGCATTCACATGATTGTCAATGTGCTGCTGCTCACTCCGTGGTGTCTGTGCAGCCCG	691
Oy	221	ArgGlnHleAlaLeuLeuTYrAsnValIlySaRhISerLeuGluValArgValIlyAsp	240
Db	692	AGGCAGCATGCTCTCTGTACAAATGTCAAGAGCACAGCTTGGAATGTGGAGTCAAGGAC	751
Oy	241	CysValIgluAsnGluAspGluGluGluValaGluIlyAsGluIyLeuGluGluGluAspGluSer	260
Db	752	TGTGTGGAAATGAGGATGAAAGGAGGACAGAGAAAGAGAGAGATTCCAGATGAGACT	811
Oy	261	GluPheArgArgGlnHleGluGluGluValIlySaAlaIyGluGluIyArgMetGluAlaIlys	280
Db	812	GAGTTTCGCCCGCACATGAAGTGAAGTCAAGGCCAAGAGGGCAGAAATGAAAGCCAAAG	871
Oy	281	AspGlySerLeuIlySaAlaIyGluGluIySerThrGlyThrSerGluSerSerValIgluAla	300
Db	872	GACCGCACGCTTAAGGCCCAAGAGAGAAACACGCGGACCAAGTGAAGTGTAGAGGCC	931
Oy	301	ArgGlySerGluGluValaArgGluSerSerThrValaIleSerAspGluSerMetGluGly	320
Db	932	AGGGGACACGAGAGAGTCAAGAGAGACACGCTGGTCCACGCAACGCGCAGCAGAGGGGT	991
Oy	321	LysGluGlySerThrIlySaIgluGluAsnSerMetIlySaIlyAspIlyGlyArgThrGlu	340
Db	992	AAGAGAGCAGACCAACAACTTAGAGAAACAGCATBAAGCAGACAAAGGTGCCACAGAG	105
Oy	341	ValaAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle	360
Db	1052	GTCACACAGTGACGACTTGGGTGAAGATGACATGAGATGTTGTGTGAAGCAGCATC	111
Oy	361	AsnPheSerGluAspAspValIgluAlaValaAsnIleProGluSerLeuProProSerArg	380
Db	1112	AATTTCAAGAGAGATGACGTCAAGGAGGAACATCCGAGAGCCTCCACCCAGTCTGT	117
Oy	381	ArgAsnSerAsnSerAsnProProLeuProArgCysTYrGlnCysIlySaAlaIlyVal	400
Db	1172	CGTAACAGACACAGCAACCTCTCTGCGCCAGGTGCTTACAGTGCAAAGTGTCTAAAGTG	123
Oy	401	IlePheIleIleIlePheSerTYrValleuSerLeuGlyProTYrCysPheIleuAlaVal	420
Db	1232	ATCTTCATCATATTTCCTATGTGCTATCCCTGGGGCCCTAAGCTTTTAAAGAGTC	129
Oy	421	LeuAlaValTTrpValaIlySaValIgluThrGlnValProGlnTTrpValIleThrIleIleIle	440
Db	1292	CTGGCGGTGTGGTGGATGTCCAAACCCAGGTACCCCAAGTGGGTGATCAACATAACATC	135
Oy	441	TrpLeuPhePheLeuGlnCysCysIleHleAspTYrValIyGlyTYrMetHleIlySaThr	460
Db	1352	TGGCTTTCTCTCTGAGTGTGCATCCACCCCTATGTCTATGGCTTACATGACAAAGACC	141
Oy	461	IleIlySaIyGluIleGlnaSpMetLeuIlySaIyPhePheCysIlySaGluIySaProProlys	480
Db	1412	ATTAGAAGAAATCCAGGACATGCTGAAGAATTTTCTGCAAGGAAAAAGCCCGGAAN	147
Oy	481	GluAspSerHisProAspLeuProGlyTYrGluGlyGlyTYrGluGlyIlySaIleValPro	500
Db	1472	GAAAGATAGCACCCAGACTGCGCCGGAACAAGAGGTGGAGTGAAGCAAGATGTCTCCT	153
Oy	501	SerTYrAspSerAlaThrPhePro	508
Db	1532	TCCTACGATTCGTACTTTTCTT	1555

RESULT 9

ACF03567
ID ACF03567 standard; cDNA, 1584 BP.

XX AC ACF03567;
XX DT 15-SEP-2003 (first entry)
XX DE Human NOV14a protein encoding cDNA SEQ ID NO:41.

KW Human; NOVX; cytostatic; cardiant; antiinflammatory; immunosuppressive;
KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
KW anorectic; antiaesthetic; nephrotropic; antiarthritic; hepatotropic;
KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
KW relaxant; anticomvulsant; hypotensive; vasodilator; antiparkinsonian;
KW vulnerrary; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
KW cardiomyopathy; arteriosclerosis; hypertension; diabetes; inflammation;
KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
KW acquired immunodeficiency syndrome; neuropathy; cirrhosis; arthritis;
KW Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
KW muscular dystrophy; epilepsy; wasting disorder; chromosome X; gene; ss.
XX OS Homo sapiens.
XX PD WO200294870-A2.
XX PN 28-NOV-2002.
XX PP 02-NOV-2001; 2001WO-US051580.
XX PR 02-NOV-2000; 2000US-0245291P.
XX PR 02-NOV-2000; 2000US-0245317P.
XX PR 07-NOV-2000; 2000US-0246562P.
XX PR 08-NOV-2000; 2000US-0246871P.
XX PR 26-JAN-2001; 2001US-0264389P.
XX PR 29-JAN-2001; 2001US-0264423P.
XX PA (CURA-) CURAGEN CORP.

P1 Grosse WM, Macdougall JR, Smitson G, Millet I, Stone DJ,
P1 Gunther E, Ellemann K, Alsobrook JP, Lepley DM, Burgess CE;
P1 Spytek KA, Edinger SR, Gangolli EA, Gorman L, Taupier RJ, Li L;
P1 Guo X, Fernandes BR, Vernet CAM, Tcheurnev VT, Casman SJ, Shenoy S;
P1 Mishra V, Furtak K, Baumgartner JC, Colman SD;
DR WPI; 2003-140359/13.
DR P-PSDB; ABR57432.

PT New NOVX polypeptide useful for preventing or treating NOVX-associated
PT disorders, e.g. cancer, cardiomyopathy, arteriosclerosis or diabetes, and
PT in chromosome mapping, tissue typing or pharmacogenomics.
XX Claim 8; Page 129; 346pp; English.

XX AC ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
XX CC TO ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic,
XX CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
XX CC antiarteriosclerotic, anorectic, antiaesthetic, nephrotropic, virucide,
XX CC antiarthritic, hepatotropic, neuroprotective, antibacterial, relaxant,
XX CC antiparasitic, anticomvulsant, hypotensive, vasodilator, antiparkinsonian,
XX CC vulnerrary, angiogenic and antiangiogenic activities, and can be used in
XX CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
XX CC be used to determine the presence or absence of (I) in a sample. The NOVX
XX CC polypeptides, polynucleotides encoding them, and antibodies against them,
XX CC are useful in manufacturing a NOVX-associated disorder such as hypertension,
XX CC syndrome associated with a NOVX-associated disorder such as hypertension,
XX CC cardiomyopathy, arteriosclerosis, cancer, diabetes, asthma, inflammation,
XX CC autoimmune disorder, allergies, blood disorders, obesity, acquired
XX CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig)A nephropathy,
XX CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
XX CC infections (e.g. bacterial, viral, parasitic), stroke, muscular

CC dystrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOX
 CC sequence, which are used in an example from the present invention
 XX

SO Sequence 1584 BP; 359 A; 457 C; 430 G; 338 T; 0 U; 0 Other;

Alignment Scores:

Prod. No.: 9,656-244 Length: 1584
 Score: 2644.00 Matches: 508
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-712-615-2 (1-508) x ACF03567 (1-1584)

```

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 31 ATGAGCTCAGCTGACCAACAGCAGCGGAGAGTAAACAGACAGCCACGTCATGCCCC 90
QY 21 LeuSerLysMetProLLeuSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 91 CTCCTCAAAATGCCATACAGCTGCGCCACGCGCATCATCCGTCACACGTCGTGTTATC 150
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 151 TTCCCTCGCGCCTCTTTCGTGGCAACATAGTGTGGCGCTAGTGTGGCGCAAGCGG 210
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 211 CAGCGCTGCGAGGTACCAACCGTTTATCTTTAACCTTCCTGTCACCACTGCTGCGAG 270
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 271 ATTGGCTCGTGGCCCCCTGGGTGGTGGCCACCTCTGTCTCTTCTGCGCCCTCAAC 330
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisAlaLeuPheAlaSerValAsn 120
DB 331 AGCCACTTCTGCACGGCCCTGGTTAGCTCACCCACCTGTTGCCCTTGCACGGCTTAC 390
QY 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 391 ACCATTGCTTGGTGTCAAGTGAATGCTGCTATCATCATCACCCTCTCTCCACCGG 450
QY 141 SerLysMetThrGlyArgArgGlyTyrLeuLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 451 TCCAAAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGACACCTGGATTGGCCATC 510
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 511 CTGCAGAGACACTCTCCACTTACGGCTGGGCGCAGGCTGCCCTTGTGATGAGCGCATGCT 570
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 571 CTCTGCTCATGATCTGGGGGGGCGACGCCACCTACATCTCACTGAGCTGTGTCCTTC 630
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValIlePheCysAlaAlaArg 220
DB 631 ATCGCATTCCTCACTGATGTCTGATGCTGCTGCTACTCCGTGTGTCTCTGTGACGCCGG 690
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleArgHisSerLeuGlnValArgValIleAsp 240
DB 691 AGGCAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGAAGTGCAGATGAGAGAC 750
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluLysValGluGluPheGlnAspGluSer 260
DB 751 TGTGTGGAAGATGAGAGATGAGAGAGGAGCAGAGAGAGAGAGAGAGTTCAGAGATGAGAT 810
QY 261 GluPheArgArgGluHisGluGluGlyValIleValAlaValGluGlyValArgMetGluAlaLys 280
DB 811 GAGTTTCGCGCGCAGATGAGAGTGAAGTGAAGGCCAAGAGAGAGGCAATGGAAGCCAAAG 870
QY 281 AspGlySerLeuLysAlaValGluGluGlySerThrGlyThrSerGluSerSerValGluAla 300

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DB 871 GACGCGACCTCGAAGCGCAAGAGAGAGCAGCGGGACCACTGAGATGATAGAGGCC 930
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 931 AGGGCAGCAGAGAGAGTCAAGAGAGCAGCAGGTCGCGACGAGCGAGCATGAGAGGT 990
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB 991 AAGGAAGCAGACCAAAAGTTGAGGAGAAACAGCATGAAGGACAGACAGAGGTGCAAG 1050
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1051 GTCAACCACTGAGCATGACTGGCTGTGAATGACATGAGATGTTGTGGAAGACACATC 1110
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProSerArg 380
DB 1111 AATTTCACTGAGATGAGTGAAGTGAAGTGAACATCCGAGAGGCTTCCACCGATGCT 1170
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysValAlaAlaLysVal 400
DB 1171 CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGCTACAGTGCAAAAGCTGCTAAAGT 1230
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1231 ATCTTCATCATCATTTTCTCTATGTCTATCCCTGGGGCCCTACTGCTTTTTCAGATC 1290
QY 421 LeuAlaValTyrPvalAspValGluThrGlnValProGlnTyrPvalIleThrIleIleIle 440
DB 1291 CTGGCCGATGGATGATGATGATGAAACCAAGTACCCAGTGGGTATATCACTAATATC 1350
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1351 TGGCTTTCTTCTGCAATGCTGATCCACCCCTATGTCTATGCTATGCAACAAGCC 1410
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProLys 480
DB 1411 ATTAAGAAAGAAATCCAGACATGCTGAAGAAATCTTCTGCAAGAAAGCCCGGAAA 1470
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB 1471 GAAGATAGCAACCCAGACCTGCCGGAACAGAGGTGGACTGAAGGCAAGATTGCTCT 1530
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1531 TCTTAGATTCTGCTACTTTTCTCT 1554

RESULT 10
ADF70610
ID ADF70610 standard; DNA; 2241 BP.
XX
AC ADF70610;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein gene SeqID233.
XX
KW ligand: orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX

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(TAKE) TAKEDA CHEM IND LTD.
XX Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX MPI: 2003-697654/66.
DR P-PSDB; ADF70508.
XX Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX Example 4; SEQ ID NO 233; 594pp; Japanese.
XX This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligand binding to an orphan receptor protein.

XX Sequence 2241 BP, 578 A, 597 C, 570 G, 496 T, 0 U, 0 Other;

Alignment Scores:

Pred. No.:	1,6e-243	Length:	2241
Score:	2644.00	Matches:	508
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-712-615-2 (1-508) x ADF70610 (1-2241)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGAGCTCCACCGCAGCAACGCGGAGATACGAGCAGCAGCGTCATGCC 60
QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATGCGCATCGCTGCGCCACGCGCATATCCGTCACACCGCTGCTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 121 TTCCTGCGCGCTCTTTCGTGCGCAACATAGTCGTGCGTATGTTGCAAGCCGCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGCTGACGGTGAACCAACGTTTATCTTAACTCTGTCACCGACCTGCGCAG 240
QY 81 IleSerLeuValAlaProTyrValAlaIleThrSerValProLeuPheTyrProLeuAsn 100
DB 241 ATTTGCGCTGTGGCGCCCTGTGGTGTGGCCACCTGTGTGCTCTTCTTGGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTTCGACGGCCCTGTGAGCTTACCCACCTGTCCTTGGCCAGCGTACAC 360
QY 121 ThrIleValIleValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGCTGTGGTGTGAGTGTGCTACTTGTCCATCATTCACCTCTCTCTCAACCG 420
QY 141 SerIleMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 421 TCCAAATGACCCAGGCGCGGTACGTGCTCTCTATGGACCTGGAAATTTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlyAlaIleAlaPheAspGluArgAsnAla 180
DB 481 CTGCAAGACATCTCTCACTACGCGCTGGGCGCAGGCTCTTTATATGAGCCATGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200

DB 541 CTCTGCTCATATCTCTGGGGGCGCAGCCCACTACACTATCTACAGCTGCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValPheCysAlaIleArg 220
DB 601 ATGTCATTTCCACTGATTTGTATGATGTGCTCTCTCTGCTGTGTCTGTGCAAGCCCG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValArgHisSerLeuGlnValArgValIleAsp 240
DB 661 AGCGACATGCTCTGCTGATCATGTCAAGAACACAGCTTGAAAGTGGAGCTCAAGAGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyIleGlyIleValIleValIleValIleValIle 260
DB 721 TGTGTGGAATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGlyIleValIleValIleValIleValIleValIleValIle 280
DB 781 GAGTTTCCGCGCAGCATTAAGGTAGGTCAAGGCCAAGAGAGAGAGAGAGAGAGAGAG 840
QY 281 AspGlySerLeuValAlaValGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGCGAGCTGAAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGluSerThrIleValGluGluAsnSerMetValAspLysGlyArgThrGlu 340
DB 961 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyIleAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCACTGACAGATTGATCTGGGTGAAATGACATGAGATTGTGTGAAGCAGCATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAlaIleProGluSerLeuProProSerArg 380
DB 1081 AATTTTCAGAGAGATGACGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysIleValAlaIleVal 400
DB 1141 CATTACAGCAAGCAACCTCTCTGCGCAGGTGCTACAGTGCAGAGCTGTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCTTTCTCTATGCTATCCCTGCGGCGCTTACTGCTTTTATGACATC 1260
QY 421 LeuAlaValIlePheValAspValGluThrGlnValProGlnTyrValIleThrIleIle 440
DB 1261 CTGCGCGTGTGGTGTGATGTCAAAACCCAGTACCCAGTGGGTGATCCCATTAATCATC 1320
QY 441 TyrLeuPhePheLeuGlnCysGlyIleHisProTyrValIleTyrMetHisIleValThr 460
DB 1321 TGGCTTTTCTTCTGAGGTGTCATCAACCTCTATGTCTATGCTATGCAACAGAC 1380
QY 461 IleIleValGluIleGlnAspMetLeuValIlePhePheCysLeuGlyIleValProLys 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAAGTTCTTTCGCAAGAAAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyIleThrGluGlyIleThrGluGlyIleValPro 500
DB 1441 GAAGATAGCACCAACCACTGCGCGGAGACAGAGGAGTGAAGCAAGAAATTTGCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTTACGATTGCTACTTTTCT 1524
RESULT 11
ACCS8886
ID ACCS8886 standard; cDNA; 4718 BP.
XX ACCS8886;
AC
XX
DT 22-SBP-2003 (first entry)

XX Human G-protein coupled receptor OM_10 cDNA.
KW G-protein coupled receptor; GPCR; OM_10; human; receptor; cardiac;
KW hypersensitive; hypotensive; antianginal; cytostatic; antiparastic;
KW analgesic; gynaecological; antidepressant; antisthmatic; osteopathic;
KW neurologic; cranquillizer; nephrotoxic; antitumor; antiallergic;
KW neurologic; anticonvulsant; neuroprotective; antiparkinsonian;
KW gene therapy; gene; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 332..1858
FT FT /*tag= a
FT FT /product= "OM_10"
XX MO200304162-A2.
XX 30-MAY-2003.
XX 12-NOV-2002; 2002WO-US036204.
XX 16-NOV-2001; 2001US-0332110P.
XX (AMHP) WYETH.
XX Blatcher M, Paulsen JE, Bates BG;
XX MPI; 2003-449811/42.
XX P-P8DB; ABR42865.
XX
XX New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
PT UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
PT Parkinson's disease, acute heart failure, hypertension, cancer or
PT osteoporosis.
XX
XX Claim 49; Page 174-178; 190pp; English.
XX
XX The present sequence is that of cDNA encoding a novel human G-protein
CC coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
CC from a genome database search using the human 5-HT₆ receptor sequence.
CC Identified regions of genomic DNA were used to predict full-length genes,
CC and these gene predictions were used to isolate the present sequence from
CC a cDNA library. OM_10 is predominantly expressed in the putamen and
CC caudate nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists
CC and antagonists of the invention are useful in drug screening assays,
CC pharmacogenomics, monitoring of effects during clinical trial, or for
CC diagnosing, preventing and treating diseases associated with enhanced or
CC inhibited GPCR activity, e.g. acute heart failure, hypotension,
CC hypertension, angina pectoris, myocardial infarction, hyperproliferative
CC diseases such as cancers and psoriasis, apoptotic diseases, pain,
CC endometriosis, anorexia, bulimia, asthma, osteoporosis, echinophrenia,
CC delirium, depression, anxiety, urinary retention, ulcers, allergies,
CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
CC syndrome, Alzheimer's disease, or Parkinson's disease
XX
XX Sequence 4718 BP; 1359 A; 1078 C; 1060 G; 1221 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 4 718-243 Length: 4718
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-712-615-2 (1-508) x ACCS8886 (1-4718)

Qy 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
Db ATGAGCTTCCACTTCCAGCCACACAGACGCGGAGAGTAAGACGACCGACGATGATGCC 391

Qy 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
Db CTCTCCAAAAGGCCATCAGCTGGCCACAGGACATCATCCGCTCAACCGTGTGTTATTC 451
Qy 41 PheLeuAlaAlaSerPheValIGLYAsnIleValLeuAlaLeuValLeuGlyArgGlyPro 60
Db TTCTCGCGCGCTCTTTGTGTGGCAACATAGTGTGGGCTTAGTGTTCACGCGAACGCG 511
Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAlaLeuLeuValThrAspLeuLeuGln 80
Db CAGTGTGTGAGGTACCAACCGTTTATCTTTAACTCTCTGTCACCGACTGTGTGAG 571
Qy 81 IleSerLeuValAlaProTyrValValAlaThrSerValProLeuPheTyrProLeuAsn 100
Db ATTTGCTGTGGGCCCCCTGGGTGTGGCCACTGTGGCTCTCTTGTGGCCCCCTCAAC 631
Qy 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaSerValAsn 120
Db AGCCACTTGTGACGCGCCCTGTGTTAGCTTCAACCTCTGTTGCTTCCGACGCTCAAC 691
Qy 121 ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db ACCATTGTCTTGATGTAGTGGATGCTACTGTTCATCATCAACCTCTGCTCTCAACCG 751
Qy 141 SerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
Db TCCAGATGACCCAGCGCGCGGTTCCTGCTCTTATGACACTCTGATTTGTGCGCATTC 811
Qy 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAspGlyArgAsnAla 180
Db CTGCAGACACTCTCTTCCCTTACGCTGGGCGCCAGGCTGCTTGTATGAGCGCATGCT 871
Qy 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
Db CTCTGCTCAAGATGTGGGGGCGCAGCCGACGTAATATTCTCAGGTGTGTCCTTC 931
Qy 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValIlePheCysAlaAlaArg 220
Db ATTCGATTTCCACTGATTTGTCATGATTCCTGCTCACTCCGCTGTGTCACCGCCGG 991
Qy 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValIleValIleValIleValIleValIle 240
Db AGGCGATGCTCTGCTCTTCAATGTCAAGACACACTTGTGAATGTGAGTCAAGAC 1051
Qy 241 CysValIGluAsnGluAspGluGluGlyValIleGluValIleValIleValIleValIle 260
Db TGTGTGAAGATGAGGATGAAGAGGAGCAGAGGAAGAGGAGGATTCACAGATGAGT 1111
Qy 261 GluPheArgArgGlnHisGluGlyGlyValIleValIleValIleValIleValIleValIle 280
Db GAGTTTCCCGCCGACATGAAGGTGAGCTCAAGCCCAAGGAGGCGCAGATGACCCCAAG 1171
Qy 281 AspGlySerLeuValIleValIleGluGlySerThrGlyThrSerGluSerValIleGluVal 300
Db GACGGCACCTGAAGGCGCAGAGAGAGGACACGGGGACAGAGTAAGTGTAAAGGCC 1231
Qy 301 ArgGlySerGluGluValArgGluSerSerThrValIleAspAspGlySerMetGluGly 320
Db AGGGCAGCGAGAGGTCAAGAGAGCAGACGCTGCGCAGCAGCGACGATGAGAGGT 1291
Qy 321 LysGluGlySerThrLysValIGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db AAGGAAGCAGACCAAGATTGAGAGGAACAGCAAGAGGACGACAAAGGTCGACAGAG 1351
Qy 341 ValaGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
Db GTCAACCAAGTCAGATTGCTGGTGAAGATGACATGAGTTGGTGAAGACGACATTC 1411
Qy 361 AsnPheSerGluAspAspValIGluValIleValIleProGluSerLeuProProSerArg 380
Db AATTTCAGTGAAGATGAGTCAAGGCACTGAACATCCCGAGAGGCTCCACCCAGTGT 1471
Qy 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysValAlaIleValIleVal 400

DB 1472 CTTAACAGACAGCAACCTCTCTGCCCAGGTGCTACAGTGCAGCAAGCTGCTAAAGTG 1531
QY 401 IIPheIleIleIlePheSerThrValLeuSerLeuGlyProGlyCysPheLeuAlaVal 420
DB 1532 ATCTTCATCATCTATTTCTCTATGCTATGCTATCCCTGGGCGCTTACTGCTTTTATGAGATC 1591
QY 421 LeuAlaValThrValAspValGluThrGlnValProGlnThrValIleThrIleIle 440
DB 1592 CTGGCGGTGGGTGGATGTCGAAACCCAGTACCCAGTGGGTGATTCACATTAATCATC 1651
QY 441 ThrPhePhePheLeuGlnCysCysIleHisProGlyValIleGlyIleThrIleIleVal 460
DB 1652 TGGCTTTTCTCTCTGAGTGGTGCATCCACCCCTATGCTATGCTACATGACCAAGACC 1711
QY 461 ILeValLeuGluIleGlnAspMetLeuValLeuValPhePheCysValLeuGluValProGly 480
DB 1712 ATTACAGAGCAATTCAGAGCATGCTGAGAGATTTCTTCTGCAAGAGAAAGCCCCGAGAA 1771
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyValThrGluGlyValIleValPro 500
DB 1772 GAAGATGACCAACCCAGTCCGCGGAGACAGAGGTGGGACTGAAAGCAAGATTGTCCCT 1831
QY 501 SerThrAspSerAlaThrPhePro 508
DB 1832 TCTACGATTCCTGCTACTTTTCT 1855
RESULT 12
ID AAL44180 standard; DNA; 1524 BP.
AC AAL44180;
XX
DT 24-OCT-2002 (first entry)
XX
DE Human G-protein coupled receptor protein coding sequence #2.
XX
KW Human; G-protein coupled receptor protein; TGR34; gene; ds;
central nervous system disease; Alzheimer's disease; metabolic disease;
diabetes; cancer; breast cancer; circulatory disease; atherosclerosis;
inflammatory disease; arthritis; respiratory disease; bronchitis;
digestive disease; stomach ulcer; immune disorder; autoimmune disease;
infection; AIDS.
XX
KW Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT 1..1524
FT /*tag= a
FT /partial
FT /product= "Human G-protein coupled receptor protein #2"
FT /note= "No stop codon is given"
XX
XX WO200259304-A1.
XX PD 01-AUG-2002.
XX
XX 22-JAN-2002; 2002WO-JP000405.
XX PF 23-JAN-2001; 2001JP-00015050.
XX PR 30-MAR-2001; 2001JP-00102560.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX PA
XX Miwa M, Ito T, Shintani Y, Miyajima N;
PI
XX MPI; 2002-557949/59.
XX DR P-PSDB; AAO15504.
XX
XX Human G-protein coupled receptor protein and DNA encoding it for design
PT of drugs and reagents for treatment and diagnosis of cancer or
PT respiratory and metabolic diseases.
XX

PS Claim 7; Page 100-101; 109pp; Japanese.
XX
CC The invention comprises the amino acid and coding sequences of two human
CC G-protein coupled receptor proteins (TGR34). The DNA and protein
CC sequences of the invention are useful for the treatment, prevention and
CC diagnosis of: central nervous system diseases (e.g. Alzheimer's disease);
CC metabolic diseases (e.g. diabetes); cancer (e.g. breast cancer);
CC circulatory diseases (e.g. atherosclerosis); inflammatory diseases (e.g.
CC arthritis); respiratory diseases (e.g. bronchitis); digestive diseases
CC (e.g. stomach ulcer); immune disorders (e.g. autoimmune diseases); and
CC infections (e.g. AIDS). The present DNA sequence encodes a human G-
CC protein coupled receptor protein
XX
SQ Sequence 1524 BP; 346 A; 439 C; 419 G; 320 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1,776-243 Length: 1524
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x AAL44180 (1-1524)
QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGACCTCCACCTGCAACCAAGCAGCGCCGAGAGTAAACGACGACACGTCATGCC 60
QY 21 LeuSerLeuMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATGCCCATCAGCTGCGCCACGCGCATCATCCGCTCAACCGCTGCTTATC 120
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValIleValLeuValLeuGlnArgValPro 60
DB 121 TTCCTGCGGCTCTTTCGTGGCAATAGTGGCCCTGAGTGTGAGCGCAAGCCG 180
QY 61 GlnLeuLeuGluValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTCAGGTACCAACCGTTTATCTTAACTCTGTCACCACTGCTGCG 240
QY 81 IleSerLeuValAlaProThrValAlaAlaThrSerValProLeuPheThrProLeuAsn 100
DB 241 ATTGCGCTGATGCGCCCTGGGTGGGCGCACCTGCTGCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTGTGACCGGCTGTGAGCCCTCACCCACCTGTGCTTGGCCAGCGTCAAC 360
QY 121 ThrIleValIleValSerValAspArgIleLeuSerIleIleHisProLeuSerThrPro 140
DB 361 ACCATTGTGCTGTGTCAGTGCATGCTCTTGTCCATCATCAACCTCTCTCTACCGG 420
QY 141 SerLeuMetThrGlnArgArgIleValLeuLeuLeuValThrThrIleValAlaIle 160
DB 421 TCCAAAGATACCAAGCGCGCGGTATCTGCTCTATGAGCACTGATGGCCATC 480
QY 161 LeuGlnSerThrProProLeuValIleValIleValIleValAlaPheAspGluArgAsnAla 180
DB 481 CTGCAGACGACTCTCCACTCAACGCTGGGGCGACGCGCTTGATAGCGCAATGCT 540
QY 181 LeuCysSerMetIleThrGlyAlaSerProSerThrThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGCCACCCCAAGCTACATTAATCTACGCTGTGCTTTC 600
QY 201 IleValIleProLeuValIleValMetIleAlaCysIleSerValValPheCysAlaAlaArg 220
DB 601 ATGCTATTCCACTGATTTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ArgGlnHisAlaLeuLeuValIleValIleValIleValIleValIleValIleValIleVal 240
DB 661 AGGACAGATGCTCTGCTGTAATGCAATGCAAGACACAGCTGTGAACTGGAGTCAAGGAC 720

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Oy 241 CysValGluAenGluAenGluGluValAgluValyluValyluGluGluPheGluAenGluSer 260
Db 721 TGTGTGAGAAATGAGATGAAAGAGAGAGAGAGAAAGAGAGATTCAGATAGAGT 780
Oy 261 GluPheAArgGluNH;agluGluValValyluValyluValyluValyluValyluValylu 280
Db 781 GAGTTTCCCGCCAGCATGAGGTAGGTACAGGCCAGAGGCGAGAGAGAGAGAGAGAGAGAG 840
Oy 281 AepGlySerLeuValyluValyluValyluValyluValyluValyluValyluValylu 300
Db 841 GACGACACCTGAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Oy 301 ArgGlySerGluGluValyluValyluValyluValyluValyluValyluValyluValylu 320
Db 901 AGGGGACACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Oy 321 LysGluGlySerThrValyluValyluValyluValyluValyluValyluValyluValylu 340
Db 961 AAGGAAAGGACAGACCAAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Oy 341 ValaenGluCysSerIleAenPheGluValyluValyluValyluValyluValyluValylu 360
Db 1021 GTCAACCAAGTCAGATTCATTTGGGTGAAGATGACATGAGATTTGGTGAAGACAGCATC 1080
Oy 361 AenPheSerGluAenPheValyluValyluValyluValyluValyluValyluValyluValylu 380
Db 1081 AATTTCAGTGAAGATGACCTCGAGGACAGAGATCCCGAGAGAGCTCCACCCAGTGTCT 1140
Oy 381 ArgAenSerAenSerAenProPheProAenGluValyluValyluValyluValyluValylu 400
Db 1141 CGTAACAGACAGACCACTCTCTGCCCCAGAGTGTACAGTGTACAGAGTGTAAAGTG 1200
Oy 401 IlePheIleIleIlePheSerThrValyluValyluValyluValyluValyluValyluValylu 420
Db 1201 ATCTTCATCATATTTCTCTATGAGTATCCCTGGGGCCCTACTGCTTTTATGACAGTC 1260
Oy 421 LeuAlaValThrValyluValyluValyluValyluValyluValyluValyluValylu 440
Db 1261 CTGGCCGCTGGGTGATGTCTGAAACCCAGGTACCCAGTGGTGTATCCCTAAATCATC 1320
Oy 441 TrpLeuPhePheLeuGluCysValyluValyluValyluValyluValyluValyluValylu 460
Db 1321 TGGCTTTCTTCTCTGAGTGTCTGATCCACCCCTATGTATTAGGCTACATGACAGAGCC 1380
Oy 461 IleIleValyluValyluValyluValyluValyluValyluValyluValyluValyluValylu 480
Db 1381 ATTGAAGAGAAATCCAGGACATGCTGAAGAGAGTCTTCTGCAAGAGAGAGAGAGAGAG 1440
Oy 481 GluAenSerHisProAenPheProGluThrGluGluValyluValyluValyluValylu 500
Db 1441 GAAGATAGCCACCCAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Oy 501 SerTyAenSerAlaThrPhePro 508
Db 1501 TCTTACGATTCTGCTACTTTTCTCT 1524

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Km antidepressant; anorectic; PCR primer; gene therapy.
XX Homo sapiens.
OS WO200162797-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US005676.
XX
XX 23-FEB-2000; 2000US-0184247P.
XX 23-FEB-2000; 2000US-0184303P.
XX 23-FEB-2000; 2000US-0184304P.
XX 23-FEB-2000; 2000US-0184305P.
XX 23-FEB-2000; 2000US-0184306P.
XX 02-MAR-2000; 2000US-0186457P.
XX 03-MAR-2000; 2000US-0186810P.
XX 09-MAR-2000; 2000US-0186854P.
XX 13-MAR-2000; 2000US-0188880P.
XX 03-APR-2000; 2000US-0194344P.
XX 23-JUN-2000; 2000US-0213861P.
XX 11-JUL-2000; 2000US-0217369P.
XX 11-JUL-2000; 2000US-0217370P.
XX 14-JUL-2000; 2000US-0218337P.
XX 20-JUL-2000; 2000US-0218492P.
XX
XX (PNUA ) PHARMACIA & UPJOHN CO.
PA
PI Vogeli G, Wood LS, Parodi LA, Lind P;
XX MPI. 2001-570628/64.
XX P-PSDB; AA0235605.
XX
XX New isolated nucleic acid encoding a new G-protein coupled receptor
XX polypeptide for detecting receptor modulators that can treat mental
XX disorders, such as schizophrenia, anxiety, depression, or obesity.
XX
XX Claim 4, Page 89-90; 279pp; English.
XX
XX Sequences AAS42806-AAS42926 represent cDNA molecules and PCR primers for
XX cDNA molecules encoding human G-protein coupled receptor (GPCR)
XX polypeptides. The protein and DNA sequences of the invention can be used
XX to identify compounds which bind to GPCR polypeptides and in screening
XX for compounds that modulate GPCR activity. By screening a human subject
XX for the presence of mutations in GPCR DNA, a GPCR-related disorder or a
XX genetic predisposition can be diagnosed. The sequences can also be used
XX for treatment and prevention of mental disorders such as schizophrenia,
XX attention deficit disorder, anxiety, depression, dementia and bipolar
XX disorder, neurological disorders such as Huntington's disease,
XX Parkinson's disease and Tourette's syndrome, metabolic disorders such as
XX obesity, anorexia and type 2 diabetes, cardiovascular disorders such as
XX thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,
XX viral infections caused by HIV and cancers
XX
XX SQ Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

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Alignment Scores:

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Pred. No.: 1.78e-243 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0

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US-10-712-615-2 (1-508) x AAS42857 (1-1527)

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Oy 1 MetThrSerThrCysThrAenSerThrArgGluSerAenSerSerHisThrCysMetPro 20
Db 1 ATGAGTCACCATCTGACCAACAGCAGCGCGAGATTAACAGACGACATGATGCC 60
Oy 21 LeuSerIleMetProIleSerLeuAlaHagIleIleIleIleIleIleIleIleIleIle 40
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QY	61	GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln	80
Db	181	CAGCTGCTGCAGGTAGCCAAACGGTTTAACTTTAACTCTGTGTCAACCACTGCTGCAG	240
QY	81	IleSerLeuValAlaProTrpValValAlaIleThrSerValProLeuPheTrpProLeuAsn	100
Db	241	ATTTCGCTGTGGCCCCCTGGGTGGGGCCACTCTGTGCTCTCTTCTGGCCCCCTCAAC	300
QY	101	SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValaAsn	120
Db	301	AGCCACTTCTGCACGGCCCTGGATTAGCTCACCAACCTGTTCGCTTCCGACGGTCAAC	360
QY	121	ThrIleValLeuValSerValAspArgTrpLeuSerIleIleHisProLeuSerTrpPro	140
Db	361	ACCAATTGTCGTGGTGCATGGATGGCTACTGTCATGATCAACCTCTCTTCCTCAACCG	420
QY	141	SerLysMetThrGlnArgArgLysTrpLeuLeuLeuLeuTrpTrpIleValAlaIle	160
Db	421	TCCAAAGATACCCACGACCGCGGATTACCTGCTCTCTTAAGCACTCGAATGTGGCAATC	480
QY	161	LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAlaAlaPheAspGlnArgAsnAla	180
Db	481	CTGCAGAGACATCTCTCACTTACGGCTGGGGCGAGGCTGGCTTGAATGAGGCAATGCT	540
QY	181	LeuCysSerMetIleTrpGlyAlaSerProSerTrpThrIleLeuSerValValSerPhe	200
Db	541	CTCTCTCTCATATATCTGGGGGGCCAGCCCCAGCTACATATCTCAGCTGTGATCTTCC	600
QY	201	IleValIleProLeuIleValMetIleAlaCysTrpSerValValPheCysAlaIleArg	220
Db	601	ATCGCATTCACATGATTTGTCAAGATTGCTGTACTCTGTGGTGTCTGTGCAGCCCCG	660
QY	221	ArgGlnHisAlaLeuLeuTrpAsnValLysArgHisSerLeuGlnValArgValLysAsp	240
Db	661	AGCGAGCAATGCTCTGTGTACATGTCAAGACACACAGCTTGGAACTGGAGTCAAGAC	720
QY	241	CysValGlnAsnGlnAspGlnGlnGlyAlaGlnLysLysGlnGlnPheGlnAspGlnSer	260
Db	721	TGTGTGAGAAATGAGGATGAAGAGGAGCAGAGAAAGAAAGAGAGATTCAGAGATGAGAT	780
QY	261	GluPheArgArgGlnHisGlnGlyGlnValLysValLysGlnGlyArgMetGlnAlaLys	280
Db	781	GAGTTTCGGCGGCAGATGAAGGTGAGGTCAAGCCMAAGAGGCGAATGGAAGGCCAAG	840
QY	281	AspGlySerLeuLysAlaLysGlnGlySerThrGlyThrSerGlnSerSerValGlnAla	300
Db	841	CACGGCAGCTTAAGGCCAAGAGAGAGACGCGGACCAAGTGAAGATTGTATAGAGCC	900
QY	301	ArgGlySerGlnGlnValArgGlnSerSerThrValAlaSerAspGlySerMetGlnGly	320
Db	901	AGGGCAGAGAGAGAGGTCAAGAGAGACAGCGGTGGCAGCGACGGCAGCATGAGGGT	960
QY	321	LysGlnGlySerThrLysValGlnGlnLysSerMetLysAlaAspLysGlyArgThrGln	340
Db	961	AAGGAGAGGACGACCAAAATTGAGGAGAACACACTGAAGGACACAAAGGTGTGCACAG	1020
QY	341	ValaAsnGlnCysSerIleAspLeuGlyGlnAspAspMetGlnPheGlyGlnAspAspIle	360
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Db	1081	AATTTCAAGAGAGATGACGTGAGGAGAGAAATATCCGGAAGAGCTCCACCACTGCT	1140
QY	381	ArgAsnSerAsnSerAsnProProLeuProArgCysTrpGlnCysLysAlaAlaLysVal	400
Db	1141	CGTAAACGACAAAGCAACCTCTCTGTGCCAGGTGTACAGTGCAAAGCTCTAAAGTG	1200

QY	401	llehelllellellepserTyrValleuSerleuGlyProTyrCyspheLeuAlaVal	420
Db	1201	ATCTTCATCATCATTTTCTCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTGGACGTC	1260
QY	421	LeuAlaValTrrpValAspValGluThrGlnValProGlnTrrpValIleThrIleIleIle	440
Db	1261	CTGGCCGGTGGGGGATGTCGAAACCCAGGTACCCCAAGGGGGAATCACCATTATATATC	1320
QY	441	TrrpLeuphePheLeuGlnCysCysAlaIleHisProTyrValTyrGlyTyrMetHisLysThr	460
Db	1321	TGGCTTTTCTTCGCGAGCTGTGATCCACCCCTATGCTTATGGCTACATGACACAAAGCC	1380
QY	461	IleLysLysGluIleGlnAspMetLeuLysIshpheCysLysGluLysProProLys	480
Db	1381	ATTAAAGAAAGAAATCCAGACATCTGTAAAGAGTTCTTTCGCAAGAGAAAAGCCCCGAAA	1440
QY	481	GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro	500
Db	1441	GAAAGTAGCCACCCAGACCTGCCCCGAAACAGAGGTGGAGCTGAAGCAAGATTGTCCCT	1500
QY	501	SerTyrAspSerAlaThrPhePro	508
Db	1501	TCTACGATTTCTGCTACTTTTCCCT	1524

RESULT 14

ID AAS07942 standard; cDNA; 1527 BP.

AC AAS07942;

DT 23-OCT-2001 (first entry)

DE Human cDNA encoding G-protein coupled receptor, hRUP15.

KW Human; G-protein coupled receptor; GPCR; hRUP15; agonist;

XX

XX

FT	CDS	
	1.	.1527

FT /product="HRUP15"

PN WO200136471-A2.

PD 25-MAY-2001.

PF 16-NOV-2000; 2000WO-US031509.

PR 17-NOV-1999; 99US-0166088P.

PR 17-NOV-1999; 99US-0166369P.

PR 23-DEC-1999; 99US-0171901P.

PR 11-FEB-2000; 2000US-0181749P.

PR 14-MAR-2000; 2000US-0189259P.

PR 10-APR-2000; 2000US-0195899P.

PR 28-APR-2000; 2000US-0200419P.

PR 12-JUN-2000; 2000US-0210741P.

PR 21-AUG-2000; 2000US-0226760P.

PR 26-SEP-2000; 2000US-0235779P.

PR 20-OCT-2000; 2000US-0242343P.

✕

DT 26-MAR-2002 (first entry)
XX Human cDNA encoding alpha adrenergic receptor-like GPCR.
XX
XX
XX Human; ss: alpha adrenergic receptor; G protein-coupled receptor; GPCR;
KW peripheral nervous system disease; central nervous system disease;
KW urinary incontinence; benign prostatic hypertrophy; infection;
KW HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Tourette's syndrome.
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
FT 1..1527
FT CDS /tag= a
FT /product= "Alpha adrenergic receptor"
XX
XX MO200188126-A2.
XX
XX 22-NOV-2001.
XX
XX 11-MAY-2001; 2001MO-EP005383.
XX
XX 15-MAY-2000; 2000US-0204145P.
XX 04-DEC-2000; 2000US-0250505P.
XX
XX (FARB) BAYER AG.
XX
XX Ramakrishnan S;
XX
XX MPI; 2002-106124/14.
XX P-PSDB; AAU11764.
XX
XX New polynucleotide, useful for treating pain, cancer, Parkinson's
XX diseases, obesity, hypertension, asthma, schizophrenia, encodes an alpha
XX (1a) adrenergic receptor-like G-protein coupled receptor (GPCR).
XX
XX Claim 1; Fig 2; 123pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding an alpha
XX adrenergic receptor-like G-protein coupled receptor (GPCR) polypeptide,
XX the encoded polypeptide, fragments, derivatives and allelic variants.
XX Also include are an expression vector comprising the polynucleotide, a
XX host cell containing the vector, screening for therapeutic agents which
XX decrease or increase the activity of the receptor by binding a test agent
XX to the protein and determining whether the activity is decreased or
XX increased. A modulator of the receptor is useful for treating alpha
XX adrenergic receptor-like GPCR disorder such as peripheral or central
XX nervous system disease, urinary incontinence or benign prostatic
XX hypertrophy. The receptor, polynucleotide or modulator is useful for
XX treating disorders such as bacterial, fungal, protozoan, and viral
XX infections, particularly those caused by HIV (human immunodeficiency
XX virus), pain, cancer, anorexia, bulimia, asthma, Parkinson's diseases,
XX obesity, acute heart failure, hypertension, hypertension, urinary
XX retention, osteoporosis, angina pectoris, myocardial infarction, ulcer,
XX allergy, benign prostatic hypertrophy, and psychotic and neurological
XX disorders, including anxiety, schizophrenia, manic depression, delirium,
XX dementia, severe mental retardation, and dyskinesias, such as
XX Huntington's disease and Tourette's syndrome. The polynucleotide is
XX useful in diagnostic assays for detecting diseases and abnormalities or
XX susceptibility to disease and abnormalities related to the presence of
XX mutations in the gene. The protein is useful to identify test compounds
XX which may act as agonists or antagonists, and for raising antibodies
XX which can block the receptor and effectively prevent ligand binding. The
XX present sequence is the cDNA encoding the alpha adrenergic receptor-
XX like GPCR
XX
XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;
XX
XX

Alignment Scores:
Pred. No.: 1,786-243 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0
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DB 1 ATGACCTCCACCTGCACCAACAGCAGCGCGAGAGTAACAGCAGCAGCGTACGCGCC 60
QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleIleArgSerThrValIleVal 40
DB 61 CTCTCCAAATGCGCCATCAGCCCTGGCCCGCATCATCTCCGTCACCGCTGCTGTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleValIleValIleValIleValIle 60
DB 121 TTCCTGCGCGCTCTTTCCTGCGCAATAGTGTGCGCTGAGTGGTGGAGCGCGCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGCTGACAGGTGACCAACCGTTTATCTTAACTCTGCTGTCACCGACCTGCTGAC 240
QY 81 IleSerLeuValAlaProTyrValValAlaIleThrSerValProLeuPheTyrProLeu 100
DB 241 ATTTGCTGTGTGGCCCCCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisIleLeuPheAlaPheAlaSerVal 120
DB 301 AGCCACTTTCGACCGCCCTGTTTACCTTACCCACCTGTGCTTGGCCGAGCTCAAC 360
QY 121 ThrIleValIleValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGTGCTGTGTGTCAGTGTGTCATCTTGTCTCATCATCACCCTCTCTCTACCG 420
QY 141 SerIleMetThrGlnArgArgGlyTyrIleLeuLeuTyrGlyThrTyrIleValAlaIle 160
DB 421 TCCAAAGATACCAAGCGCGCGGTACCTGCTCTTACGCGACCTGCGATTTGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAspGluArgAsnAla 180
DB 481 CTGACAGACATCTCTCTCACTTACGCTGCGCGCGCGCTTGTGATGAGCGCAATGCT 540
QY 181 IleuCysSerMetIleTyrPylValAspProSerTyrThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGCGACGCCACACTACATATCTCAGCGTGGTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValValPheCysAlaAlaArg 220
DB 601 ATCGTCATTCACCTGATGTCTGATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValAspHisSerLeuGlnValArgValIleAsp 240
DB 661 AGCGACGATGCTCTGTGTGACATGTCAAGACACAGCTTGAAGTGGAGTCAAGAGAC 720
QY 241 CysValGluAsnGluAspGluGluGluValAlaGluTyrSlyGluGluIlePheGlnAspGluSer 260
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DB 781 GAGTTTCCGCGCGCACACATGAAGTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 281 AspGlySerLeuValAlaGluGluGluSerThrGlyThrSerGluSerSerValGluVal 300
DB 841 GACGGGAGCTTAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
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Qy 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
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Qy 361 AsnPheSerGluAspAspValGluValAlaAsnIleProGlnSerLeuProPheSerArg 380
Db 1081 AATTTCAGTGAAGATGAGGTCCAGGACAGTGAACATCCGAGAGCCTCCACCCAGTCGT 1140
Qy 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysAlaAlaLysVal 400
Db 1141 CGTACACAGCAACAGACCCCTCTGCCCCAGGTGCTACAGTGCACAAGCTGCTAAAGTG 1200
Qy 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
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Qy 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
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Qy 501 SerTyrAspSerAlaThrPhePro 508
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Job time : 634 secs

Db 121 TIVVSVDRYLSIIHPLSTPSKMTORRGYLLLYGTWIVAILOSTPPLVYGWGAAPDERNA 180
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Db 361 NFSEDDVAVNIPESLPSPRRNSNPNPLPRCYCKAKAVIIFISYVLSLGPYCFYAV 420
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Db 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 2

US-10-293-983-9

; Sequence 9, Application US/10293983
; Publication No. US20030149998A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Blatcher, Maria

; APPLICANT: Paulsen, Janet

; APPLICANT: Bates, Brian G

; TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Therefor

; FILE REFERENCE: AM100476

; CURRENT APPLICATION NUMBER: US/10/293,983

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-983-9

Query Match 100.0%; Score 2644; DB 4; Length 508;

Best Local Similarity 100.0%; Pred. No. 3e-182;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Qy 61 QLOVNTNFIFNLVLTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Db 61 QLOVNTNFIFNLVLTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSTPSKMTORRGYLLLYGTWIVAILOSTPPLVYGWGAAPDERNA 180
Db 121 TIVVSVDRYLSIIHPLSTPSKMTORRGYLLLYGTWIVAILOSTPPLVYGWGAAPDERNA 180
Qy 181 LCSMTMGASPSYTIILSVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Db 181 LCSMTMGASPSYTIILSVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Qy 241 CVENDEBGAKEKEFEPODESEFRROHEGEVAKKEGMEAKDGSLLAKEGSTGTSSSVEA 300
Db 241 CVENDEBGAKEKEFEPODESEFRROHEGEVAKKEGMEAKDGSLLAKEGSTGTSSSVEA 300
Qy 301 RGESEVRSSSTVASDGSMEGEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDI 360
Db 301 RGESEVRSSSTVASDGSMEGEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDI 360

Db 301 RGESEVRSSSTVASDGSMEGEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDI 360
Qy 361 NFSEDDVAVNIPESLPSPRRNSNPNPLPRCYCKAKAVIIFISYVLSLGPYCFYAV 420
Db 361 NFSEDDVAVNIPESLPSPRRNSNPNPLPRCYCKAKAVIIFISYVLSLGPYCFYAV 420
Qy 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEKPPK 480
Db 421 LAVWVDETQVPOWVITIIIMLFLOCCIHPPYVGYMKTIKKEIQDMLKKFCEKEKPPK 480
Qy 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 3

US-10-712-615-2

; Sequence 2, Application US/10712615

; Publication No. US20040214317A1

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGP8RMY8, EXPRESSED

; FILE REFERENCE: D0047A-CIP

; CURRENT APPLICATION NUMBER: US/10/712,615

; PRIOR FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: U.S. 09/992,238

; PRIOR FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: U.S. 60/248,285

; PRIOR FILING DATE: 2000-11-14

; PRIOR APPLICATION NUMBER: U.S. 60/268,581

; PRIOR FILING DATE: 2001-02-14

; PRIOR APPLICATION NUMBER: U.S. 60/308,285

; PRIOR FILING DATE: 2001-07-27

; PRIOR APPLICATION NUMBER: U.S. 60/317,166

; PRIOR FILING DATE: 2001-09-04

; NUMBER OF SEQ ID NOS: 134

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-712-615-2

Query Match 100.0%; Score 2644; DB 4; Length 508;

Best Local Similarity 100.0%; Pred. No. 3e-182;

Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Db 1 MTSTCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLOKRP 60
Qy 61 QLOVNTNFIFNLVLTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Db 61 QLOVNTNFIFNLVLTDLQISLVAPWVAVTSVPLFMPLNHFCTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSTPSKMTORRGYLLLYGTWIVAILOSTPPLVYGWGAAPDERNA 180
Db 121 TIVVSVDRYLSIIHPLSTPSKMTORRGYLLLYGTWIVAILOSTPPLVYGWGAAPDERNA 180
Qy 181 LCSMTMGASPSYTIILSVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Db 181 LCSMTMGASPSYTIILSVSVFIVIPLIWIMACYSVFCAARQHALLVNKRSLSEVRVD 240
Qy 241 CVENDEBGAKEKEFEPODESEFRROHEGEVAKKEGMEAKDGSLLAKEGSTGTSSSVEA 300
Db 241 CVENDEBGAKEKEFEPODESEFRROHEGEVAKKEGMEAKDGSLLAKEGSTGTSSSVEA 300
Qy 301 RGESEVRSSSTVASDGSMEGEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDI 360
Db 301 RGESEVRSSSTVASDGSMEGEGSTKVEENSMKADKGRTEVNQCSIDLGEDDMEFGEDI 360

QY 361 NSEDDVEAVNIPESLPSPRRNSNPNLPKCYOCAAAYVPIIIFSYLISGPGYCFNAV 420
| | | | |
DB 361 NSEDDVEAVNIPESLPSPRRNSNPNLPKCYOCAAAYVPIIIFSYLISGPGYCFNAV 420
QY 421 LAWVDVEVQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFFCEKPEPK 480
| | | | |
DB 421 LAWVDVEVQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFFCEKPEPK 480
QY 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
| | | | |
DB 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508

RESULT 4
US-10-505-486-131
; Sequence 131, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 131
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-131

Query Match 100.0%; Score 2644; DB 5; Length 746;
Best Local Similarity 100.0%; Pred. No. 4.9e-182;
Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTCTNSTRESNSSHCTCPKMPISLAHGIIIRSTVVIIFLAASFGNIVLALVLOKRP 60
| | | | |
DB 1 MSTCTNSTRESNSSHCTCPKMPISLAHGIIIRSTVVIIFLAASFGNIVLALVLOKRP 60
QY 61 QLLQVITNRFIFMLVITDLDQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
| | | | |
DB 61 QLLQVITNRFIFMLVITDLDQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSYSPKMTQRGYLLYGTVIIVAILQSTPPLVYGMQGAAPDERNA 180
| | | | |
DB 121 TIVLVSVDRLYSIIHPLSYSPKMTQRGYLLYGTVIIVAILQSTPPLVYGMQGAAPDERNA 180
QY 181 LCSMTWGSAPSTYIIISVVSFVIYPLIWMACYSVVFCARRQHALINYNKRSLEVRVD 240
| | | | |
DB 181 LCSMTWGSAPSTYIIISVVSFVIYPLIWMACYSVVFCARRQHALINYNKRSLEVRVD 240
QY 241 CVENEDDEGAKEKEEFRODESEFRROHEGEVKAKEGMEKADSLKXEGSTGTSSESSVA 300
| | | | |
DB 241 CVENEDDEGAKEKEEFRODESEFRROHEGEVKAKEGMEKADSLKXEGSTGTSSESSVA 300
QY 301 RSESEVRESSTVADSGMEKEGSTVEENSMKADKRTVEVNOCSIDLGEDMEFGEDDI 360
| | | | |
DB 301 RSESEVRESSTVADSGMEKEGSTVEENSMKADKRTVEVNOCSIDLGEDMEFGEDDI 360
QY 361 NSEDDVEAVNIPESLPSPRRNSNPNLPKCYOCAAAYVPIIIFSYLISGPGYCFNAV 420
| | | | |
DB 361 NSEDDVEAVNIPESLPSPRRNSNPNLPKCYOCAAAYVPIIIFSYLISGPGYCFNAV 420
QY 421 LAWVDVEVQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFFCEKPEPK 480
| | | | |
DB 421 LAWVDVEVQVQWVITIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKKEFFCEKPEPK 480
QY 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
| | | | |

DB 481 EDSHPDLPETEGTEGKIVPSYDSATFP 508
| | | | |

RESULT 5
US-09-791-932-112
; Sequence 112, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1el G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; PRIOR APPLICATION NUMBER: 2001-02-23
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-932-112

Query Match 99.9%; Score 2641; DB 3; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTCTNSTRESNSSHCTCPKMPISLAHGIIIRSTVVIIFLAASFGNIVLALVLOKRP 60
| | | | |
DB 1 MSTCTNSTRESNSSHCTCPKMPISLAHGIIIRSTVVIIFLAASFGNIVLALVLOKRP 60
QY 61 QLLQVITNRFIFMLVITDLDQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
| | | | |
DB 61 QLLQVITNRFIFMLVITDLDQISLVAPWVAVTSVPLFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVLVSVDRLYSIIHPLSYSPKMTQRGYLLYGTVIIVAILQSTPPLVYGMQGAAPDERNA 180
| | | | |

Db 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLELLYGTWIVAILQSTPPLVXGMOAFAEDERNA 180
Qy 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Db 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360
Qy 301 RGSSEVRESSTVADSGMEGKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGDDI 360
Db 301 RGSSEVRESSTVADSGMEGKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGDDI 360
Qy 361 NFSDEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Db 361 NFSDEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Qy 421 LAVWVDVETQVPOVWITIIIMLFLOCCIHPPYVGYMKHTIKKEIQDMLKKFCEKRPK 480
Db 421 LAVWVDVETQVPOVWITIIIMLFLOCCIHPPYVGYMKHTIKKEIQDMLKKFCEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 6
US-10-094-417-6

; Sequence 6, Application US/10094417
; Publication No. US20030045685A1

; GENERAL INFORMATION:

; APPLICANT: Tian, Hui

; APPLICANT: Zhao, Jiayang

; APPLICANT: Chen, Jin-long

; APPLICANT: Cutler, Gene

; APPLICANT: Tularek Inc.

; TITLE OF INVENTION: NO. US20030045685A1e1 Receptors

; FILE REFERENCE: 018781-008110US

; CURRENT APPLICATION NUMBER: US/10/094,417

; PRIOR FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: US 09/802,803

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: US 60/276,649

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 6

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36

; US-10-094-417-6

Query Match

Best Local Similarity 99.8%; Score 2641; DB 4; Length 508;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTNRFINLAVTDLQISLVAPMWVATSVPLFPLNSHFTALVSLTHLFAFASVN 120
Db 61 QLLQVTNRFINLAVTDLQISLVAPMWVATSVPLFPLNSHFTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLELLYGTWIVAILQSTPPLVXGMOAFAEDERNA 180
Db 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLELLYGTWIVAILQSTPPLVXGMOAFAEDERNA 180
Qy 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Db 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240

Db 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360
Qy 301 RGSSEVRESSTVADSGMEGKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGDDI 360
Db 301 RGSSEVRESSTVADSGMEGKEGSTKVEENSMKADKGRTEVNOCSIDLGEDMEFGDDI 360
Qy 361 NFSDEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Db 361 NFSDEDDVEAVNIPESLPPSRNNSNPPLPRCYCKAAKVIIFIIIFSIVLSLGPYCLAV 420
Qy 421 LAVWVDVETQVPOVWITIIIMLFLOCCIHPPYVGYMKHTIKKEIQDMLKKFCEKRPK 480
Db 421 LAVWVDVETQVPOVWITIIIMLFLOCCIHPPYVGYMKHTIKKEIQDMLKKFCEKRPK 480
Qy 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 7
US-10-345-332-2

; Sequence 2, Application US/10345332
; Publication No. US20030129705A1

; GENERAL INFORMATION:

; APPLICANT: Li et al.

; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED

; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR

; FILE REFERENCE: CL000754CON

; CURRENT APPLICATION NUMBER: US/10/345,332

; PRIOR FILING DATE: 2003-01-16

; PRIOR APPLICATION NUMBER: 09/769,741

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/205,166

; PRIOR FILING DATE: 2000-05-18

; PRIOR APPLICATION NUMBER: 09/638,018

; PRIOR FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PasteSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 508

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-345-332-2

Query Match

Best Local Similarity 99.8%; Score 2641; DB 4; Length 508;

Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSCTNSTRESNSHTCMPLSKMPISLAHGIIIRSTVIVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTNRFINLAVTDLQISLVAPMWVATSVPLFPLNSHFTALVSLTHLFAFASVN 120
Db 61 QLLQVTNRFINLAVTDLQISLVAPMWVATSVPLFPLNSHFTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLELLYGTWIVAILQSTPPLVXGMOAFAEDERNA 180
Db 121 TIVVSVDRYLSIIHPLSPSKMTQRGYLELLYGTWIVAILQSTPPLVXGMOAFAEDERNA 180
Qy 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Db 181 LCSMIMGASPSYTIISVVSFIVIPLIWIMACYSVVFCARROHALLNVKHSLEVRVKD 240
Qy 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360
Db 241 CVENDEBGAKEKEEFODESEFRROHGEVAKEGRMADKGRTEVNOCSIDLGEDMEFGDDI 360

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QY 301 RSESEVRESSTVASDGSMEGKSGTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RSESEVRESSTVASDGSMEGKSGTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NFESEDVEAVNPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
DB 361 NFESEDVEAVNPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
QY 421 LAWVVDVEVQVQWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKFFCKEKKPK 480
DB 421 LAWVVDVEVQVQWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKFFCKEKKPK 480
QY 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508

RESULT 8
US-10-088-726-21
; Sequence 21, Application US/10088726
; Publication No. US20030157558A1
; GENERAL INFORMATION:
; APPLICANT: Matsumoto et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AN
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088,726
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-088-726-21

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCPLSKMPLSLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCPLSKMPLSLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIFMLVTDLQISLVAPWVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIFMLVTDLQISLVAPWVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120
QY 121 TIVVSVVDYRLSIHPLSPSKMTQRGYLLLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
DB 121 TIVVSVVDYRLSIHPLSPSKMTQRGYLLLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
QY 181 LGSMTWGAASPSYTIISVSVFIVPLIWMIACYSVFCARROHALLVNNKRSLEVRVD 240
DB 181 LGSMTWGAASPSYTIISVSVFIVPLIWMIACYSVFCARROHALLVNNKRSLEVRVD 240
QY 241 CVENEDDEGABKEEFQDSEFRRQHEGVKAKEGMEAKDGLKAKEGSTGTSSSVYA 300
DB 241 CVENEDDEGABKEEFQDSEFRRQHEGVKAKEGMEAKDGLKAKEGSTGTSSSVYA 300
QY 301 RGSSEVRESSTVASDGSMEGKSGTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
DB 301 RGSSEVRESSTVASDGSMEGKSGTVEENSMKADGRTEVNOCSIDLGEDDMEFGEDDI 360
QY 361 NFESEDVEAVNPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
DB 361 NFESEDVEAVNPESLPPSRNSNSNPPLPRCYQCAAKVIFIIISYVLSLGPYCFLLAV 420
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QY 421 LAWVVDVEVQVQWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKFFCKEKKPK 480
DB 421 LAWVVDVEVQVQWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKFFCKEKKPK 480
QY 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508
DB 481 EDSHPDLPCTEGTEGKIIVPSYDSATFP 508

RESULT 9
US-10-321-807-16
; Sequence 16, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Rupong
; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: NO. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-16

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSSHCTCPLSKMPLSLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
DB 1 MTSTCTNSTRESNSSHCTCPLSKMPLSLAHGIIRSTVLVIFLAASFVGNIVLALVQRKP 60
QY 61 QLLQVTRNRFIFMLVTDLQISLVAPWVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120
DB 61 QLLQVTRNRFIFMLVTDLQISLVAPWVATSVPLFWPLNSHCTALVSLTHLFAFASVN 120
QY 121 TIVVSVVDYRLSIHPLSPSKMTQRGYLLLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
DB 121 TIVVSVVDYRLSIHPLSPSKMTQRGYLLLYGTWIVAILOSTPPLVYGMGAAPDERNA 180
QY 181 LGSMTWGAASPSYTIISVSVFIVPLIWMIACYSVFCARROHALLVNNKRSLEVRVD 240
DB 181 LGSMTWGAASPSYTIISVSVFIVPLIWMIACYSVFCARROHALLVNNKRSLEVRVD 240
QY 241 CVENEDDEGABKEEFQDSEFRRQHEGVKAKEGMEAKDGLKAKEGSTGTSSSVYA 300
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Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGLAKGSGTGTSSSEVEA 300
Qy 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Db 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Db 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 10
US-10-276-243-3
; Sequence 3, Application US/10276243
; Publication No. US20030187219A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN alpha1 ADRENERGIC RECEPTOR-LIKE G
; FILE REFERENCE: PROTEIN-COUPLED RECEPTOR
; CURRENT FILING DATE: 2002-11-14
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/250,505
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-243-3

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVA PWVATSVLPFWPLNSHFCALVSLTHLPAPASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVA PWVATSVLPFWPLNSHFCALVSLTHLPAPASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTORRGYLLYGTMIVAILQSTPPLVGMGQAADFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTORRGYLLYGTMIVAILQSTPPLVGMGQAADFDERNA 180
Qy 181 LCSMWGASPSYTIILSVSFIVIPLIWIAACYSVFCARRQHALLVNKRHSLERVYKD 240
Db 181 LCSMWGASPSYTIILSVSFIVIPLIWIAACYSVFCARRQHALLVNKRHSLERVYKD 240
Qy 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGLAKGSGTGTSSSEVEA 300
Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGLAKGSGTGTSSSEVEA 300
Qy 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Db 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Db 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420

Db 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 11
US-10-436-715-14
; Sequence 14, Application US/10436715
; Publication No. US20040018976A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; FILE REFERENCE: D0262 NP
; CURRENT FILING DATE: 2003-05-13
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-436-715-14

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSHTCMPISKMPISLAHGIIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTRNFIFNLVTDLQISLVA PWVATSVLPFWPLNSHFCALVSLTHLPAPASVN 120
Db 61 QLLQVTRNFIFNLVTDLQISLVA PWVATSVLPFWPLNSHFCALVSLTHLPAPASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTORRGYLLYGTMIVAILQSTPPLVGMGQAADFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTORRGYLLYGTMIVAILQSTPPLVGMGQAADFDERNA 180
Qy 181 LCSMWGASPSYTIILSVSFIVIPLIWIAACYSVFCARRQHALLVNKRHSLERVYKD 240
Db 181 LCSMWGASPSYTIILSVSFIVIPLIWIAACYSVFCARRQHALLVNKRHSLERVYKD 240
Qy 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGLAKGSGTGTSSSEVEA 300
Db 241 CVENDEGAKEKEFEODESEFRQHEGEVAKKEGRMEAKDGLAKGSGTGTSSSEVEA 300
Qy 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Db 301 RGSSEVRESSTVASDGSMEGKEGSTKVEENSMKADKRTENVQCSIDLGEDDMEFGEDDI 360
Qy 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Db 361 NFSEDDVEAVNIPESLPPSRNSNSNPPLPRCYCKAKAKVFIIFISYVLSLGPYCFPLAV 420
Qy 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Db 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPRVYVGYMHKTIKKEIOMLKKPFCKEKPRK 480
Qy 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 12
US-10-343-650A-90
; Sequence 90, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-343-650A-90

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182; Indels 0; Gaps 0;
Matches 507; Conservative 1; Mismatches 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPLSLAHGIIRSTVLVIPLAASFGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPLSKMPLSLAHGIIRSTVLVIPLAASFGNIVLALVLRKP 60
QY 61 QLLQVTRNRFIPLVLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFAPASVN 120
DB 61 QLLQVTRNRFIPLVLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFAPASVN 120
QY 121 TIVVSVDRYLSIHPILSPSKMQRGGLLYGTWIVAILLOSTPPLVYGMGOAAFDERNA 180
DB 121 TIVVSVDRYLSIHPILSPSKMQRGGLLYGTWIVAILLOSTPPLVYGMGOAAFDERNA 180
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARROHALLVNVKRSLEVRVD 240
DB 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARROHALLVNVKRSLEVRVD 240
QY 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVBA 300
DB 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVBA 300
QY 301 RSESEVRRESSTVASDGSMEGKSGSTKVEBNSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
DB 301 RSESEVRRESSTVASDGSMEGKSGSTKVEBNSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
QY 361 NSESDDEAVANIPESLPERSRNSNSNPPLPRCYOCAAIVIFIIIFSIVLSIGPYCFLAV 420
DB 361 NSESDDEAVANIPESLPERSRNSNSNPPLPRCYOCAAIVIFIIIFSIVLSIGPYCFLAV 420
QY 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKKEFCCKEPPK 480
DB 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKKEFCCKEPPK 480
QY 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 13

US-10-321-807-16
; Sequence 16, Application US/10321807
; Publication No. US20040137563A9
; GENERAL INFORMATION:

; APPLICANT: Dang, Huong T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Human G Protein-Coupled Receptors

; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-321-807-16

Query Match 99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182; Indels 0; Gaps 0;
Matches 507; Conservative 1; Mismatches 0;

QY 1 MTSTCTNSTRESNSSHTCMPLSKMPLSLAHGIIRSTVLVIPLAASFGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSSHTCMPLSKMPLSLAHGIIRSTVLVIPLAASFGNIVLALVLRKP 60
QY 61 QLLQVTRNRFIPLVLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFAPASVN 120
DB 61 QLLQVTRNRFIPLVLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCALVSLTLFAPASVN 120
QY 121 TIVVSVDRYLSIHPILSPSKMQRGGLLYGTWIVAILLOSTPPLVYGMGOAAFDERNA 180
DB 121 TIVVSVDRYLSIHPILSPSKMQRGGLLYGTWIVAILLOSTPPLVYGMGOAAFDERNA 180
QY 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARROHALLVNVKRSLEVRVD 240
DB 181 LCSMTWGAASPSYTIISVSVFIVPLIWMACYSVFCARROHALLVNVKRSLEVRVD 240
QY 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVBA 300
DB 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKEGSTGTSSESVBA 300
QY 301 RSESEVRRESSTVASDGSMEGKSGSTKVEBNSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
DB 301 RSESEVRRESSTVASDGSMEGKSGSTKVEBNSMKADKGRTEVNOCSIDLGEDMEFGEEDI 360
QY 361 NSESDDEAVANIPESLPERSRNSNSNPPLPRCYOCAAIVIFIIIFSIVLSIGPYCFLAV 420
DB 361 NSESDDEAVANIPESLPERSRNSNSNPPLPRCYOCAAIVIFIIIFSIVLSIGPYCFLAV 420
QY 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKKEFCCKEPPK 480
DB 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIVYGYMHTIKKEIODMLKKEFCCKEPPK 480
QY 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSDPDLPGTEGTEGKIVPSYDSATFP 508

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RESULT 14
US-10-314-048A-16
; Sequence 16, Application US/10314048A
; Publication No. US20040142377A1
; GENERAL INFORMATION:
; APPLICANT: Unetel, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22.US6.CIP
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-048A-16

Query Match          99.9%; Score 2641; DB 4; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182; Indels 0; Gaps 0;
Matches 507; Conservative 1; Mismatches 0;

Qy 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTNRFIFNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCIALVSLTHLFAFASVN 120
Db 61 QLLQVTNRFIFNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCIALVSLTHLFAFASVN 120
Qy 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Db 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Qy 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Db 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
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Db 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Qy 241 CVENDEGAEKKEFEODESEFRROHEGEVAKKEGRMEAKDGLAKKEGSTGTSSSVEA 300
Db 241 CVENDEGAEKKEFEODESEFRROHEGEVAKKEGRMEAKDGLAKKEGSTGTSSSVEA 300
Qy 241 CVENDEGAEKKEFEODESEFRROHEGEVAKKEGRMEAKDGLAKKEGSTGTSSSVEA 300
Db 241 CVENDEGAEKKEFEODESEFRROHEGEVAKKEGRMEAKDGLAKKEGSTGTSSSVEA 300
Qy 301 RGSSEVRSSSTVASTGSMWEGKSTKVENSMKAKGRTEVNVOCSIDLGEDDMEGEEDI 360
Db 301 RGSSEVRSSSTVASTGSMWEGKSTKVENSMKAKGRTEVNVOCSIDLGEDDMEGEEDI 360
Qy 301 RGSSEVRSSSTVASTGSMWEGKSTKVENSMKAKGRTEVNVOCSIDLGEDDMEGEEDI 360
Db 301 RGSSEVRSSSTVASTGSMWEGKSTKVENSMKAKGRTEVNVOCSIDLGEDDMEGEEDI 360
Qy 361 NFSEDDVAVNIPESLPBSRRNSNPPLPRCYOCKAAKAVIFIIIFSYVLSLGPYCFILAV 420
Db 361 NFSEDDVAVNIPESLPBSRRNSNPPLPRCYOCKAAKAVIFIIIFSYVLSLGPYCFILAV 420
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Qy 421 LAWVVDVETQVPOWVITIIILWLFLOCCIHRYVYGVNKHKTKEIOMLKKFCKEKP 480
Db 421 LAWVVDVETQVPOWVITIIILWLFLOCCIHRYVYGVNKHKTKEIOMLKKFCKEKP 480
Qy 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 15
US-10-897-815-16
; Sequence 16, Application US/10897815
; Publication No. US20050004178A1
; GENERAL INFORMATION:
; APPLICANT: Unetel, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22.US6.CIP
; CURRENT FILING DATE: 2004-07-23
; PRIOR APPLICATION NUMBER: US/10/314,048
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-897-815-16

Query Match          99.9%; Score 2641; DB 5; Length 508;
Best Local Similarity 99.8%; Pred. No. 5e-182; Indels 0; Gaps 0;
Matches 507; Conservative 1; Mismatches 0;

Qy 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Db 1 MTSTCTNSTRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLRKP 60
Qy 61 QLLQVTNRFIFNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCIALVSLTHLFAFASVN 120
Db 61 QLLQVTNRFIFNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFCIALVSLTHLFAFASVN 120
Qy 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Db 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Qy 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Db 121 TIVVSVVRYSIIHPLSPSKMQRGVLILGYTWIVAILIOSTPPLVGMGOAFADERNA 180
Qy 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Db 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Qy 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Db 181 LCSMWGASPSYTIISVVSFIVIPLIWIMACYSVFCAARQHALLVNKKHSLSEVRVYD 240
Qy 241 CVENDEGAEKKEFEODESEFRROHEGEVAKKEGRMEAKDGLAKKEGSTGTSSSVEA 300
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Db	241	CVENEDBEGAERKEEFQDESEFRROHGEVKAKEGRMEAKDGLKAKEGSGTGTSSSVYA	300
Qy	301	RGSEEVRESSIVASDGSMEKEGSTYVENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI	360
Db	301	RGSEEVRESSIVASDGSMEKEGSTYVENSMKADKGRTEVNQCSIDLGEDDMEFGEDDI	360
Qy	361	NFSEDDVEAVNIPESLPFSRRNSNSNPPLPRCYCKAKAVIFIIIPSYVLSLGPYCFLAV	420
Db	361	NFSEDDVEAVNIPESLPFSRRNSNSNPPLPRCYCKAKAVIFIIIPSYVLSLGPYCFLAV	420
Qy	421	LAVWVDETQVPOWVTTIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKEFCCKEKPX	480
Db	421	LAVWVDETQVPOWVTTIIIMLFLOCCIHPPYVGYMHTIKKEIODMLKEFCCKEKPX	480
Qy	481	EDSHPDLPSTEGTCKIVPSYDSATFP	508
Db	481	EDSHPDLPSTEGTCKIVPSYDSATFP	508

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Job time : 136.35 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:25:56 ; Search time 38.1 Seconds

(without alignments)
1102.342 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
3: /cgn2_6/prodata/1/1aa/H COMB.pep:*
4: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:*
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6: /cgn2_6/prodata/1/1aa/backfills.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2641	99.9	508	US-10-314-048A-16	Sequence 16, Appl
2	2641	99.9	926	US-10-314-048A-104	Sequence 104, App
3	2636	99.7	508	US-10-314-048A-92	Sequence 92, Appl
4	391	14.8	407	US-09-364-425B-23	Sequence 23, Appl
5	388.5	14.7	454	US-08-748-485-1	Sequence 1, Appl
6	371	14.0	529	US-08-467-568-2	Sequence 2, Appl
7	371	14.0	529	US-09-030-582-2	Sequence 2, Appl
8	371	14.0	529	PCT-US94-09051-2	Sequence 2, Appl
9	343.5	13.0	422	US-07-817-920-3	Sequence 3, Appl
10	343.5	13.0	422	US-08-370-542-3	Sequence 3, Appl
11	343.5	13.0	422	US-08-117-006-3	Sequence 3, Appl
12	343.5	13.0	422	US-08-216-594-3	Sequence 3, Appl
13	343.5	13.0	422	US-08-542-358-3	Sequence 3, Appl
14	343.5	13.0	422	US-08-157-185-13	Sequence 13, Appl
15	343.5	13.0	422	US-08-281-526B-13	Sequence 13, Appl
16	343.5	13.0	422	US-09-018-351-3	Sequence 3, Appl
17	343.5	13.0	422	US-09-332-837-13	Sequence 13, Appl
18	343.5	13.0	422	PCT-US93-00149-3	Sequence 3, Appl
19	340.5	12.9	422	US-09-341-446B-10	Sequence 10, Appl
20	338.5	12.8	466	US-08-334-698-6	Sequence 6, Appl
21	338.5	12.8	466	US-08-228-932-6	Sequence 6, Appl
22	338.5	12.8	466	US-08-468-939-6	Sequence 6, Appl
23	338.5	12.8	466	US-08-722-001-28	Sequence 28, Appl
24	338.5	12.8	466	US-08-406-855A-6	Sequence 6, Appl
25	338.5	12.8	466	US-08-722-190-6	Sequence 6, Appl
26	338.5	12.8	466	US-08-244-354-6	Sequence 6, Appl
27	338.5	12.8	466	US-09-206-899-6	Sequence 6, Appl

28	338.5	12.8	466	2	US-09-444-783-6	Sequence 6, Appl
29	338.5	12.8	466	2	US-09-688-415-6	Sequence 6, Appl
30	338.5	12.8	466	2	US-09-444-783-6	Sequence 6, Appl
31	338.5	12.8	466	4	PCT-US95-04203-6	Sequence 6, Appl
32	333.5	12.6	429	1	US-08-748-485-7	Sequence 7, Appl
33	333.5	12.6	429	2	US-09-919-039-6	Sequence 6, Appl
34	333.5	12.6	466	1	US-08-722-001-12	Sequence 12, Appl
35	333.5	12.6	466	1	US-08-467-568-11	Sequence 11, Appl
36	333.5	12.6	466	1	US-09-030-582-11	Sequence 11, Appl
37	328	12.4	421	2	US-09-450-790A-13	Sequence 13, Appl
38	325.5	12.3	466	2	US-09-688-415-11	Sequence 11, Appl
39	324.5	12.3	466	2	US-08-406-855A-23	Sequence 23, Appl
40	324.5	12.3	466	2	US-09-206-899-23	Sequence 23, Appl
41	324	12.3	421	2	US-09-826-509-425	Sequence 425, App
42	314.5	11.9	501	1	US-08-722-001-14	Sequence 14, Appl
43	314.5	11.9	501	1	US-08-467-568-9	Sequence 9, Appl
44	314.5	11.9	501	1	US-09-030-582-9	Sequence 9, Appl
45	314.5	11.9	572	1	US-08-334-698-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-10-314-048A-16
; Sequence 16, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unetec, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22 US 6 CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-048A-16

Query Match      99.9%; Score 2641; DB 2; Length 508;
Best Local Similarity 99.8%; Pred. No. 2.6e-205;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTSTCTNSRESNSSHTCMPLSKMPISLAHGIRSTVIVIFLAASFVGVIVATLVQRKP 60
        |||||||
DB      1 MTSTCTNSRESNSSHTCMPLSKMPISLAHGIRSTVIVIFLAASFVGVIVATLVQRKP 60
QY      61 QLTQVTRRFIFMLVLTDLQISLVAPVWVATSVPLFWPLNSHFCRTALVSLTHLFAFASVN 120
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Db 61 QLVQVTRFIFNLVLTDLQISLVAPWVATSVLPFLNSHFCTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVPLIYMIACYSVVFCAARQHALLVNVKHSLEVRVKD 240
Db 181 LCSMWGASPSYTIISVSVFIVPLIYMIACYSVVFCAARQHALLVNVKHSLEVRVKD 240
Qy 241 CVENDEEGAEKKEEFQDESEFRQHEGEVYAKEGRMEAKDGLKAKEGSTGTSSESVYA 300
Db 241 CVENDEEGAEKKEEFQDESEFRQHEGEVYAKEGRMEAKDGLKAKEGSTGTSSESVYA 300
Qy 301 RGSEVRRESSVYASDGSMEGEGSTKYBENSMDKDKRTENVQCSIDLGEDMFEGBDDI 360
Db 301 RGSEVRRESSVYASDGSMEGEGSTKYBENSMDKDKRTENVQCSIDLGEDMFEGBDDI 360
Qy 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYCKAKAVFIIFISYVLSLGPYCFLAY 420
Db 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYCKAKAVFIIFISYVLSLGPYCFLAY 420
Qy 421 LAVWVDETQVQWVITIIIMLFLOCCIHBYVGYMKTIKKEIQDMLKKXFCCKEKPX 480
Db 421 LAVWVDETQVQWVITIIIMLFLOCCIHBYVGYMKTIKKEIQDMLKKXFCCKEKPX 480
Qy 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
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RESULT 2
US-10-314-048A-104
; Sequence 104, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 104
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Homo sapiens and Rat
US-10-314-048A-104
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Query Match 99.9%; Score 2641; DB 2; Length 926;
Best Local Similarity 99.8%; Pred. No. 5,56-205;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1
1 MTCTCTNSTRESSNSHTCMPLSKMPIISLHGIIIRSTVLVIFLASPVGNIVLAVLQRP 60
1 MTCTCTNSTRESSNSHTCMPLSKMPIISLHGIIIRSTVLVIFLASPVGNIVLAVLQRP 60
Db 1 MTCTCTNSTRESSNSHTCMPLSKMPIISLHGIIIRSTVLVIFLASPVGNIVLAVLQRP 60
Qy 61 QLVQVTRFIFNLVLTDLQISLVAPWVATSVLPFLNSHFCTALVSLTHLFAFASVN 120
Db 61 QLVQVTRFIFNLVLTDLQISLVAPWVATSVLPFLNSHFCTALVSLTHLFAFASVN 120
Qy 121 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRRGYLLYGTWIVAILQSTPPLYGWQAAFDERNA 180
Qy 181 LCSMWGASPSYTIISVSVFIVPLIYMIACYSVVFCAARQHALLVNVKHSLEVRVKD 240
Db 181 LCSMWGASPSYTIISVSVFIVPLIYMIACYSVVFCAARQHALLVNVKHSLEVRVKD 240
Qy 241 CVENDEEGAEKKEEFQDESEFRQHEGEVYAKEGRMEAKDGLKAKEGSTGTSSESVYA 300
Db 241 CVENDEEGAEKKEEFQDESEFRQHEGEVYAKEGRMEAKDGLKAKEGSTGTSSESVYA 300
Qy 301 RGSEVRRESSVYASDGSMEGEGSTKYBENSMDKDKRTENVQCSIDLGEDMFEGBDDI 360
Db 301 RGSEVRRESSVYASDGSMEGEGSTKYBENSMDKDKRTENVQCSIDLGEDMFEGBDDI 360
Qy 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYCKAKAVFIIFISYVLSLGPYCFLAY 420
Db 361 NFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYCKAKAVFIIFISYVLSLGPYCFLAY 420
Qy 421 LAVWVDETQVQWVITIIIMLFLOCCIHBYVGYMKTIKKEIQDMLKKXFCCKEKPX 480
Db 421 LAVWVDETQVQWVITIIIMLFLOCCIHBYVGYMKTIKKEIQDMLKKXFCCKEKPX 480
Qy 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIYPSYDSATFP 508
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RESULT 3
US-10-314-048A-92
; Sequence 92, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
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/ PRIOR FILING DATE: 2002-09-13
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 92
/ LENGTH: 508
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-314-048A-92

Query Match 99.7%; Score 2636; DB 2; Length 508;
Best Local Similarity 99.6%; Pred. No. 6,5e-205;
Matches 506; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSTCNSTRESNSSHCHMPISLKHGIIRSTLVITPLAASFGNIVLALVQRP 60
DB 1 MTSTCNSTRESNSSHCHMPISLKHGIIRSTLVITPLAASFGNIVLALVQRP 60
QY 61 QLLQVTNRFTLNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 61 QLLQVTNRFTLNLVTDLLQISLVAPWVAVTSVPLFWPLNSHFTALVSLTHLFAFASVN 120
QY 121 TLVAVSVDRYLSIHLSPSKMKTORGVLILYGTWIVALLQSTPPLVGMGAAPDERNA 180
DB 121 TLVAVSVDRYLSIHLSPSKMKTORGVLILYGTWIVALLQSTPPLVGMGAAPDERNA 180
QY 181 LCSMIGASPSYTIISVGFIVPLIVMIACYSVFCARQHALYNKRSLERVRD 240
DB 181 LCSMIGASPSYTIISVGFIVPLIVMIACYSVFCARQHALYNKRSLERVRD 240
QY 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKESGTGTSSESVRA 300
DB 241 CVENEDDEGAKEKEEFODESEFRROHEGEVKAKEGMEAKDGLKAKESGTGTSSESVRA 300
QY 301 RSESEPRESTYASDGSMEGKSGSTVENSMKADRGREVNOCSDLDGEDMEFEEDDI 360
DB 301 RSESEPRESTYASDGSMEGKSGSTVENSMKADRGREVNOCSDLDGEDMEFEEDDI 360
QY 361 NSESDDEAVNIIPESLPPSRNSNPNP.PRCYQCAKAVIFIIISYVLSIGPYCEFLAV 420
DB 361 NSESDDEAVNIIPESLPPSRNSNPNP.PRCYQCAKAVIFIIISYVLSIGPYCEFLAV 420
QY 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIYVYGMAHTIKKEIDMDLKEFECKEPPK 480
DB 421 LAWVVDVETQVPOWVITIIIMLFLOCCIHPIYVYGMAHTIKKEIDMDLKEFECKEPPK 480
QY 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIIVSYDSATFP 508

RESULT 4
US-09-364-425B-23
/ Sequence 23, Application US/09364425B
/ Patent No. 6653086
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Chen, Ruoping
/ TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-coupled Orphan Receptor
/ FILE REFERENCE: Arent0047
/ CURRENT APPLICATION NUMBER: US/09/364,425B
/ CURRENT FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: 60/094,879
/ PRIOR FILING DATE: 1998-07-31
/ PRIOR APPLICATION NUMBER: 60/106,300
/ PRIOR FILING DATE: 1998-10-30
/ PRIOR APPLICATION NUMBER: 60/110,906
/ PRIOR FILING DATE: 1998-12-04
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26

/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 23
/ LENGTH: 407
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-364-425B-23

Query Match 14.8%; Score 391; DB 2; Length 407;
Best Local Similarity 23.6%; Pred. No. 1.5e-23;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

QY 31 GIIRSTVIVIFLAASFV--GNIVLALVLRKQFOLLQVNRFTLNLVTDLLQISLVAPW 88
DB 25 GVITFOFALIVITIFVCLGNLIVITLYKKSYYLLTNSKFVFSITLSNFIPLSVLPLPV 84
QY 89 VATSVPLFWPLNSHFTALVSLTHLFAFASVTVIVSVDRYLSIHLSPSKMKTORG 148
DB 85 VTSSIRREWIFGVWNCPSALLYLLISSASMLTLGVIAIDRYAVAVLPVVPKKTGNRA 144
QY 149 YLLYGTWIVALLQSTPPLVGMGAAPDERNALCSMIGASPSYTIISVGFIVPLIVM 208
DB 145 VVALVYIMLSLIGCLPLPGMSVFEDEFKMCMVAAMHREGTAFMQIWALFPLVYM 204
QY 209 IACYSVFCARQHALYNKRSLERVRDQVENEDEGAKEKEEFODESEFRROHEG 268
DB 205 LVYCGFIRVAR-----VKARKHCGTVIVIE-EDAQ----- 235
QY 269 EVKAKEGMEAKDGLKAKESGTGTSSESVKARGSEEVRESSTVYASDGSMEGKSGTKVE 328
DB 236 ---RTGR-----KNSSTSTSSSG----- 250
QY 329 ENSMKADRGREVNOCSDLDGEDMEFEEDDIINSESDDEAVNIIPESLPPSRNS----- 383
DB 251 -----SRNAFQGV 260
QY 384 -NSNPPLPCYQCAKAVIFIIISYVLSIGPY-CFLAVLAW--VDVETQVPOWVITII 439
DB 261 YSAN-----QCKALITLIVLGNFMVTGWGVVIVASEALMGSSVSPSLETA----- 309
QY 440 IMLFLOCCIHPIYVYGMAHTIKKEIDMDLKEFECKEPPK 468
DB 310 TWLSFASAVCHPLIYGLMKNKTIVRKEILLGM 338

RESULT 5
US-08-748-485-1
/ Sequence 1, Application US/08748485
/ Patent No. 5817480
/ GENERAL INFORMATION:
/ APPLICANT: Au-Young, Janice
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Goli, Surya K.
/ APPLICANT: Murty, Luyun E.
/ TITLE OF INVENTION: NOVEL HISTAMINE H2 RECEPTOR
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCTE PHARMACEUTICALS, INC.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/748,485
/ FILING DATE: Herewith
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0159 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Consensus
; CLONE: 1722180
;
; US-08-748-485-1

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Query Match      14.7%; Score 388.5; DB 1; Length 454;
Best Local Similarity 22.9%; Pred. No. 2.8e-23;
Matches 103; Conservative 72; Mismatches 129; Indels 145; Gaps 10;

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QY 31 GIINSTVLVIFLAASFV--GNIVLALVLQKFPOLLQVTRFTFNLLVTDLQISLVAPMV 88
DB 25 GIIITFOAIIVITTFVCLGNLVIVTVLYKSKYLLTSLNKFVFSLLSFLSLVLPFV 84
QY 89 VATSVLPMPNLNHSHTCLVSLTHLPFASVTVLVSVDRSLTIHPLSPSKMTQRG 148
DB 85 VTSSIRREWIFGVVWGNFSALYLLISASMLTGLVIALDRYAVLVPMVYPMKLTGNRA 144
QY 149 YLLVGTIVAILQSTPPLYGWGOAFDERNALCSMINGASPSYITLVSFTVPLIYV 208
DB 145 VMALYYIYVLSLIGCLPPLFGWSSVPEDFKMKCAAHMREBGYAFQIMCALPPLVM 204
QY 209 IACISVVFCAARQHALLYNVKHSLEVRVKDCVENEDEGAKEEFPQDESEFRQHEG 268
DB 205 LVCTYFIFRVAR----- 216
QY 269 EVKAEKGMKADKSLKAKEGSTGTSESVKRGSEVRESESTVASDGSMEKSGSTKVE 328
DB 217 -VKAR-----KVNCGTVVVEEDAQGTG---VKNSSTSTSS----- 250
QY 329 ENSMKADKRGTEVNOCSIDLGEDDMEFGEDINFSEDVEAVNIPESLPPSRNS----- 383
DB 251 -----GSRNAPQGV 261
QY 384 -NSNPPLRCYQCKAKAVIFIIIFSYVLSLGPY-CFLAVLAVM--VDVETQVPOWVITTI 439
DB 262 YSAN-----QCKALITILVLVLAGPMVWGPYVNVVIASEALMGKSVSPSLETWA----- 310
QY 440 IMLPFLQCCIHPPYVVGVMHKTIKKEIQDM 468
DB 311 TWLSPASAVCHPLIYGLMKNKTIVKELGM 339

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RESULT 6
US-08-467-568-2
; Sequence 2, Application US/08467568
; Patent No. 5817477
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
; ADDRESS: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
;
;
;

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; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,568
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-324
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
; US-08-467-568-2

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Query Match      14.0%; Score 371; DB 1; Length 529;
Best Local Similarity 23.1%; Pred. No. 8.9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;

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QY 6 TNSRE-----SNSHTCMPLSKMPSISLHGIIINSTVLVIFLAASFVNIVLALVLRKP 60
DB 14 SNLVEEGEGEASSPSSPSLSP-----FLSA--WGNLVIVTVLYKKS 56
QY 61 QLVQVTRFIFNLVTDLQISLVAPMVVATSVPLFPLNHSFCTALVSLTHLPFASVN 120
DB 57 YLITLSNKFVSLTSLNLSLVLPFYVTSIRREHIFGVVWGNFSALYLLISASML 116
QY 121 TIVLVSDRYLSIHPISYPSKMTQRGYYLLVGTWIVAILQSTPPLYGWGOAFDERNA 180
DB 117 TLGVIALDRYVAVLVPMYPMKLTGNRAVMALVYIMLSLIGCLPPLFGWSSVEYGENKW 176
QY 181 LCSMTWGSPSYITLVSFTVPLIYVIACTSVVFCAARQHALLYNVKHSLEVRKXD 240
DB 177 MCVAAHREPYTAFWQIMCALPFLVWLVCYGFIFRVAR-----VKARKVHCGTV 228
QY 241 CVENEDEGAKKEEFPQDESEFRQHEGEVAKEGMEAKDGLKAKEGSTGTSESVYA 300
DB 229 IVE-EDAQ-----RTGR-----KNISSTSS----- 249
QY 301 RGSSEVRESESTVASDGSMEKSGSTKVEENSMKADKRGTEVNOCSIDLGEDDMEFGEDDI 360
DB 250 -----GR----- 251
QY 361 NFSEDVEAVNIPESLPPSRNS-----NSNPPLRCYQCKAKAVIFIIIFSYVLSLGP 414
DB 252 -----RRNAFGVVYSAN-----QCKALITILVLVLAGPMVWGP 285
QY 415 Y-CFLAVLAVM--VDVETQVPOWVITTIIMLPFLQCCIHPPYVVGVMHKTIKKEIQDM 468
DB 286 YMWVIASEALMGKSVSPSLETWA-----TWLSPASAVCHPLIYGLMKNKTIVKELGM 338

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RESULT 7
US-09-030-582-2
; Sequence 2, Application US/09030582
; Patent No. 5994506
; GENERAL INFORMATION:
; APPLICANT: SOPPET, DANIEL R
; TITLE OF INVENTION: ADRENERGIC RECEPTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Giffillan, Cecchi,
; ADDRESS: Stewart & Olstein
;
;
;

```

STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,582
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-324
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-030-582-2

Query Match 14.0%; Score 371; DB 1; Length 529;
Best Local Similarity 23.1%; Pred. No. 8,9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;
QY 6 TNSTRE-----SNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFGNIVLALVLRKP 60
DB 14 SNTLEEKGEGASSPSSPSLSSP-----FLSA--WGNLVIVTLTKKS 56
QY 61 QLLQVTRNFIENLVTDLQISLVAPWVYATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 57 YLLTISNKFVPSLTLNLFSLVLPVVTSSIREMIFGVWCMFSAALLYLISASWL 116
QY 121 TIVLVSVDRIYLIHPLSPSKMTORRGYLLXGTWIVAILOSTPPLYGMOGAADPERNA 180
DB 117 TLGVIAIDRYAVLIPMYIPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKM 176
QY 181 LCSMTWGPSYTYILSVSFIVIPLIWMIACYSVFCARQHALLVNKRHSLEVRVD 240
DB 177 MCVAAWHREPGYTAAWQICALFPLVMLVCYGFIFRVAR-----VKARKVHCITV 228
QY 241 CVENDEBGAKEKEFEODESEFRROHGEVKAKEGMEAKDGLKAKGSGTSSSVYA 300
DB 229 IVE-BDAQ-----RTGR-----KNSSTSSS----- 249
QY 301 RGSSEVRSSSTVASDGSMEKGSGTKVEENSMKADKGRTEVNQCSIDLGEDMGEDEDI 360
DB 230 -----GR----- 251
QY 361 NFESEDDVEAVNIPESLPSRRNS-----NSNPPLPRCYQCKAKAVIPIIFSYVLSGP 414
DB 252 -----RRNAFGVVYSAN-----QCKALLITILVVLGAFMVTWCP 285
QY 415 Y-CFLAVLAVW--VDVETQVPOWVITIIWLFLOCCIHPIYVYGWYMKTIKKEIDM 468
DB 286 YWVVIASEALMGKSSVSPSLSTWA-----TWLSFASAVCHPLIYIGLMNKTKVRKELGM 338

RESULT 8
PCT-US94-09051-2
; Sequence 2, Application PC/TUS9409051
; GENERAL INFORMATION:

APPLICANT: LI, ET AL.
TITLE OF INVENTION: Adrenergic Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09051
FILING DATE: Submitted herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
PCT-US94-09051-2

Query Match 14.0%; Score 371; DB 4; Length 529;
Best Local Similarity 23.1%; Pred. No. 8,9e-22;
Matches 110; Conservative 69; Mismatches 132; Indels 166; Gaps 14;
QY 6 TNSTRE-----SNSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFGNIVLALVLRKP 60
DB 14 SNTLEEKGEGASSPSSPSLSSP-----FLSA--WGNLVIVTLTKKS 56
QY 61 QLLQVTRNFIENLVTDLQISLVAPWVYATSVPLFWPLNSHFTALVSLTHLFAFASVN 120
DB 57 YLLTISNKFVPSLTLNLFSLVLPVVTSSIREMIFGVWCMFSAALLYLISASWL 116
QY 121 TIVLVSVDRIYLIHPLSPSKMTORRGYLLXGTWIVAILOSTPPLYGMOGAADPERNA 180
DB 117 TLGVIAIDRYAVLIPMYIPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSSVEYGENKM 176
QY 181 LCSMTWGPSYTYILSVSFIVIPLIWMIACYSVFCARQHALLVNKRHSLEVRVD 240
DB 177 MCVAAWHREPGYTAAWQICALFPLVMLVCYGFIFRVAR-----VKARKVHCITV 228
QY 241 CVENDEBGAKEKEFEODESEFRROHGEVKAKEGMEAKDGLKAKGSGTSSSVYA 300
DB 229 IVE-BDAQ-----RTGR-----KNSSTSSS----- 249
QY 301 RGSSEVRSSSTVASDGSMEKGSGTKVEENSMKADKGRTEVNQCSIDLGEDMGEDEDI 360
DB 250 -----GR----- 251
QY 361 NFESEDDVEAVNIPESLPSRRNS-----NSNPPLPRCYQCKAKAVIPIIFSYVLSGP 414
DB 252 -----RRNAFGVVYSAN-----QCKALLITILVVLGAFMVTWCP 285
QY 415 Y-CFLAVLAVW--VDVETQVPOWVITIIWLFLOCCIHPIYVYGWYMKTIKKEIDM 468


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Db      31 VVTSYQVITSLTGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLWVSVL 88
      84 VAPMVAVTSVPLFPLNHSFCTALVSLTHLPAPASVNTVLVSVDRLYSIIHPLSPSKM 143
      89 VLPMAALYQVNLKMTLGOVTCDFIALDVLCTCTSIHLCAIALDRYMAITDPIDYVNRK 148
Qy      144 TORRGVLLYGTWIVAILOSTPPLVGMGOAFDERNALCSMIMGASPSYTIISVVSFIYI 203
      149 TRRRAAALISLTWILGFLISIPMLGMTRP--EDRSDPACTISKDHGTTIYSTGCAFYI 206
Db      204 PLIWIACSVVFCARQHALLYNKRSLVRVDCVENEDEBGAEKKEFODESEFR 263
      207 PLLMLVLVYGRIFRAR-----FRIRKTYKKVKEKTGADTRHGASPAPOK 251
Qy      264 ROHEBEVAKKEGRM--EAKDGL-----KAKGSGTSSSEVSEARGSEVRSSSTVASDG 316
      252 KSVNGESGRNWRLLVSESKAGALCANGAVRQDDGALLEVIVH----- 296
Db      317 SMEKGEKSTKVEENSKADKGRTEVNOCSIDLGEEDMERGEDDINFSEDDVEAVNIPESL 376
      297 ----RVGNSK-BHLPLPSEAGPTPCAPASFE----- 322
Qy      377 PPSRRNSNPNPLPRCYOCKAKAVIIFIISVYLSLGPYCFIPLAVLWVDTETVPQWVI 436
      323 RGRERNAEKRMALAREKTKVTGLIINGTFLICWLPFFIVALVLPFCSSSCHMPTLLG 382
Db      437 TIIIMFLQCCIHPIVYVGYMKTIKKEIODMLKKEPFCKE 476
      383 AIINWLGYSNLSLNPVIYAVFNKDFONAFKKIICLFCRQ 422

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RESULT 11

US-08-117-006-3

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; Sequence 3, Application US/08117006
; Patent No. 5639652
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR AND
; TITLE OF INVENTION: US5 THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,006
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1795/39318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear

```

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; IMMEDIATE SOURCE:
; CLONE: 5-HT1A
US-08-117-006-3

```

Query Match 13.0%; Score 343.5; DB 1; Length 422;
 Best local similarity 22.0%; Pred. No. 1.1e-19;
 Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

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Qy      26 ISLAHGIIRSTVLVIFLASFVGN--IVLAVLQRRKPOLLOVNTNPIFNLTVDLQISL 83
      31 VVTSYQVITSLTGLTIFCAVGNACVVAIALER--SLQNVANYLIGSLAVTDLWVSVL 88
Db      84 VAPMVAVTSVPLFPLNHSFCTALVSLTHLPAPASVNTVLVSVDRLYSIIHPLSPSKM 143
      89 VLPMAALYQVNLKMTLGOVTCDFIALDVLCTCTSIHLCAIALDRYMAITDPIDYVNRK 148
Qy      144 TORRGVLLYGTWIVAILOSTPPLVGMGOAFDERNALCSMIMGASPSYTIISVVSFIYI 203
      149 TRRRAAALISLTWILGFLISIPMLGMTRP--EDRSDPACTISKDHGTTIYSTGCAFYI 206
Db      204 PLIWIACSVVFCARQHALLYNKRSLVRVDCVENEDEBGAEKKEFODESEFR 263
      207 PLLMLVLVYGRIFRAR-----FRIRKTYKKVKEKTGADTRHGASPAPOK 251
Qy      264 ROHEBEVAKKEGRM--EAKDGL-----KAKGSGTSSSEVSEARGSEVRSSSTVASDG 316
      252 KSVNGESGRNWRLLVSESKAGALCANGAVRQDDGALLEVIVH----- 296
Db      317 SMEKGEKSTKVEENSKADKGRTEVNOCSIDLGEEDMERGEDDINFSEDDVEAVNIPESL 376
      297 ----RVGNSK-BHLPLPSEAGPTPCAPASFE----- 322
Qy      377 PPSRRNSNPNPLPRCYOCKAKAVIIFIISVYLSLGPYCFIPLAVLWVDTETVPQWVI 436
      323 RGRERNAEKRMALAREKTKVTGLIINGTFLICWLPFFIVALVLPFCSSSCHMPTLLG 382
Db      437 TIIIMFLQCCIHPIVYVGYMKTIKKEIODMLKKEPFCKE 476
      383 AIINWLGYSNLSLNPVIYAVFNKDFONAFKKIICLFCRQ 422

```

RESULT 12

US-08-216-594-3

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; Sequence 3, Application US/08216594
; Patent No. 5652113
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Branchek, Theresa
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1F RECEPTOR
; TITLE OF INVENTION: AND US5 THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216,594
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39318
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
TELEX: 422523 COOP UT
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
IMMEDIATE SOURCE:
CLONE: 5-HT1A
US-08-216-594-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1,1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAHGIIRSVTLVIFLASFVGN--IVLALVLRKPOLLOVTRFIFNLVTLDTLQISTL 83
DB 31 VTSVQVITSLTLGLTIFCAVLGNACVVAIALER--SLQNVANVYLSLAVTDLMSVL 88
QY 84 VAPWVAVSVPLFWPLNSHFCALVSLTHLFAFASVNTIVLVSDRYLSIHPSPSKM 143
DB 89 VLPMAALYQVLMKMTLGOVTCDFIALDVLCTSSILHLCAIALDRVYALTDPIQVNR 148
QY 144 TORRGYLLYGTWVAIIQSTPPLYGWQAADFERNALCSMIWASPSYTLISVSVFVI 203
DB 149 TPRRAAALISLTWLGFLISIPMLGWRTP--EDRSDPDACTISKDHGTIYSTFGAFYI 206
QY 204 PLIWIACYSVFCARQHALLVNKRHSLEVRVYKCVENEDGAEKKEEFQDESEFR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASPAQPK 251
QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSTGTSESSVEARGSEVRRESSTVASDG 316
DB 252 KSVNDESSSRMRRLVESKAGALCANGAVRQDDGALAEVFN----- 296
QY 317 SMEKSGSTKYVENSMKADKGRTEVNOCSIDLGEDMEGDDINFSDDVAVNIPESL 376
DB 297 ----RVGNSK-EHLPLSEAGTPCAPASFE----- 322
QY 377 PPSRRNSNSNPPLPRCYCCKAKAVIFIIIFSYVLSLGPYCFILAVAVDVETQVPQWVI 436
DB 323 RKNERNAAKRMALARRKTVKTGIIMGTFILCMLPFIYALVLPCESSCHMPTLLG 382
QY 437 TIIIVLFLQCCIHPPYVGVYMKTIKKEIQDMLKKFPCKE 476
DB 383 AIIIMWLGYSNLNPLVYAYFNKDFQNAFKKIICLFCRQ 422

RESULT 13
US-08-542-358-3
Sequence 3, Application US/08542358
Patent No. 5786155
GENERAL INFORMATION:
APPLICANT: Weinshank, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Hartig, Paul R.
TITLE OF INVENTION: DNA ENCODING A HUMAN 5-HT1E RECEPTOR AND USES THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/542,358
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1795/39317-2Z/JPW/MAT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-542-358-3

Query Match 13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1,1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLAHGIIRSVTLVIFLASFVGN--IVLALVLRKPOLLOVTRFIFNLVTLDTLQISTL 83
DB 31 VTSVQVITSLTLGLTIFCAVLGNACVVAIALER--SLQNVANVYLSLAVTDLMSVL 88
QY 84 VAPWVAVSVPLFWPLNSHFCALVSLTHLFAFASVNTIVLVSDRYLSIHPSPSKM 143
DB 89 VLPMAALYQVLMKMTLGOVTCDFIALDVLCTSSILHLCAIALDRVYALTDPIQVNR 148
QY 144 TORRGYLLYGTWVAIIQSTPPLYGWQAADFERNALCSMIWASPSYTLISVSVFVI 203
DB 149 TPRRAAALISLTWLGFLISIPMLGWRTP--EDRSDPDACTISKDHGTIYSTFGAFYI 206
QY 204 PLIWIACYSVFCARQHALLVNKRHSLEVRVYKCVENEDGAEKKEEFQDESEFR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASPAQPK 251
QY 264 ROHEGEVAKEGRM--EAKDGL-----KAKGSTGTSESSVEARGSEVRRESSTVASDG 316
DB 252 KSVNDESSSRMRRLVESKAGALCANGAVRQDDGALAEVFN----- 296
QY 317 SMEKSGSTKYVENSMKADKGRTEVNOCSIDLGEDMEGDDINFSDDVAVNIPESL 376
DB 297 ----RVGNSK-EHLPLSEAGTPCAPASFE----- 322
QY 377 PPSRRNSNSNPPLPRCYCCKAKAVIFIIIFSYVLSLGPYCFILAVAVDVETQVPQWVI 436
DB 323 RKNERNAAKRMALARRKTVKTGIIMGTFILCMLPFIYALVLPCESSCHMPTLLG 382
QY 437 TIIIVLFLQCCIHPPYVGVYMKTIKKEIQDMLKKFPCKE 476
DB 383 AIIIMWLGYSNLNPLVYAYFNKDFQNAFKKIICLFCRQ 422

RESULT 14
US-08-157-185-13
Sequence 13, Application US/08157185
Patent No. 5985585
GENERAL INFORMATION:
APPLICANT: Baird A. Jonathan

```

: APPLICANT: Branchek A. Theresa
: APPLICANT: Weinsthank L. Richard
: TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
: TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/157,185
: FILING DATE: 15-JUN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 41908-A-PCT-US/JPW/MAT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 422 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-157-185-13

Query Match      13.0%; Score 343.5; DB 1; Length 422;
Best Local Similarity 22.0%; Pred. No. 1.1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLANGIIRSTVLVFLAASPVGN--IVLALVLRKRPOLLQVTRNFILNLTVDLQISL 83
DB 31 VVVSQVITSLTLGLTIFCAVLGNACVVAIALER--SLQNVANVLIQSLAVTDLMAVSYL 88
QY 84 VAPMVAVTSVPLFWPLNSHFTALVSLTHLFAFASVNTIVLVSVDVRYLSIHPLSYPSKM 143
DB 89 VLPMAALYQVINKWTLGQVTCDFIALDVLCTSSILHLCAIALDRYMAITPIDVYVKR 148
QY 144 TORRGYLLYGTWIVAIILQSTPTPLYGWGOAEDERNALCSMIWGASPSYTIISVSFIYI 203
DB 149 TPRRAAALISLWTLGLFISIPMLGWRTP--EDRSDPDACTISKDHGTTIYSTGAFYI 206
QY 204 PLIVMIACYSVVFCAARQHALLVNKRSHLEVRKDCVNEDEGAKEKEEFODESEFR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASPAPOK 251
QY 264 RQHEBEVAKKEGRM--EAKDGSL-----KAKEGSTSTSSSEVARGSEEVRESSYVASDG 316
DB 252 KSVNBSGSGRMNRLGVESKAGALCANGAVRQGDGAALVEIEVA----- 296
QY 317 SMEGEGSTKVEENMKADKGRTEVNQCSIDLGEDMEFGEDDINFSDVEAVNIPESL 376
DB 297 ----RVGNK-EHLPLPSEAGPTPCAPASF----- 322
QY 377 PPSRRNSNPNPLPRCYOCKAKAVIFIIIFSVLSLGPYCFLAVLAVWVDETQVPQWVI 436
DB 323 RKNERAAEKAKRKAALAREKRTVLTIGITGTFILCMLPFIIVLALVLPFCSSCHMPTLLG 382
QY 437 TIIIMLFYQCCIHPRVYGVYMKTIKKEIQDMLKRFCKE 476
DB 383 AIIIMLGYSNLSLNPVLYVAFNKPONAFKTIKCLFCFRQ 422
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RESULT 15
US-08-281-526B-13
: Sequence 13, Application US/08281526B
: Patent No. 6083749
: GENERAL INFORMATION:
: APPLICANT: Bard A. Jonathan
: APPLICANT: Branchek A. Theresa
: APPLICANT: Weinsthank L. Richard
: TITLE OF INVENTION: DNA ENCODING A HUMAN SEROTONIN
: TITLE OF INVENTION: RECEPTOR (5-HT4B) AND USES THEREOF
: NUMBER OF SEQUENCES: 17
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Cooper & Dunham LLP
: STREET: 1185 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/281,526B
: FILING DATE: 27-JUL-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: White P., John
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 41908-1/JPW
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-0400
: TELEFAX: (212) 391-0525
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 422 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-281-526B-13

Query Match      13.0%; Score 343.5; DB 2; Length 422;
Best Local Similarity 22.0%; Pred. No. 1.1e-19;
Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

QY 26 ISLANGIIRSTVLVFLAASPVGN--IVLALVLRKRPOLLQVTRNFILNLTVDLQISL 83
DB 31 VVVSQVITSLTLGLTIFCAVLGNACVVAIALER--SLQNVANVLIQSLAVTDLMAVSYL 88
QY 84 VAPMVAVTSVPLFWPLNSHFTALVSLTHLFAFASVNTIVLVSVDVRYLSIHPLSYPSKM 143
DB 89 VLPMAALYQVINKWTLGQVTCDFIALDVLCTSSILHLCAIALDRYMAITPIDVYVKR 148
QY 144 TORRGYLLYGTWIVAIILQSTPTPLYGWGOAEDERNALCSMIWGASPSYTIISVSFIYI 203
DB 149 TPRRAAALISLWTLGLFISIPMLGWRTP--EDRSDPDACTISKDHGTTIYSTGAFYI 206
QY 204 PLIVMIACYSVVFCAARQHALLVNKRSHLEVRKDCVNEDEGAKEKEEFODESEFR 263
DB 207 PLLMLLVLYGRIFRAAR-----FRIRKTVKVEKGTGADTRHGASPAPOK 251
QY 264 RQHEBEVAKKEGRM--EAKDGSL-----KAKEGSTSTSSSEVARGSEEVRESSYVASDG 316
DB 252 KSVNBSGSGRMNRLGVESKAGALCANGAVRQGDGAALVEIEVA----- 296
QY 317 SMEGEGSTKVEENMKADKGRTEVNQCSIDLGEDMEFGEDDINFSDVEAVNIPESL 376
DB 297 ----RVGNK-EHLPLPSEAGPTPCAPASF----- 322
QY 377 PPSRRNSNPNPLPRCYOCKAKAVIFIIIFSVLSLGPYCFLAVLAVWVDETQVPQWVI 436
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Db	323	RKNERNAEAKRKWALAREKTVKTLGIMGTFLCMLPPFIWALVLPFCSSCHMPTLLG	382
Qy	437	TIIMLFPLQCCIHPEYVYGYMHKTIKEIODMLKKFCKE	476
Db	383	AIINWLGYSNSLNPVIYAFNKPQNAFKKIICLFCRQ	422

Search completed: December 3, 2005, 06:37:51
Job time : 41.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:36:57 ; Search time 6.92727 Seconds
(without alignments)
351.144 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MISTCTNSTRESNHSHTCMP.....GTEGTEGKIYPSYDSTATFP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US08_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppaa/PCT_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2641	99.9	508	6	US-10-980-388-112 Sequence 112, App
2	791	29.9	204	6	US-10-980-388-68 Sequence 68, Appl
3	204.5	7.7	352	7	US-11-068-686-20 Sequence 20, Appl
4	198	7.5	417	6	US-10-992-577-44 Sequence 44, Appl
5	197.5	7.5	419	7	US-11-067-884-8 Sequence 8, Appl1
6	194.5	7.4	352	7	US-11-068-686-2 Sequence 2, Appl1
7	191.5	7.2	432	6	US-10-992-577-2 Sequence 2, Appl1
8	186.5	7.1	355	7	US-11-068-686-4 Sequence 4, Appl1
9	184.5	7.0	440	6	US-10-502-893-2 Sequence 2, Appl1
10	175.5	6.6	430	6	US-10-992-577-8 Sequence 8, Appl1
11	174.5	6.6	420	6	US-10-992-577-6 Sequence 6, Appl1
12	174.5	6.6	522	6	US-10-510-018-2 Sequence 2, Appl1
13	171.5	6.5	409	6	US-10-627-633-4 Sequence 4, Appl1
14	166	6.3	352	6	US-10-627-633-2 Sequence 2, Appl1
15	164.5	6.2	345	6	US-10-627-633-6 Sequence 6, Appl1
16	164	6.2	340	6	US-10-980-388-117 Sequence 117, App
17	163.5	6.2	342	6	US-10-980-388-118 Sequence 118, App
18	144	5.4	360	6	US-10-851-667A-26 Sequence 26, Appl
19	137.5	5.2	481	6	US-10-980-388-100 Sequence 100, App
20	137	5.2	485	6	US-10-821-234-934 Sequence 934, App
21	131.5	5.0	358	6	US-10-980-388-96 Sequence 96, Appl
22	131.5	5.0	389	6	US-10-980-388-116 Sequence 116, App
23	128.5	4.9	271	6	US-10-980-388-67 Sequence 67, Appl
24	125.5	4.7	347	6	US-10-131-826A-18 Sequence 18, Appl1
25	120.5	4.6	350	6	US-10-502-145-1 Sequence 1, Appl1

26	114	4.3	337	6	US-10-980-388-115 Sequence 115, App
27	114	4.3	353	7	US-11-067-884-6 Sequence 6, Appl1
28	111.5	4.2	351	7	US-11-067-884-4 Sequence 4, Appl1
29	111	4.2	349	6	US-10-131-826A-424 Sequence 424, App
30	106	4.0	313	7	US-11-095-093-2 Sequence 2, Appl1
31	106	4.0	364	7	US-11-067-884-2 Sequence 2, Appl1
32	100	3.8	313	6	US-10-980-388-63 Sequence 63, Appl
33	99	3.7	1388	6	US-10-821-234-1143 Sequence 1143, Ap
34	96	3.6	793	7	US-11-060-914-2 Sequence 2, Appl1
35	95	3.6	287	6	US-10-980-388-66 Sequence 66, Appl
36	94.5	3.6	356	6	US-10-980-388-70 Sequence 70, Appl
37	93	3.5	543	6	US-10-689-742-78 Sequence 78, Appl
38	93	3.5	858	6	US-10-645-441-18 Sequence 18, Appl
39	92	3.5	432	7	US-11-055-822-1096 Sequence 1096, Ap
40	91.5	3.5	431	7	US-11-092-140-6 Sequence 6, Appl1
41	91.5	3.5	790	6	US-10-131-826A-204 Sequence 204, App
42	91	3.4	312	6	US-10-858-730-122 Sequence 122, App
43	91	3.4	782	6	US-10-793-626-2352 Sequence 2352, Ap
44	91	3.4	858	6	US-10-645-441-23 Sequence 23, Appl
45	90.5	3.4	615	6	US-10-982-545-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-980-388-112
; Sequence 112, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 112
; TYPE: PRT
; LENGTH: 508
; ORGANISM: Homo sapiens
; US-10-980-388-112
Query Match 99.9%; Score 2641; DB 6; Length 508;
Best local Similarity 99.8%; Pred. No. 4,4e-198;

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Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESNSHTCMPISLAHGIIIRSTVLVIFLAASFVGNIVLAVLQKRP 60
Db 1 MTSTCTNSTRESNSHTCMPISLAHGIIIRSTVLVIFLAASFVGNIVLAVLQKRP 60
QY 61 QLLQVTRNFIFNLVTDLLQISLVAWPVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db 61 QLLQVTRNFIFNLVTDLLQISLVAWPVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGKYLGYTWIYVAILQSTPPLVGMGOAARDEBNA 180
Db 121 TIVVSVDRYLSIIHPLSYPSKMTQRGKYLGYTWIYVAILQSTPPLVGMGOAARDEBNA 180
QY 181 LCSMIMGASPSYTLISVVSFIVIPLIWIAVCSVVFCAARQHALLVNWKSHLEVRVYD 240
Db 181 LCSMIMGASPSYTLISVVSFIVIPLIWIAVCSVVFCAARQHALLVNWKSHLEVRVYD 240
QY 241 CVENEDDEGAEKKEFQDESEFRROHGEVYAKEGRMAKOGSLKAKGSGTGTSSSYEA 300
Db 241 CVENEDDEGAEKKEFQDESEFRROHGEVYAKEGRMAKOGSLKAKGSGTGTSSSYEA 300
QY 301 RGSSEVRRESSTVYASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDI 360
Db 301 RGSSEVRRESSTVYASDGSMEKSGSTKVEENSMKADKGRTEVNOCSIDLGEDDMERGEDI 360
QY 361 NFSEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIIFSIVLSLGPYCFNAV 420
Db 361 NFSEDDVAVNIPESLPPSRNSNSNPPLPRCYCKAKAVIFIIIFSIVLSLGPYCFNAV 420
QY 421 LAWVAVDETQVQWVITIIIMLFLOCCIHPPVYGVYKTKKEIQDMLKRFCEKRPK 480
Db 421 LAWVAVDETQVQWVITIIIMLFLOCCIHPPVYGVYKTKKEIQDMLKRFCEKRPK 480
QY 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508
Db 481 EDSHPDLPGTEGTEGKIIVPSYDSATFP 508

RESULT 2
US-10-980-388-68
; Sequence 68, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325-US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370

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; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 68
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-68

Query Match 23.9%; Score 791; DB 6; Length 204;
Best Local Similarity 98.7%; Pred. No. 4,46-55;
Matches 156; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTSTCTNSTRESNSHTCMPISLAHGIIIRSTVLVIFLAASFVGNIVLAVLQKRP 60
Db 47 MTSTCTNSTRESNSHTCMPISLAHGIIIRSTVLVIFLAASFVGNIVLAVLQKRP 106
QY 61 QLLQVTRNFIFNLVTDLLQISLVAWPVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 120
Db 107 QLLQVTRNFIFNLVTDLLQISLVAWPVAVTSVPLFWPLNSHFCTALVSLTHLFAFASVN 166
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGKYLGYTWIY 158
Db 167 TIVVSVDRYLSIIHPLSYPSKMTQRGKYLGYTWIY 204

RESULT 3
US-11-068-686-20
; Sequence 20, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicki L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greca E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 7.7%; Score 204.5; DB 7; Length 352;
Best Local Similarity 26.3%; Pred. No. 2,7e-09;

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Db 287 QASKLGLMSLQPP-----QMSIDMG----- 307
Qy 357 EDDINFSEDDVAVNIPESLPSPRRNSNSNPPLPRCYOCKAKAVIIFIIFSYSLGPGYC 416
Db 308 -----FKTRAFITLLILFAVFIYCMNAFT 331
Qy 417 FLAVLAV-----WVDVETQVPQVVTIITLWFLPQCCIPHPYGVYGMKTIKKEIQ 466
Db 332 TYSIVATSPSKHPYQHNFFETIST-----W-----LMLCYLKSALNPLIYWM----- 373
Qy 467 DMLKKEF--CKEKPKEDSHRDLPGTEGTECKIYPS 501
Db 374 -RIKKEFDACLDMPK--SFKEFLPOLPGHTKRIRPS 407

RESULT 6
US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Report, Carol J.
; Title of Invention: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 7.4%; Score 194.5; DB 7; Length 352;
Best Local Similarity 25.0%; Pred. No. 1.6e-08;
Matches 58; Conservative 51; Mismatches 104; Indels 19; Gaps 7;
Qy 16 HTCMPLSMPT-SLAHGIIIRSTVIVIFLAASFGNIVLALVQRPQLQVNRIRINUL 74
Db 15 YTSECCQKINVKQIAARLLPPLYSLVFI-FGFVGMMVLVLLINCKRLKSMMDIYLNLA 73
Qy 75 VTDLQISLVAPWVATSVPLFWPLNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSII 134
Db 74 ISDLFFLLVPPW--AHYAAAGMDFGNTMCQLLTGLYFIFGFSGIFPITILLIDRIYLV 131

Qy 135 HPLSYPSKMTORRGVLLYGTWIVAILOSTPPLPYGMGAADERNALCS-----MIW 186
Db 132 HAVFALKARTYTFGVNYSVITWVAVFASLPGIIL-FTRSQEGAHYTCSSHPFSQYQFW 190
Qy 187 GASPSYTLISVSVFVPLIYMIACYSVFCFAARQNALYVNVKHSLEVRV 238
Db 191 --KNFQILKIVILGLVLPFLVMVICYSIGILKTLR---CNEKKRRRAVNL 236

RESULT 7
US-10-992-577-2
; Sequence 2, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P. G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; Title of Invention: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT APPLICATION NUMBER: US/10/992,577
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-2

Query Match 7.2%; Score 191.5; DB 6; Length 432;
Best Local Similarity 16.6%; Pred. No. 3.6e-08;
Matches 94; Conservative 64; Mismatches 144; Indels 265; Gaps 17;
Qy 2 TSTCTNSRRESNSHTCMPLSKMPTSLAHGIIIRSTVIVIFLAASFGNIVLALVQRPQ 61
Db 24 TSMATSLTFSSYYQHS-SPVAM-----PIAAVILFLIC--MVGNTLVCFVLKRRH 73
Qy 62 LLQVTNRIFNLVLTDLQISLVAPWVATSVPLFWPLNSHFCIALVSLTHLFAFASVNT 121
Db 74 MRYVTNMFILNMAVSDLVGIFCMFPTLLVDMLITGMFPDNTCKMSGLVQMSVASVFT 133
Qy 122 IVLVSVDVRYLSIHPPLSYPSKMTORRGVLLYGTWIVAILOSTP----- 165
Db 134 LVATLVERFRICIVHD--FREKTLRKALFTTAVYVWALMLMCSAVTLTYTREBHHML 191
Qy 166 -----PLYGMGAADERNALCSMIW---GASPSYTLISVSVFVPLIYMIACYSVV 215
Db 192 DARNRSYPLYS-----CMEAMPBKGMKRYTAVFAHYLVLPALLIVMY--- 236
Qy 216 FCAARRQHALLYNVKHSLEVRVYKDCVENDEBGAKEKEEPQDSSEFRQHEGVAKEG 275
Db 237 -----VRIARKLC----- 244
Qy 276 RMEAKDSLKAKESGTSTSESVARSGSEVRRESSTVASDSMEKSGSTKVEENSMKAD 335
Db 245 -----QAPGPARDTEA-----VAE 259
Qy 336 KGRTEVNOCSIDLGEDWMEFGEDINFSEDDVAVNIPESLPSPRRNSNSNPPLPRCYQC 395
Db 260 GGR-----SRR-----RA 268
Qy 396 KAAKVIIFIIFSYSLGPGYCFLAVLAVWVDVETQVPQWITITII----- 440

Db 269 RRVHKLWVAFPTLS-----W-----LPWVLLLDIDYSELQHLHLSV 310
Qy 441 -----WLFLOCCIHPIVYGYMHTIKKEIDMLKKEFC-----KEKP----- 478
Db 311 VAFPLAHMLAFHSSANPIIYGFYFNENFRGFOAARAOICWPMMAHKQAYSERPNRL 370
Qy 479 -----PKEDSHDLPTEGCTEG 496
Db 371 RRRVVVDVQPSDGLPSESGLSPG 397

RESULT 8
US-11-068-686-4
; Sequence 4, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; ; Schmeickart, Vicky L.
; ; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88-2B amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-068-686-4

Query Match 7.1%; Score 186.5; DB 7; Length 355;
Best Local Similarity 24.0%; Pred. No. 6.9e-08;
Matches 47; Conservative 48; Mismatches 86; Indels 15; Gaps 5;

Qy 40 IFLAASFGVNIVLALVQRKPOLQVTRNFIFPLVLTDLQISLVAIPWVAVSPLFWPL 99
Db 43 LVFTVGLLGNVVMMLIKRRIRMTNYYLNLALSDLLFVTLTFWVHYVR-GNNWVF 101
Qy 100 NSHFTALVSLTHLFAFASVNTIVLSVDRYLSIHPLSYPSKMTGRGYLLYGTWIVA 159
Db 102 GCGMCKLTLGFGYHTGYSIFILLITIDRYLAIVAVPALRARTVTFGVITSIVTWGLA 161
Qy 160 ILQSTFP-LYGMGOAFAFDERNALCSMIMGASPSY-----TILSVSFIVIPLIYVACY 212
Db 162 VLAALPEFIYETELFER--TLCSALYRBDIVYSWRHPTLMTITCLVLPILVACIY 219

Qy 213 SVVF-----CAARRQH 223
Db 220 TGIITKLRCPSKKY 235

RESULT 9
US-10-502-893-2
; Sequence 2, Application US/10502893
; Publication No. US20050255529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer HealthCare AG
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; FILE REFERENCE: Ica 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; PRIOR FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-502-893-2

Query Match 7.0%; Score 184.5; DB 6; Length 440;
Best Local Similarity 26.7%; Pred. No. 1.3e-07;
Matches 56; Conservative 35; Mismatches 76; Indels 43; Gaps 7;

Qy 35 STVLVIFLAASFGVNIVLALVQRKPOLQVTRNFIFNLVTDLIQISVAP----- 86
Db 30 AALCVVIALTAANSILIALICTOPALNTSNFVLSFTSDLMGLVMPAMLNALY 89
Qy 87 --WVAVTSVPLFWPUNSHRCTALVSLTHLFAFASVNTIVLSVDRYLSIHPLSYPSKMT 144
Db 90 GHWVLARGLCLMTAPDVNCS-----ASTINLCLISLDRLTLISPLRYKLRT 139
Qy 145 QRRGYLLYGTWIVAILQS--TPLYGW-----GOAFAFDERNALCSMIMGASPSY 192
Db 140 PLRALALVIGANSLAALASFLPLLGMHGLHARPPVVGQ-----CRLL-ASLPV 189
Qy 193 TILSVSFIVIPLIYVACIYSVFCAARRQ 222
Db 190 LVASGLTFE-LPSGAICFTYCRILLAAARKQ 218

RESULT 10
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerold, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JFM
; CURRENT APPLICATION NUMBER: US/10/992,577
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22

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;; PRIOR APPLICATION NUMBER: 09/161,113
;; PRIOR FILING DATE: 1998-09-25
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 8
;; LENGTH: 430
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match      6.6%; Score 175.5; DB 6; Length 430;
Best Local Similarity 25.1%; Pred. No. 6,3e-07;
Matches 61; Conservative 39; Mismatches 90; Indels 53; Gaps 9;

QY 6 TNSRESNSHTCMPLSKMPISLHAGIRSTVLVIFLAASFVGNITVALVQKPKQLQV 65
DB 28 TNLFFSYXQHT-SPVAMFI-VAVAL-----IFLLC-MVGNLTVCFIVLKNHMTV 77
QY 66 TNRFFNLVLDLQISLVAAPVAVTSVPLFPLNSHCTALVSLTHFAPASVNTIVLV 125
DB 78 TMMFLNLAVSDLVGIFCMPTTLVDNLITGMPFDNATCKMSGLVQGSVASVFTLVAI 137
QY 126 SVDRYLSIHPSPSKMTRGRGYLLVGTWIVALTGSTP----- 165
DB 138 AVERPRCIVHP--FRKLTIRKALVTIVATMALIMCPASVTLTVTRREHFNVDARN 195
QY 166 ---PLYGWGQAADERNALCSMIW---GASPSYTLISVSVFIVPLIWMACYSV---F 216
DB 196 RSYPLYS-----CMEAWPEKGMRRVYTTVLFSHYIADLALIVMVARIAKL 243
QY 217 CAA 219
DB 244 CQA 246

RESULT 11
US-10-992-577-6
; Sequence 6, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT APPLICATION NUMBER: US/10/992,577
; CURRENT FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-6

Query Match      6.6%; Score 174.5; DB 6; Length 420;
Best Local Similarity 18.7%; Pred. No. 7,3e-07;
Matches 84; Conservative 74; Mismatches 145; Indels 147; Gaps 14;

QY 33 IRSTVLVIFLAASFVGNITVALVQKPKQLQVTRNRFNLTIVLDLQISLVAAPVAVTS 92
DB 49 IISYFLIFFLC--MNGNTVVCFTIVNRKNKMTVTNLFLNLAIISDLVIGIFCMPTITLDN 106
```

```
QY 93 VPLFPLNSHCTALVSLTHFAPASVNTIVLVSVDRYLSIHPSPSKMTRGRGYLL 152
DB 107 IIAGMFGNTMCKISGLVQGSVAASVFTLVAVDVFQCVVP--FRPKLTITAFVII 164
QY 153 YGTWIVALTGSTPPLYGWGQAADERNALCSMIWGASPYTLISVSEFIVPLIWIACY 212
DB 165 MIWVLAI-----TIMS-----PSAVML--- 182
QY 213 SVFECAARRQHALLYNVNRKSLFVRVXDCVENEDBEAGKEEFODESEFRORHEGEVKA 272
DB 183 -----HYGEKXYRRLNS-----QNKTSPLYWCGEDWP----- 211
QY 273 KEGMEAKDGLKAKESGTGSESSVEARSGSEVREESTYVADSOSMGKEGSTVEENSM 332
DB 212 -----NOEMRKXYT-----TVLFANIT 228
QY 333 KADGRTEVNCSIDLGEDDMEFGEDDINSEDDVEAVNIPESLPSPRRNSNPPLPRC 392
DB 229 LA-----PLSLIYIMYGRIGISLFR-----AAVPHT--GRKQDEQHHVYSRK 268
QY 393 YQCAKAVIFIIIPSYVLSLGPYCFVLAVAVDVEVTOVPQWVTITII-----WLFPLQC 447
DB 269 KQ-KIKMLLIVALLFILSMPLWTMLMSDYADLSNBLQ-INIYIYPEAHMLAFGNS 326
QY 448 CIHPYVYGYMAKTIKGIQDMKKPFCEK 477
DB 327 SVNPIIYGFENENFRGRFOEAFQLOLOCR 356

RESULT 12
US-10-510-018-2
; Sequence 2, Application US/10510018
; Publication No. US20050244896A1
; GENERAL INFORMATION:
; APPLICANT: Golz, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Weingarten, Bernhard
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with
; FILE REFERENCE: Le A 35 945
; CURRENT APPLICATION NUMBER: US/10/510,018
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: PCT/EP2003/002962
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: EP 02007270.8
; PRIOR FILING DATE: 2002-04-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-510-018-2

Query Match      6.6%; Score 174.5; DB 6; Length 522;
Best Local Similarity 18.7%; Pred. No. 9,6e-07;
Matches 84; Conservative 74; Mismatches 145; Indels 147; Gaps 14;

QY 33 IRSTVLVIFLAASFVGNITVALVQKPKQLQVTRNRFNLTIVLDLQISLVAAPVAVTS 92
DB 151 IISYFLIFFLC--MNGNTVVCFTIVNRKNKMTVTNLFLNLAIISDLVIGIFCMPTITLDN 208
QY 93 VPLFPLNSHCTALVSLTHFAPASVNTIVLVSVDRYLSIHPSPSKMTRGRGYLL 152
DB 209 IIAGMFGNTMCKISGLVQGSVAASVFTLVAVDVFQCVVP--FRPKLTITAFVII 266
QY 153 YGTWIVALTGSTPPLYGWGQAADERNALCSMIWGASPYTLISVSEFIVPLIWIACY 212
DB 267 MIWVLAI-----TIMS-----PSAVML--- 284
QY 213 SVFECAARRQHALLYNVNRKSLFVRVXDCVENEDBEAGKEEFODESEFRORHEGEVKA 272
```



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Db 285 -----HVQEEKYRVRRLNS-----QNKTSPPVWCREDWP----- 313
Qy 273 KEGREAKDGLKAKEGSTGTSESSVEARGSEEVESSTVASDGSMEKSGSTKVEENSM 332
Db 314 -----NOEMKITYT-----TULFANITY 330
Qy 333 KADKGRTEVNOCSIDLGEDDMEFEGEDDINFSEDDVEAVNIPESLPPSRNSNSNPPLPRC 392
Db 331 LA-----PLSLIVIMYGRIGISLFR-----AAVPHPT-----GRKNGQOMHVSRK 370
Qy 393 YCCAKAVFIILIFSVLSLGPYCFALAVAVNDVETQVPQWVITITL-----WLFELQC 447
Db 371 KQ-KIIMLLIYALLFILSMPLMTLMLSDYADLSPEMLQ-IINIIYIPFAHWLAFGNS 428
Qy 448 CIHPYVGYVMKTIKKEIDMLKKFPCXK 477
Db 429 SVNPIIIGFFENFRGRFOEAFOLQOLCGR 458
```

```
RESULT 13
US-10-627-633-4
; Sequence 4, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennamd, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-627-633-4
```

```
Query Match 6.5%; Score 171.5; DB 6; Length 409;
Best Local Similarity 25.6%; Pred. No. 1.2e-06;
Matches 46; Conservative 37; Mismatches 90; Indels 7; Gaps 3;

Qy 40 IFLAA-----SFVGNIVLALVLRKPQLQVTRRFENLLVTDLQISLVAWVAVTSVPL 95
Db 64 IFGALMLFSGNSIVCLVIRSRRTOSTNYFVVSACADLLISVASTPFLVLOFTTG 123
Qy 96 FWPJNSHCFCTALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSYPSKMTQRRGYLLVGT 155
Db 124 RWTLSAMCKVRYRQYVLPQVYVLSICIDRFYTIYPLSF--KVSREKAKKMIAS 181
Qy 156 WTVALLQSTPPLYGQGAADFERNALCSMIMGASPSYTLISVSVFIVPLIMACYSV 215
Db 182 WILDAFVTVPVFFFGSNMDSHCNIFLPPSMEGT-AYVIHFLVGVFVLSIILFYQKV 240
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RESULT 14
US-10-627-633-2
; Sequence 2, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennamd, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
```

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; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-627-633-2
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Query Match 6.3%; Score 166; DB 6; Length 415;
Best Local Similarity 24.3%; Pred. No. 3.3e-06;
Matches 49; Conservative 43; Mismatches 104; Indels 6; Gaps 3;
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Qy 14 SHTCMPSKRPISLAHGISTVIVTFLASFVNITVLALVLRKPQLQVTRRFIRLU 73
Db 51 SNQTDLHVLRKGEVATASIFPGILMLF--SIFGNSIVCLVIRSRRTOSTNYFVVS 107
Qy 74 LVTDLQISLVAWVAVTSVPLFWPJNSHCFCTALVSLTHLFAFASVNTIVLVSDRYLSI 133
Db 108 ACADLLISVASTPFLVLOFTTGKMTLSATCKVRYRQYVLPQVYVLSICIDRFYTI 167
Qy 134 IHPISYPSKMTQRRGYLLVGTWIVALLQSTPPLYGQGAADFERNALCSMIMGASPSY 193
Db 168 VYPLSF--KVSREKAKKMIASWIFDAGFVTPVLPFFYGSNMDSHCNIFLPPSMEGT-AYT 224
Qy 194 ILSVSVFIVPLIMACYSV 215
Db 225 VIHFLVGVFVLSIILFYQKV 246
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RESULT 15
US-10-627-633-6
; Sequence 6, Application US/10627633
; Publication No. US20050250720A1
; GENERAL INFORMATION:
; APPLICANT: Charles, Andrew David
; APPLICANT: Brennamd, John Charles
; APPLICANT: Hart, Kevin Anthony
; TITLE OF INVENTION: Novel Compound
; FILE REFERENCE: 1991-221
; CURRENT APPLICATION NUMBER: US/10/627,633
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 09/722,342
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/172,146
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-627-633-6
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Query Match 6.2%; Score 164.5; DB 6; Length 352;
Best Local Similarity 24.4%; Pred. No. 3.5e-06;
Matches 44; Conservative 38; Mismatches 91; Indels 7; Gaps 3;
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Qy 40 IFLAA-----SFVGNIVLALVLRKPQLQVTRRFENLLVTDLQISLVAWVAVTSVPL 95
Db 29 IFGALMLFSGNSIVCLVIRSRRTOSTNYLVVSACADLLISVASTPFLVLOFTTG 88
Qy 96 FWPJNSHCFCTALVSLTHLFAFASVNTIVLVSDRYLSIIHPLSYPSKMTQRRGYLLVGT 155
Db 89 RWTLSAMCKVRYRQYVLPQVYVLSICIDRFYTIYPLSF--KVSREKAKKMIAS 146
Qy 156 WTVALLQSTPPLYGQGAADFERNALCSMIMGASPSYTLISVSVFIVPLIMACYSV 215
Db 147 WILDAFVTVPVFFFGSNMDSHCNIFLPPSMEGT-AYVIHFLVGVFVLSIILFYQKV 205
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Search completed: December 3, 2005, 06:55:54
Job time : 8.92727 sec8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:45 ; Search time 28.8636 Seconds
(without alignments)
1693.415 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTEGTEKIVPSYDSTRPP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir80: *
2: pir1: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	343.5	13.0	490	2 A35546	muscarinic acetylch
2	340.5	12.9	422	2 I38209	serotonin receptor
3	340	12.9	477	2 S71323	alpha-1A adrenergic
4	336	12.7	466	2 I57959	alpha-1C adrenergic
5	335.5	12.7	421	2 I49375	serotonin receptor
6	333.5	12.6	429	2 S65656	alpha-1C adrenergic
7	333.5	12.6	466	2 JH0765	alpha-1C adrenergic
8	333.5	12.6	499	2 S65657	alpha-1C adrenergic
9	331.5	12.5	422	2 JH0315	serotonin receptor
10	325.5	12.3	466	2 A35375	alpha-1-adrenergic
11	319	12.1	509	2 A47174	serotonin receptor
12	314.5	11.9	501	2 JH0447	alpha-1A adrenergic
13	314.5	11.9	572	2 I39369	alpha-1A adrenergic
14	312.5	11.8	484	2 S48657	muscarinic acetylch
15	306.5	11.6	560	2 A38731	muscarinic acetylch
16	304.5	11.5	601	2 JH0170	octopamine receptor
17	296.5	11.2	601	2 S12004	tyramine receptor
18	294	11.1	466	2 S10856	muscarinic acetylch
19	294	11.0	466	2 JH0197	muscarinic acetylch
20	291	11.0	479	2 S10127	muscarinic acetylch
21	289	10.9	466	2 A27386	muscarinic acetylch
22	288	10.9	468	2 T15941	hypothetical prote
23	288	10.9	515	2 S10125	alpha-1B adrenergic
24	287	10.9	466	2 S10126	muscarinic acetylch
25	285	10.8	610	2 T32917	hypothetical prote
26	283	10.7	515	2 A40491	alpha-1B adrenergic
27	283	10.7	517	2 A45121	alpha-1B adrenergic
28	282.5	10.7	478	2 C29514	muscarinic acetylch
29	282	10.7	479	2 S33776	muscarinic acetylch

30	280	10.6	466	2 A40972	muscarinic acetylch
31	279.5	10.6	516	2 JCS042	G protein-coupled
32	277.5	10.5	437	2 UT0531	muscarinic acetylch
33	276	10.4	564	2 A38271	serotonin receptor
34	275.5	10.4	484	2 S58868	G protein-coupled
35	275.5	10.4	532	2 UT0530	muscarinic acetylch
36	273	10.3	443	1 D7H02	dopamine receptor
37	273	10.3	445	2 A48881	serotonin receptor
38	270	10.2	448	2 A47519	serotonin receptor
39	268	10.1	448	2 S36402	serotonin receptor
40	267.5	10.1	442	1 D7H02	dopamine receptor
41	265	10.0	501	2 T18863	hypothetical prote
42	262.5	9.9	445	2 T42203	serotonin receptor
43	260	9.8	430	2 T16079	hypothetical prote
44	259.5	9.8	589	2 B29514	muscarinic acetylch
45	258	9.8	460	2 A31897	muscarinic acetylch

ALIGNMENTS

RESULT 1

A35546
muscarinic acetylcholine receptor M4 - chicken
C/Species: Gallus gallus (chicken)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C/Accession: A35546
R/Tietje, K.M.; Goldman, P.S.; Nathanson, N.M.
J. Biol. Chem. 265, 2828-2834, 1990
A/Title: Cloning and functional analysis of a gene encoding a novel muscarinic acetylch
A/Reference number: A35546; PMID:90153912; PMID:2154460
A/Accession: A35546
A/Molecule type: DNA
A/Residues: 1-490 <TIE>
A/Cross-references: UNIPROT:P17200; UNIPARC:UP1000004E75B; GB:J05218; NID:G211067; PIDN
C/Superfamily: Vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem
F/42-67/Domain: transmembrane #status predicted <TM1>
F/80-104/Domain: transmembrane #status predicted <TM2>
F/117-138/Domain: transmembrane #status predicted <TM3>
F/158-181/Domain: transmembrane #status predicted <TM4>
F/203-226/Domain: transmembrane #status predicted <TM5>
F/413-433/Domain: transmembrane #status predicted <TM6>
F/445-466/Domain: transmembrane #status predicted <TM7>

Query Match 13.0%; Score 343.5; DB 2; Length 490;
Best Local Similarity 23.7%; Pred. No. 1.1e-15;

Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

QY	36	TVLVIFLA-----	ASFGNIVLALVQRKPOLQVNRPIFNLTVDL-----	QISL 83
		::		::
QY	84	VAPWVATSVPLFWPLNSHFTALVSLTLFAFASVNTIVLVSVDRLYSIHPLSYSKM 143		
		:::	:::	:::
DB	39	TYELVFIAITVTSGLSLTVVSNILWLSTKNRQLOTUNNYLFSLACDLIIQVSSML 98		
		::		::
QY	99	YTVYTIKG---YWPFGAVVCDMLADLVVSNASVWMLLISFDYFCVTKELTPARR 154		
		:::	:::	:::
QY	144	TQRRGVLIXGTWIVAILIISTPPLXW---GQAAPDENALCSMTWGSPTTILSVS 199		
		:::	:::	:::
DB	155	TYKMGALMTAAWIIISFILMAPILFWOPIVKRTVHERE--CYIOFLSNPAVTFGTATA 212		
		::		::
QY	200	FIVIPLIWIAQSVYVFCAROHALLVYVKHSLVLR-----VKDCVEN 244		
		::		::
DB	213	APFLPVIMTVLYIHLSLSRSR-----VRHKHPSRKRRGKSLFFKAPPVYKONNN 266		
		::		::
QY	245	EDEGAKEKEEFQDESEFRHGEYKAKEGMEAKDGLKAKESGTSSSEVARGSE 304		
		:::	:::	:::
DB	267	SPRAVEKVEVRN-----GKV-----DDPSAQTEATQOE-----KE 301		
		::		::
QY	305	EYRESSTVASDMSMEKESGTVKEENSMKADGRTEVNCSDIDLGDDHPEFEDDINPSE 364		
		::		::
DB	302	TSNESSTVSMOTYTKDKP--TTEILPAGGQSPAHPRVNPIS-----KMSKIKLVTKO 352		
		::		::

Oy 365 DDVAVNNPEELP-----PSREN--SNSNP-LPCY-----OCKAKV 400
 Db 353 TGTSTVAIEIVPAKAGSDHNSLRPNVAVKAFASIASQVRKKQMAAREKKTRT 412
 Oy 401 IFIIIFSVYLGPCEFAVAVWVDVETQVPOWITIIIMLFLOCCIHPPYGVYMAKT 460
 413 IFAILLATILWTPTPNVWVLTNTF--CETCVPETWYISGVLYLCVNSTINACALCNAT 470
 Oy 461 IKKEIQDML 469
 471 FKKTFKHLL 479
 Db
 RESULT 2
 138209 serotonin receptor 1A - human
 N.Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
 C.Species: Homo sapiens (man)
 C.Date: 06-Sep-1996 #sequence revision 15-May-1998 #text_change 09-Jul-2004
 C.Accession: 138209; 137104; 507343; 156176; 831438
 R.Jacobson, U.S.; Reifel, L.M.; Conley, M.P.; Sambamurti, K.; Humayun, M.Z.
 Mutat. Res. 179, 89-101, 1987
 A.Title: DNA replication-blocking properties of adducts formed by aflatoxin B1-2,3-dichloroacetate
 A.Reference number: 138209; MUID:87258013; PMID:3110609
 A.Accession: 138209
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-422 <JAC>
 A.Cross-references: UNIPROT:P08908; UNIPARC:UPI0000124F1A; EMBL:X57629; NID:g36428; PIDN:
 R.Parks, C.U.; Chang, L.S.; Shenk, T.
 Nucleic Acids Res. 19, 7155-7160, 1991
 A.Title: A polymerase chain reaction mediated by a single primer: cloning of genomic sequences
 A.Reference number: 137104; MUID:92115564; PMID:1766875
 A.Accession: 137104
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-9 <PAR>
 A.Cross-references: UNIPARC:UPI00000077A; EMBL:Z11168; NID:g1033027; PIDN:CAA77560.1; E
 R.Koblik, B.K.; Ffiele, T.; Collins, S.; Yang-Feng, T.; Koblik, T.S.; Francke, U.; Le
 Nature 329, 75-79, 1987
 A.Title: An intronless gene encoding a potential member of the family of receptors coupled
 A.Reference number: 807343; MUID:87315369; PMID:3041227
 A.Accession: 807343
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-151, 'R', 155-171, 'I', 173-417, 'N', 419-422 <KOB>
 A.Cross-references: UNIPARC:UPI00000503D; EMBL:X13556; NID:g95523; PIDN:CAA31908.1; PID
 A.Note: the authors translated the codon ATC for residue 172 as Met
 R.Aune, T.M.; McGrath, K.M.; Sarr, T.; Bombard, M.P.; Kelley, K.A.
 J. Immunol. 151, 1175-1183, 1993
 A.Title: Expression of 5HT1A receptors on activated human T cells. Regulation of cyclic
 A.Reference number: 156176; MUID:93329096; PMID:8393041
 A.Accession: 156176
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 'RPV', 203-227, 'R', 229-244, 'A', 245-354, 'T', 356-362, 'MRP' <AUN>
 A.Cross-references: UNIPARC:UPI0000116D78; GB:S64045; NID:g404416; PIDN:ADJ13945.1; PID
 C.Genetics:
 A.Gene: GDB:HTT1A; ADBR2RL1; ADBRRL1
 A.Cross-references: GDB:120686; CMTM:109760
 A.Map position: Scen-5q11
 C.Superfamily: vertebrate rhodopsin
 C.Keywords: G protein-coupled receptor; glycoprotein; 11oprotein; neurotransmitter receptor
 F.37-62/Domain: transmembrane #status predicted <TM>
 F.74-98/Domain: transmembrane #status predicted <TM>
 F.110-132/Domain: transmembrane #status predicted <TM>
 F.153-178/Domain: transmembrane #status predicted <TM>
 F.192-211/Domain: transmembrane #status predicted <TM>
 F.346-367/Domain: transmembrane #status predicted <TM>
 F.379-403/Domain: transmembrane #status predicted <TM>
 F.10-11,24/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F.109-187/Disulfide bond: #status predicted
 F.1420/Binding site: palmitate (Cys) (covalent) #status predicted

[illegible]

```

Db      191 YAIFAVSGSYFLPLAILIILAMCYRVYVNAKESRGL-----KEG-Q 229
Qy      252 KKEEFODESEFRQHEGEVAKEGMEAKDGLKAKEGSTGTSESSVEARGSEVRESST 311
Db      230 KIEKADSEQVILIRMG-----NTT 249
Qy      312 VASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDMEFGEEDINFSEDDVEAVN 371
Db      250 VSED-----EALRSRT-----HFLRLRLKFSREK----- 273
Qy      372 IPESLPPSRBNSNSNPRLPRCYOCCAARKIFITIIISYVLSLGPYCPFLAVLAWVDVEYOV 431
Db      274 -----KAAKTLGIWGCFLVLCWLP--FFVLTPGISIFPAYR 307
Qy      432 P-QWVITIIIMLFLOCCIHPIYVGYMHTIKKEIDOMLKKPFCKEKPKEDSHDLPCT 490
Db      308 PSDYFKITFMGLYNSCINPIIYLCSONEFAKAFQSL-GVHCILRMTFRAHH-HLSVG 365
Qy      491 EGGTEG-KIVPSYDSATFP 508
Db      366 QSGTGHSLTSLDCKAP 384

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RESULT 4

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alpha-1C adrenergic receptor - rat
157959
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: 157959; 152862; PC2179
Rilaz, T.M.; Forray, C.; Smith, K.E.; Bard, J.A.; Vayssie, P.J.; Branchek, T.A.; Weinshan
Mol. Pharmacol. 46, 414-422, 1994
A>Title: The rat homologue of the bovine alpha 1C-adrenergic receptor shows the pharmac
A:Reference number: 157959; MUID:95021119; PMID:7935320
A:Accession: 157959
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-466 <RES>
A:Cross-references: UNIPROT:P43140; UNIPARC:UPI00004E761; EMBL:U07126; NID:9595275; PID
R:Stewart, A.F.; Rokosh, D.G.; Bailey, B.A.; Karns, L.R.; Chang, K.C.; Long, C.S.; Katiy
Circ. Res. 75, 796-802, 1994
A>Title: Cloning of the rat alpha 1C-adrenergic receptor from cardiac myocytes. alpha 1C
A:Reference number: 152862; MUID:95008062; PMID:7923624
A:Accession: 152862
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-38, 'L', 40-66, 'G', 68-466 <RE2>
A:Cross-references: UNIPARC:UPI000016761; EMBL:U13368; NID:9555851; PIDN:AAA52103.1; PI
R:Rokosh, D.G.; Bailey, B.A.; Stewart, A.F.R.; Karns, L.R.; Long, C.S.; Simpson, P.C.
Biochem. Biophys. Res. Commun. 200, 1177-1184, 1994
A>Title: Distribution of alpha 1C-adrenergic receptor mRNA in adult rat tissues by RNase
A:Reference number: PC2179; MUID:94241969; PMID:8185565
A:Accession: PC2179
A:Molecule type: mRNA
A:Residues: 102-279 <ROK>
A:Cross-references: UNIPARC:UPI00001778AF
A:Experimental source: cardiac myocyte
C:Comment: This factor comprises a multigene family. As do alpha-2 and beta-adrenergic r
C:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor; transmembrane protein
F:26-42/Domain: transmembrane #status predicted <TM1>
F:73-89/Domain: transmembrane #status predicted <TM2>
F:104-120/Domain: transmembrane #status predicted <TM3>
F:147-163/Domain: transmembrane #status predicted <TM4>
F:195-211/Domain: transmembrane #status predicted <TM5>
F:276-292/Domain: transmembrane #status predicted <TM6>
F:306-329/Domain: transmembrane #status predicted <TM7>

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Query Match 12.7%; Score 336; DB 2; Length 466;

Best Local Similarity 21.3%; Pred. No. 3, 3e-15;

Matches 108; Conservative 79; Mismatches 186; Indels 134; Gaps 11;

7 NSTRESNHSHTCMPKSIKPISLAHGIIRSTVLVIFLAASFGNIVLAVLQRRKPLQVLT 66

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Db      7 NASEGNSCTH-----PPARVNIISKAILLGVLLGLLIFGVGLNILLVLSVACHRLHAST 61
Qy      67 NRIFFNLVTDLQISLVAIPVWATSVLPFPLNSHFCCTALVSLTHLPASVNTIVLAS 126
Db      62 HYIYNLAVADLLTSTVLPSPATFELIGYAFGVFCINAAVDVLCCTASIMGLCTIS 121
Qy      127 VDRYLSTIHPLSYSPKMTQRRGTYLLVGTWIVAILQSTPPLVYGQAAFDERNALCSMTW 186
Db      122 IDRYIGVSPRLRYPTIVQRRGVRLLCWVLSTVISIGPLFGMRPA-PEDETICQI-- 178
Qy      187 GASPEYTLISVSVFVILVIMACYSVFCAARQHLNINVKHSLSEVRKDCVENED 246
Db      179 NEEPYVLFSAIGSYVPLAIIILVMYCRVYVAKR-----ESRG 217
Qy      247 EBGAKKEEFODESEFRQHEGEVAKEGMEAKDGLKAKEGSTGTSESSVEARGSEEV 306
Db      218 LKSGLKTDKSDSEQVTLIIRKNVPAEG-----GVSA----- 251
Qy      307 RESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGEDMEFGEEDINFSEDD 366
Db      252 -----KKKT-----HFSVRLKFSREK 268
Qy      367 VEAVNIPESLPPSRBNSNSNPRLPRCYOCCAARKIFITIIISYVLSLGPYCPFLAVLAWVD 426
Db      269 -----KAAKTLGIWGCFLVLCWLP--FLWMPIGSGFF 298
Qy      427 VETQVPOWVITIIIMLFLOCCIHPIYVGYMHTIKKEIDOMLKKPFCKEKPKEDS--- 483
Db      299 PDFKSEVTFKIVFLGYLNSCINPIIYPCSSQEFKAPQNVLRIOCLRROSKHALGY 358
Qy      484 --HPDLPTGEGTEGKI--VPSYDSATF 507
Db      359 TLHPPSQALBEGHRMVRIPVSGSETF 385

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RESULT 5

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149375
serotonin receptor 1A - mouse
N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 149375; A57508
R:Charcst, A.; Wainer, B.H.; Albert, P.R.
J. Neurosci. 13, 5164-5171, 1993
A>Title: Cloning and differentiation-induced expression of a murine serotonin1A receptor
A:Reference number: 149375; MUID:94076019; PMID:8254366
A:Accession: 149375
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-421 <CHA>
A:Cross-references: UNIPROT:O64264; UNIPARC:UPI000029964; EMBL:U9391; NID:g1066325; PI
R:Milkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G.
Genomics 18, 175-184, 1993
A>Title: Identification, chromosomal location, and genome organization of mammalian G-pr
A:Reference number: A48909; MUID:94116980; PMID:8288218
A:Accession: A57508
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 136-176, 'T', 178-241, 'L', 243-246, 'V', 248-262, 'W', 264-303, 'H', 305-329, 'T', 331-
A:Cross-references: UNIPARC:UPI00001778E8; GB:120339
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:37-62/Domain: transmembrane #status predicted <TM1>
F:74-98/Domain: transmembrane #status predicted <TM2>
F:110-132/Domain: transmembrane #status predicted <TM3>
F:153-178/Domain: transmembrane #status predicted <TM4>
F:192-217/Domain: transmembrane #status predicted <TM5>
F:346-367/Domain: transmembrane #status predicted <TM6>
F:379-403/Domain: transmembrane #status predicted <TM7>
F:410,11,24,30/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:109-187/Disulfide bonds: #status predicted

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[illegible]

QY 68 RPIFLMLTDLTQISLVAMWVATSVPLFPLNSHCFTALVSLTHLPAPASVNTIVLVSV 127
Db 63 YIVVLAADVADLLTSTVLPFSALFEVLGYWAGRWFCNIMAAADVLCCTASINGLCTISI 122
QY 128 DRYLSIHPILSPYSKMTQRRGYLLLYGTWIVAILOSTPPLPYGCGQAFAFERNALCSMIWG 187
Db 123 DRYIGSVPLRPTIVTQRRGLMALLCVWALSLVIGSLPFGWRQPA-PEDETIQQ--N 179
QY 188 ASPSTILSVSFIVIPLIWMTACYSVVFCAARQHALLYNKRHSLERVKDCVENEDE 247
Db 180 EEPGYVLFSALGSPFLPLAILIIMWYCRVYVYAKR-----ESRGL 218
QY 248 EGAEKKEQEDSEFRRQHEGEVKAKEGMEAKDGLAKKEGSTGTSSESSVEARGSEVR 307
Db 219 KSLGLTDSQSDSQVTLRLRHKNAPA-----GGSGMASATKTHPSVRL- 261
QY 308 ESSVTAASDGSMEGKSGSTKYEENSMKADKRGTEVNOCSIDLGEDDMFEGEDDINFSEDDV 367
Db 262 -----LKFSRK- 268
QY 368 EAVNIPESLPSRRNSNSNPPLPRCYQCAAKYFIIFISYVLSDGYPCLAVLAVWV 427
Db 269 -----KAAKTGLGVGCGFVLCWLPF-FLVMPIGSFPF 299
QY 428 ENQVQWVITIIIMFLFLOCCIHPPYVGYMHTIKKEIODMLKKPFCKEKPREDS---- 483
Db 300 DKPSSEYTFKIVFWLGYLNSCINPIIITPCSSQSEFKAFQVNLRIQCLRRQSSKHALGYT 359
QY 484 -HPDLPGTGTEGTEGKI-VPSYDAPF 507
Db 360 LHPPSQAVEGQHKDMVRLPVGSRFP 385
RESULT 7
JUN0765
alpha-1c-adrenergic receptor - human
C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C.Accession: JUN0765; 184635; J02333; G01419
R.Hirasawa, A.; Horie, K.; Tanaka, T.; Takagaki, K.; Murai, M.; Yano, J.; Tsujimoto, G.
Biochem. Biophys. Res. Commun. 195, 902-909, 1993
A.Title: Cloning, functional expression and tissue distribution of human CDNA for the alpha-1c-adrenergic receptor
A.Reference number: JUN0765; PMID:93384619; PMID:8396931
A.Accession: JUN0765
A.Molecule type: mRNA
A.Residues: 1-466 <HTR>
A.Cross-references: UNIPARC:P35348; UNIPARC:UPI0000503BE; GB:L31774; NID:G666892; PIDN:--
R.Diehl, N.L.; Shreeve, S.M.
Eur. J. Pharmacol. 268, 393-398, 1994
A.Title: Identification of the alpha-1c-adrenergic receptor in rabbit arteries and the human ear
A.Reference number: I47013; PMID:95104335; PMID:7805763
A.Accession: I84635
A>Status: preliminary; translated from GB/EMBL/DBDJ
A.Molecule type: mRNA
A.Residues: 202-344 <DE>
A.Cross-references: UNIPARC:UPI000016B46A; GB:S76001; NID:G913817; PIDN:AAD14205.1; PID:--
R.Weinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1236-1304, 1994
A.Title: Cloning, expression and characterization of human alpha adrenergic receptors alpha-1c
A.Reference number: J02333; PMID:94296402; PMID:8024574
A.Accession: J02333
A.Molecule type: mRNA
A.Residues: 1-130, 'F', 132-140, 'P', 142-166, 'C', 168-247, 'H', 249-337, 'C', 339-430, 'Q', 432-466, 'E', 468-507, 'L', 509-534, 'P', 536-561, 'S', 563-588, 'D', 590-615, 'N', 617-642, 'K', 644-669, 'R', 671-696, 'G', 698-723, 'A', 725-750, 'V', 752-777, 'I', 779-804, 'M', 806-831, 'Y', 833-858, 'C', 860-885, 'L', 887-912, 'P', 914-939, 'T', 941-966, 'S', 968-993, 'K', 995-1020, 'R', 1022-1047, 'Q', 1049-1074, 'N', 1076-1101, 'D', 1103-1128, 'E', 1130-1155, 'G', 1157-1182, 'A', 1184-1209, 'V', 1211-1236, 'I', 1238-1263, 'M', 1265-1290, 'Y', 1292-1317, 'C', 1319-1344, 'L', 1346-1371, 'P', 1373-1398, 'T', 1400-1425, 'S', 1427-1452, 'K', 1454-1479, 'R', 1481-1506, 'G', 1508-1533, 'A', 1535-1560, 'V', 1562-1587, 'I', 1589-1614, 'M', 1616-1641, 'Y', 1643-1668, 'C', 1670-1695, 'L', 1697-1722, 'P', 1724-1749, 'T', 1751-1776, 'S', 1778-1803, 'K', 1805-1830, 'R', 1832-1857, 'Q', 1859-1884, 'N', 1886-1911, 'D', 1913-1938, 'E', 1940-1965, 'G', 1967-1992, 'A', 1994-2019, 'V', 2021-2046, 'I', 2048-2073, 'M', 2075-2100, 'Y', 2102-2127, 'C', 2129-2154, 'L', 2156-2181, 'P', 2183-2208, 'T', 2210-2235, 'S', 2237-2262, 'K', 2264-2289, 'R', 2291-2316, 'G', 2318-2343, 'A', 2345-2370, 'V', 2372-2397, 'I', 2399-2424, 'M', 2426-2451, 'Y', 2453-2478, 'C', 2480-2505, 'L', 2507-2532, 'P', 2534-2559, 'T', 2561-2586, 'S', 2588-2613, 'K', 2615-2640, 'R', 2642-2667, 'Q', 2669-2694, 'N', 2696-2721, 'D', 2723-2748, 'E', 2750-2775, 'G', 2777-2802, 'A', 2804-2829, 'V', 2831-2856, 'I', 2858-2883, 'M', 2885-2910, 'Y', 2912-2937, 'C', 2939-2964, 'L', 2966-2991, 'P', 2993-3018, 'T', 3020-3045, 'S', 3047-3072, 'K', 3074-3099, 'R', 3101-3126, 'G', 3128-3153, 'A', 3155-3180, 'V', 3182-3207, 'I', 3209-3234, 'M', 3236-3261, 'Y', 3263-3288, 'C', 3290-3315, 'L', 3317-3342, 'P', 3344-3369, 'T', 3371-3396, 'S', 3398-3423, 'K', 3425-3450, 'R', 3452-3477, 'Q', 3479-3504, 'N', 3506-3531, 'D', 3533-3558, 'E', 3560-3585, 'G', 3587-3612, 'A', 3614-3639, 'V', 3641-3666, 'I', 3668-3693, 'M', 3695-3720, 'Y', 3722-3747, 'C', 3749-3774, 'L', 3776-3801, 'P', 3803-3828, 'T', 3830-3855, 'S', 3857-3882, 'K', 3884-3909, 'R', 3911-3936, 'G', 3938-3963, 'A', 3965-3990, 'V', 3992-4017, 'I', 4019-4044, 'M', 4046-4071, 'Y', 4073-4098, 'C', 4100-4125, 'L', 4127-4152, 'P', 4154-4179, 'T', 4181-4206, 'S', 4208-4233, 'K', 4235-4260, 'R', 4262-4287, 'Q', 4289-4314, 'N', 4316-4341, 'D', 4343-4368, 'E', 4370-4395, 'G', 4397-4422, 'A', 4424-4449, 'V', 4451-4476, 'I', 4478-4503, 'M', 4505-4530, 'Y', 4532-4557, 'C', 4559-4584, 'L', 4586-4611, 'P', 4613-4638, 'T', 4640-4665, 'S', 4667-4692, 'K', 4694-4719, 'R', 4721-4746, 'Q', 4748-4773, 'N', 4775-4800, 'D', 4802-4827, 'E', 4829-4854, 'G', 4856-4881, 'A', 4883-4908, 'V', 4910-4935, 'I', 4937-4962, 'M', 4964-4989, 'Y', 4991-5016, 'C', 5018-5043, 'L', 5045-5070, 'P', 5072-5097, 'T', 5099-5124, 'S', 5126-5151, 'K', 5153-5178, 'R', 5180-5205, 'G', 5207-5232, 'A', 5234-5259, 'V', 5261-5286, 'I', 5288-5313, 'M', 5315-5340, 'Y', 5342-5367, 'C', 5369-5394, 'L', 5396-5421, 'P', 5423-5448, 'T', 5450-5475, 'S', 5477-5502, 'K', 5504-5529, 'R', 5531-5556, 'Q', 5558-5583, 'N', 5585-5610, 'D', 5612-5637, 'E', 5639-5664, 'G', 5666-5691, 'A', 5693-5718, 'V', 5720-5745, 'I', 5

C:Comment: This protein plays critical roles in the regulation of a variety of physiolog

C:Genetics:

A:Gene: GDB:ADRA1C; ADRA1L1

A:Cross-references: GDB:128088; OMIM:104221

A:Map position: 8p21-8p11.2

A:Introns: 295/3

A>Note: the list of introns may be incomplete

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; glycoprotein; receptor; transmembrane protein

F:26-31/Domain: transmembrane #status predicted <TM1>

F:66-90/Domain: transmembrane #status predicted <TM2>

F:101-123/Domain: transmembrane #status predicted <TM3>

F:144-165/Domain: transmembrane #status predicted <TM4>

F:183-205/Domain: transmembrane #status predicted <TM5>

F:274-298/Domain: transmembrane #status predicted <TM6>

F:306-329/Domain: transmembrane #status predicted <TM7>

F:7,13,22/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 333.5; DB 2; Length 466;

Best Local Similarity 21.1%; Pred. No. 4.8e-15;

Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

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QY      8 STRENSSHTCMPISLAHGIRSVTVIFLAASFVGNIVLVLQKRPQLQVTN 67
      5 SCNASDSSNCTOP--PAPVNISKAILLGVLGGLLFGVLGNILVLSVACHRHLSVTH 62
      68 RIFNLVTLDDLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVNTTVLSV 127
      63 YIIVNLAVADLLTSTVLPFSAIFEVLAGYAFGRVFCNMAAVDVLCTASIMGLCIISI 122
      128 DRYLSIHPLSYPSKMTORRGVLLYGTWIVAILDSTPPLYGWGOAAPERNAALCSMIG 187
      123 DRYIGVSYPLRPTVTYTORGLMALLCWALSLVISIGLFGWRQPA-PEDETIQI--N 179
      188 ASPSTYILSVSFYIPLVIMTACSVVFCARROHALLYNKRHSLEVRVDCVENDE 247
      180 EEPGYLVFALGSPFLPLAILVMYCRYVYVAKR-----ESRGL 218
      248 EGAEKKEEFODESEFRROHGEVKAKEGMEAKDGLKAKEGSTGTSSESVEARGSEYR 307
      219 KSGLTKDSDSEQVTLRIHRKNAFA-----GSGMASAKTKTHFSVRL- 261
      308 EESTVADSGSMGKSGSTVEENSMKADKGRTEVNOCISIDLGEDDMFEDDINPSEDDV 367
      262 -----LKFSREK- 268
      368 EAVNIPESLPSPRRNSNPNPLPRCYOCCAKEYIFIIIFSIVLSLCPYCFPLAVLAWVDV 427
      269 -----KAAKTIGIVGCFVLCLWLPF-FLVMPIGSFPP 299
      428 ETQVPQWVITIIIMLFFLOCCIHPPVYGVMHTIKKEIQDMLKKFFCKEKPRKEDS---- 483
      300 DKPSETVFKIVFWLGYLNSCINPIIYPCSSQSEFKAFQNVLRICLRRKQSSKHALGYT 359
      484 -HPDLPGTEGTEGKI-VPSYDSATP 507
      360 LHPPSQAVEGQHKDMVRIPIVGSRETF 385
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RESULT 8

S65657

N:Alternate names: alpha-1C-adrenoreceptor splice form 2 - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004

C:Accession: S65657; S65655

R:Tanaka, T.

submitted to the EMBL Data Library, July 1994

A:Reference number: S65656

A:Accession: S65657

A:Molecule type: mRNA

A:Residues: 1-499 <TAN>

A:Cross-references: UNIPROT:Q13675; UNIPARC:UPI000004875B; EMBL:D32202; NID:9927208; PID

R:Hirasawa, A.; Shibata, K.; Horie, K.; Takei, Y.; Obika, K.; Tanaka, T.; Muramoto, N.;

FEBS Lett. 363, 256-260, 1995

A:Title: Cloning, functional expression and tissue distribution of human alpha(1C)-adre

A:Reference number: S65654; MUID:9555557; PMID:7737411

A:Accession: S65655

A:Molecule type: mRNA

A:Residues: 424-499 <HIR>

A:Cross-references: UNIPARC:UPI00001778AB; EMBL:D32202

C:Genetics:

A:Gene: GDB:ADRA1C; ADRA1L1

A:Cross-references: GDB:128088; OMIM:104221

A:Map position: 8p21-8p11.2

C:Superfamily: vertebrate rhodopsin

C:Keywords: alternative splicing; neurotransmitter receptor

Query Match 12.6%; Score 333.5; DB 2; Length 499;

Best Local Similarity 21.1%; Pred. No. 5.2e-15;

Matches 107; Conservative 79; Mismatches 189; Indels 131; Gaps 10;

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QY      8 STRENSSHTCMPISLAHGIRSVTVIFLAASFVGNIVLVLQKRPQLQVTN 67
      5 SCNASDSSNCTOP--PAPVNISKAILLGVLGGLLFGVLGNILVLSVACHRHLSVTH 62
      68 RIFNLVTLDDLQISLVAPWVAVTSVPLFMPINSHFCTALVSLTHLFAFASVNTTVLSV 127
      63 YIIVNLAVADLLTSTVLPFSAIFEVLAGYAFGRVFCNMAAVDVLCTASIMGLCIISI 122
      128 DRYLSIHPLSYPSKMTORRGVLLYGTWIVAILDSTPPLYGWGOAAPERNAALCSMIG 187
      123 DRYIGVSYPLRPTVTYTORGLMALLCWALSLVISIGLFGWRQPA-PEDETIQI--N 179
      188 ASPSTYILSVSFYIPLVIMTACSVVFCARROHALLYNKRHSLEVRVDCVENDE 247
      180 EEPGYLVFALGSPFLPLAILVMYCRYVYVAKR-----ESRGL 218
      248 EGAEKKEEFODESEFRROHGEVKAKEGMEAKDGLKAKEGSTGTSSESVEARGSEYR 307
      219 KSGLTKDSDSEQVTLRIHRKNAFA-----GSGMASAKTKTHFSVRL- 261
      308 EESTVADSGSMGKSGSTVEENSMKADKGRTEVNOCISIDLGEDDMFEDDINPSEDDV 367
      262 -----LKFSREK- 268
      368 EAVNIPESLPSPRRNSNPNPLPRCYOCCAKEYIFIIIFSIVLSLCPYCFPLAVLAWVDV 427
      269 -----KAAKTIGIVGCFVLCLWLPF-FLVMPIGSFPP 299
      428 ETQVPQWVITIIIMLFFLOCCIHPPVYGVMHTIKKEIQDMLKKFFCKEKPRKEDS---- 483
      300 DKPSETVFKIVFWLGYLNSCINPIIYPCSSQSEFKAFQNVLRICLRRKQSSKHALGYT 359
      484 -HPDLPGTEGTEGKI-VPSYDSATP 507
      360 LHPPSQAVEGQHKDMVRIPIVGSRETF 385
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RESULT 9

JH0315

N:serotonin receptor 1A - rat

N:Alternate names: 5-hydroxytryptamine receptor 1A (5-HT1A)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004

C:Accession: JH0315; A35181

R:Fujitawa, Y.; Nelson, D.L.; Kashiwara, K.; Varga, E.; Roeweke, W.R.; Yamamura, H.I.

Life Sci. 47, 127-132, 1990

A:Title: The cloning and sequence analysis of the rat serotonin-1A receptor gene.

A:Reference number: JH0315; MUID:90355775; PMID:2167416

A:Accession: JH0315

A:Molecule type: DNA

A:Residues: 1-422 <FUJ>

A:Cross-references: UNIPROT:P19327; UNIPARC:UPI00001778BE

J:Alibert, P.R.; Zhou, Q.Y.; Van Tol, H.H.M.; Bunzow, J.R.; Civelli, O.

J. Biol. Chem. 265, 5825-5832, 1990


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Db 185 HLVAIMADRYAVT-SIDYIRRRSARRILIMVWIVALFISIPPLFCWRDPNDPDKT 243
Qy 180 ALCSMIWGASPSYTIISVSVFIVPLIWIACYSVVCARROHALLVNVKHSLEVRK 239
Db 244 GTC--IIISODKGYTIFSTYGAPFLPLVMIIYIRIWLVARSR-----IRDKPQMTGA 295
Qy 240 DCVENDEEGAEKKEEFODESEFRQHEGEVAKKEGMEA-----KDGSLK 285
Db 296 RLKTEETTLVVASPKTEYSVAVSDCNGCNSPDSTTEKKRRAPFKSYGCSPREKKRRAK 355
Qy 286 AEGSGTSESSVEANGSEVR-ESSTVSDSGMEKEGSTKVEENSMADKGRTEVNC 344
Db 356 LPENANGVSNSSSSRLQIOIETVAEPANGCAE--EASIMLE-----RQC 401
Qy 345 SIDLGEDMEFGEEDINFSEDDVEAVNIPESLPPSRNSNSNPPLRCYCQAKAVIFI 404
Db 402 N-----NGKKISNDTPYRTREKLEKRR-----KAAKTLAI 436
Qy 405 IFSYVLSIGPYCFPLAVLVAVDEVQVPMVITIIIMLFLOCCHPYVYGVMKTIKE 464
Db 437 TCAFLICMLPFLIALIGFVDPBE-GIPPFARSFVLMGLYFNSLNPITITIFSPFRSA 495
Qy 465 IODML 469
Db 496 FOKIL 500

RESULT 12
JH0447
alpha-1a-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: JH0447
R/Bruno, J.F.; Whitaker, J.; Song, J.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991
A/Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic
A/Reference number: JH0447; MUID:9202892; PMID:1656955
A/Accession: JH0447
A/Molecule type: mRNA
A/Residues: 1-501 <BRU>
A/Genes: GDB:ADRA1A; ADRAL; ADRAIR
A/Cross-references: UNIPROT:P25100; UNIPARC:UPI0000149ED3; GB:M76446; NID:g177806; PIDN:
A/Experimental source: h1ppocampus
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
F:56-79/Domain: transmembrane #status predicted <TM1>
F:93-116/Domain: transmembrane #status predicted <TM2>
F:128-151/Domain: transmembrane #status predicted <TM3>
F:172-196/Domain: transmembrane #status predicted <TM4>
F:210-233/Domain: transmembrane #status predicted <TM5>
F:308-331/Domain: transmembrane #status predicted <TM6>
F:339-363/Domain: transmembrane #status predicted <TM7>

Query Match 11.9%; Score 314.5; DB 2; Length 501;
Best Local Similarity 23.0%; Pred. No. 1e-13;
Matches 102; Conservative 64; Mismatches 158; Indels 119; Gaps 10;
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Db 248 AGCKERG-----KASEVLR--IHCRAATGACGA--- 276
Qy 328 EENSKADGRTEVNCSDIDGEDMGEEDINFSEDDVEAVNIPESLPPSRNSNSNP 387
Db 277 --HGMSAKGHTFRSSLSVRL-----LKSRRK----- 302
Qy 388 PLPRCYCQAKAVIFIIFSYYLSGPGCFPLAVLVAVDEVQVPMVITIIIMLFLOC 447
Db 303 -----KAAKTLAIIVGVFVLCWPFPPFFVLPDS-LFPQLKPSGVEKVIWLGYSNS 353
Qy 448 CIHPVYGYMKTIKKEIODMLK 470
Db 354 CVMPLIYPCSSREFKRAFRLRLR 376

RESULT 13
I39369
alpha-1A-adrenergic receptor - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: I39369; J02331
R/Sbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Mineman, K.P.;
Mol. Pharmacol. 47, 977-985, 1995
A/Title: Cloning of the human alpha 1d-adrenergic receptor and inducible expression of
A/Reference number: I39369; MUID:95265059; PMID:7746284
A/Accession: I39369
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-572 <RES>
A/Cross-references: UNIPROT:P25100; UNIPARC:UPI00003B078; GB:D29952; NID:g914933; PIDN:
A/Reinberg, D.H.; Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A/Title: Cloning, expression and characterization of human alpha adrenergic receptors
A/Reference number: J02331; MUID:94296402; PMID:8024574
A/Accession: J02331
A/Molecule type: mRNA
A/Residues: 1-30, 'G', 32-521, 'P', 523-572 <WEI>
A/Cross-references: UNIPARC:UPI000168433
A/Note: the authors translated the codon CCC for residue 522 as Arg
C/Genes: GDB:ADRA1A; ADRAL; ADRAIR
A/Cross-references: GDB:118749; OMIM:104219
A/Map position: 20pter-20qter
A/Introns: 37/3
C/Superfamily: vertebrate rhodopsin
C/Keywords: glycoprotein; neurotransmitter receptor; transmembrane protein
F:89-123/Domain: transmembrane #status predicted <TM1>
F:132-162/Domain: transmembrane #status predicted <TM2>
F:172-197/Domain: transmembrane #status predicted <TM3>
F:208-235/Domain: transmembrane #status predicted <TM4>
F:254-278/Domain: transmembrane #status predicted <TM5>
F:344-374/Domain: transmembrane #status predicted <TM6>
F:380-414/Domain: transmembrane #status predicted <TM7>
F:55/2/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.9%; Score 314.5; DB 2; Length 572;
Best Local Similarity 23.0%; Pred. No. 1.2e-13;
Matches 102; Conservative 64; Mismatches 158; Indels 119; Gaps 10;
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Db 270 IVWYCRYVVAR-----STTRSL 289
Qy 268 GEVKAKEGMEAKDGLAKKEGSTGTSSSEVARGSEVERESSSTVADSGMEKGEKSTKV 327
Db 290 AGVKEKRG-----KASEVLR---IHCGAALGADGA--- 318
Qy 328 EENSMKADKGRTEVNOCSIDIGEDDMERGEDDINFSEDDEAVNIPESLPPSRNSNSNP 387
Db 319 --HGMRSAKGHTFRSSLSVRL-----LKFSREK----- 344
Qy 388 PLPRCYCKAKAVTIIIFSVYLSGPRCYFLAVLAWVDVETQVQWVITIIIMFLPLOC 447
Db 345 -----KAKTALIVGVFLCMFPPEFVPLDGS-LPPOLKPEGVFKVIFMLGYTNS 395
Qy 448 CIHPYVGYMKTIKKEIOMDK 470
Db 396 CVNPLIPCSSREFKAFRLRL 418

RESULT 14

548657
muscarinic acetylcholine receptor MR - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S48657; S24948
C:Accession: S48657; S24948
C:Herrera, L.; Carvallo, P.; Antoneilli, M.; Olate, J.
FEBS Lett. 352, 175-179, 1994
A:Title: Cloning of a Xenopus laevis muscarinic receptor encoded by an intronless gene.
A:Reference number: S48657; MUID:95010703; PMID:7925970
A:Accession: S48657
A:Molecule type: mRNA
A:Residues: 1-484 <HER>
A:Cross-references: UNIPROT:P03544; UNIPARC:UPI00001778CB; GB:X65865; NID:g64900; PIDN:C
R:Olate, J.
submitted to the EMBL Data Library, April 1992
A:Reference number: S24948
A:Accession: S24948
A:Molecule type: mRNA
A:Residues: 1-131, 'X', 133-484 <OLA>
A:Cross-references: UNIPARC:UPI00001252BD; EMBL:X65865; NID:g64900; PID:g64901
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:33-58/Domain: transmembrane #status predicted <TM1>
F:71-95/Domain: transmembrane #status predicted <TM2>
F:108-139/Domain: transmembrane #status predicted <TM3>
F:148-172/Domain: transmembrane #status predicted <TM4>
F:194-217/Domain: transmembrane #status predicted <TM5>
F:407-427/Domain: transmembrane #status predicted <TM6>
F:439-460/Domain: transmembrane #status predicted <TM7>

Query Match 11.8%; Score 312.5; DB 2; Length 484;
Best Local Similarity 21.0%; Pred. No. 1.3e-13;
Matches 110; Conservative 105; Mismatches 209; Indels 99; Gaps 16;

Qy 7 NSTRESNHSHTCMPKSPISLAHGIRSTVLVFLA-----ASFGNITVLVLQR 58
Db 3 NDTWENESSASVHSIDENTIVEIRGKY--QTMEMIFLATVGSLSLVTVGNILWLSIKV 60
Qy 59 KPQLQVNNRPIFNLLVDL---QISLVARVAVATSVPLFWPLNSHCTALVSLTHLF 114
Db 61 NRQLQTVNNYFLFSACADLLIGVSMNLSLYIKG---YMPLGPIVCDMLMLADYV 116
Qy 115 AFAVNTVIVLVSDVYLSIHPISYPSKKTORGVLIVGTVIVALLGSTPLVYGGOA 174
Db 117 SNASVWMLIISLEKIFCYTKPLTPARTTGMAGLMIAMWLSFELMAPILFW-QPI 175
Qy 175 FDER---NALCSMIGASPSYTLISVSPFIVPLIVMTIACSVVFCARQHALYNNVR 231
Db 176 VQGRVVPSEGCYIQLPSNPAVTFGTAIAFYLPVIMTLIYHISLASR-----VRR 229
Qy 232 HSLERVVDQVENEDEGAKEKEEFODESEFRQHEGVEKAKEGMEAKDGLAKKEG-S 290

Db 230 HCPETR-----OEKKPISSMKSLIIKOTKIP---KQADGKRVKKNVS 273
Qy 291 TGTSESSVARGSEVERESSSTVADSGM-----EKEGSTKVEENSMK--ADKG 337
Db 274 NGKTEKSWTNQTAEKETSNESSASLSHNHPREKQPLSEASSGVLAFTQSMPLPAKA 333
Qy 338 RTE-----VNQCSIDIGEDDMERGEDDINFSEDDEAVNIPE 374
Db 334 NTASKMSKIKIVTKQNGECYTAIEIPECAIPE-----QANNRPVNNAR 380
Qy 375 SLPPSRNSNSNPPLPRCYCKAKAVTIIIFSVYLSGPRCYFLAVLAWVDVETQVQW 434
Db 381 KPASTARQVRKKROMAAREKVTTRTIPALLAFITITPTNNWMLINTF---COTCIPE 438
Qy 435 VITIIIMFLPLOCCHIPPVYGYMKTIKKEIOMDKKPFCKEK 477
Db 439 IWYIGVWLCYNNSTINPACVALCNATFKTKHL---MCGYK 478

RESULT 15

A38731
alpha-1A adrenergic receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A38731; A53280
C:Accession: A38731; A53280
C:Riomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.
J. Biol. Chem. 266, 6365-6369, 1991
A:Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recept
A:Reference number: A38731; MUID:91177889; PMID:1706716
A:Accession: A38731
A:Molecule type: mRNA
A:Residues: 1-560 <LOW>
A:Cross-references: UNIPROT:P23944; UNIPARC:UPI000015AB77; GB:M60654; NID:g202761; PIDN:
R.Perez, D.M.; Placik, M.T.; Graham, R.M.
Mol. Pharmacol. 40, 876-883, 1991
A:Title: Solution-phase library screening for the identification of rare clones: isolati
A:Reference number: A53280; MUID:92100054; PMID:1661838
A:Accession: A53280
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-36, 'P', 38-58, 'Y', 60-202, 'I', 204-305, 'R', 307-366, 'I', 368-370, 'I', 372-559 <F
A:Cross-references: UNIPARC:UPI00000E7159
A:Experimental source: hippocampus
A:Note: sequence extracted from NCBI backbone (NCBI:73541)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 11.6%; Score 306.5; DB 2; Length 560;
Best Local Similarity 23.0%; Pred. No. 3.9e-13;
Matches 102; Conservative 59; Mismatches 163; Indels 119; Gaps 10;

Qy 29 AHGIRSTVLVIFLASFPVGNIVLAVLQRRKQLQVNNRPIFNLLVTDLLQISLVAPMV 88
Db 88 AOGVGVGFPLAFITAVAGNVLVLSVACNRHLQTVNNTIVNLVADLLLSAVALPFS 147
Qy 89 VATSVPLFWPLNSHCTALVSLTHLFAFASVNTIVLVSDRYLSIHPISYPSKKTORG 148
Db 148 ATMEVLGFMAARGRCFCDVMAVADVLCCTASILSLCTISVDVRYGVRSIKYPAIMTERKA 207
Qy 149 YLLVGTIVVAILGSTPLVYGWQ--AARDERNALCSMIGASPSYTLISVSPFIVPLIV 207
Db 208 AAILLALVAVLVSVGLGLKMKKEVPDER--FCGIT--BEVGYAIFSSVCSFYLPNAV 263
Qy 208 MIACSVVFCARQHALYNNKHSLEVRVYDQVENEDEGAKEKEEFODESEFRQHE 267
Db 264 IVWYCRYVVAR-----TRSLDAGLK-----REP 290
Qy 268 GEVKAKEGMEAKDGLAKKEGSTGTSSSEVARGSEVERESSSTVADSGMEKGEKSTKV 327
Db 291 GKASEVVRHICRGAAATSAK-GYPTQSS----- 318
Qy 328 EENSMKADKGRTEVNOCSIDIGEDDMERGEDDINFSEDDEAVNIPESLPPSRNSNSNP 387

Db 319 -----KGHTLRSLSLVRL-----LKFSREK----- 338

Qy 368 PLPRCYCKAAVYIIIIISVYSLGPGYGLAVLAWVNDVENOVQGVNIIITWLEFLOC 447

Db 339 -----KAAKTLIAVSGVFVDCMPFFFFVPLGS-IFFPQLKPSGSEFNVITMIGYFNS 389

Qy 448 CIHPVYVGYMHTIKKEIOMDK 470

Db 390 CVPNLIYPOSSREFFKKAFLRLRLR 412

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Job time : 31.8636 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 06:23:01 ; Search time 170.873 Seconds
(without alignments)
2097.517 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSSTRNSHTCMP.....GTGGTEGKIYPSYDSTAFP 508

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2641	99.9	508	1 GP101_HUMAN	Q96P66 homo sapien
2	2641	99.9	508	2 Q5JSM8_HUMAN	Q5JSM8 homo sapien
3	588	22.2	229	2 Q4RPS9_TETNG	Q4RPS9 tetraodon n
4	576	21.8	200	2 Q4SUM2_TETNG	Q4SUM2 tetraodon n
5	392.5	14.8	526	2 Q90X46_BRARE	Q90X46 brachydanto
6	391	14.8	407	2 Q5TGK0_HUMAN	Q5TGK0 homo sapien
7	391	14.8	529	1 GP161_HUMAN	Q8N6U8 homo sapien
8	391	14.8	529	2 Q5TGK1_HUMAN	Q5TGK1 homo sapien
9	373	14.1	535	2 Q4S0K3_TETNG	Q4S0K3 tetraodon n
10	343.5	13.0	490	1 ACMA_CHICK	P17200 gallus gall
11	343	13.0	77	1 GP101_MOUSE	Q96P62 mus musculu
12	343	13.0	466	2 Q96RER_HUMAN	Q96RER homo sapien
13	341	12.9	427	2 Q8BUES_MOUSE	Q8BUES mus musculu
14	341	12.9	466	2 Q8BV77_MOUSE	Q8BV77 mus musculu
15	340.5	12.9	422	1 SH71A_HUMAN	P08908 homo sapien
16	340.5	12.9	422	2 SH71A_PANTR	Q929X8 pan troglod
17	340.5	12.9	422	2 Q5ZGX3_HUMAN	Q5ZGX3 homo sapien
18	340	12.9	425	2 Q9MZU2_RABIT	Q9MZU2 oryctolagus
19	340	12.9	429	2 Q9MZU3_RABIT	Q9MZU3 oryctolagus
20	340	12.9	466	1 ADA1A_RABIT	Q02824 oryctolagus
21	340	12.9	470	1 ADA1A_RABIT	Q91175 oryctolagus
22	339.5	12.8	408	2 Q98998_XETILA	Q98998 xenopus lae
23	339.5	12.8	422	1 SH71A_GORGO	Q9N297 gorilla gor
24	339.5	12.8	490	2 Q5MBX1_COULLI	Q5MBX1 columba liv
25	338.5	12.8	466	1 ADA1A_HUMAN	P35348 homo sapien
26	337.5	12.8	466	1 ADA1A_CAVPO	Q9W425 cavia porce
27	336	12.7	466	1 ADA1A_PAT	P43140 rattus norv
28	335.5	12.7	421	1 SH71A_MOUSE	Q64264 mus musculu
29	335.5	12.7	422	1 SH71A_PONY	Q9N296 pongo pygma
30	334.5	12.7	423	1 SH71A_VULVU	Q6XXY0 vulpes vulp
31	333.5	12.6	423	2 Q8HYB0_CANFA	Q8HYB0 canis fami

32	333.5	12.6	466	2 Q4VBW7_HUMAN	Q4VBW7 homo sapien
33	333	12.6	423	1 SH71A_FUGRU	Q42385 fugu rubrip
34	333	12.6	466	1 ADA1A_MOUSE	P97718 mus musculu
35	332.5	12.6	422	1 SH71A_PAT	P19327 rattus norv
36	331.5	12.5	421	2 Q8BGS4_MOUSE	Q8BGS4 m mus muscu
37	331.5	12.5	423	1 SH71A_CANFA	Q6XXK9 canis fami
38	330.5	12.5	421	2 Q8BZP1_MOUSE	Q8BZP1 mus musculu
39	330	12.5	422	2 Q4T0Z1_TETNG	Q4T0Z1 tetraodon n
40	328.5	12.4	466	1 Q4T2Y7_TETNG	Q4T2Y7 tetraodon n
41	325.5	12.3	436	2 ADA1A_BOVIN	P18130 bos taurus
42	324	12.3	416	2 Q6XPX2_OREMO	Q6XPX2 oreochromis
43	324	12.3	466	2 Q9TSM7_PIG	Q9TSM7 sus scrofa
44	321	12.1	481	2 Q5U3D5_BRARE	Q5U3D5 brachydanto
45	320	12.1	341	2 Q4RX90_TETNG	Q4RX90 tetraodon n

ALIGNMENTS

RESULT 1
GP101_HUMAN STANDARD; PRT; 508 AA.
ID GP101_HUMAN
AC Q96P66; Q8NG93;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable G-protein coupled receptor 101.
GN Name=GPR101;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21458557; PubMed=1574155; DOI=10.1016/S0378-1119(01)00651-5;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhibko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22040266; PubMed=12044879; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsubesuni S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bat N.K.,
RA Hopline R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carinci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy M., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Boultard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schenker A., Schein U.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Orphan receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC
DR EMBL; AF411115; AAL26486.1; -; Genomic DNA.
DR EMBL; AB083588; BAB89301.1; -; Genomic DNA.
DR EMBL; AB065937; BAC06152.1; ALT_INIT; Genomic DNA.
DR EMBL; BC069439; AAH69439.1; -; mRNA.
DR Ensembl; ENSG00000165370; Homo sapiens.
DR HGNC; HGNC:14963; GPR101.
DR MIM; 300393; -.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 35 Extracellular (Potential).
FT TRANSMEM 1 35 1 (Potential).
FT TOPO_DOM 57 56 Cytoplasmic (Potential).
FT TRANSMEM 57 68 2 (Potential).
FT TOPO_DOM 69 89 Extracellular (Potential).
FT TRANSMEM 90 106 Extracellular (Potential).
FT TOPO_DOM 107 127 3 (Potential).
FT TRANSMEM 107 129 Cytoplasmic (Potential).
FT TOPO_DOM 128 147 4 (Potential).
FT TRANSMEM 150 170 4 (Potential).
FT TOPO_DOM 171 196 Extracellular (Potential).
FT TRANSMEM 197 217 5 (Potential).
FT TOPO_DOM 218 399 Cytoplasmic (Potential).
FT TRANSMEM 400 420 6 (Potential).
FT TOPO_DOM 421 433 Extracellular (Potential).
FT TRANSMEM 434 454 7 (Potential).
FT TOPO_DOM 455 508 Cytoplasmic (Potential).
FT CARBOHYD 7 13 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
FT DISULFID 104 182 By similarity.
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B5 CRC64;

Query Match 99.9%; Score 2641; DB 1; Length 508;
Best Local Similarity 99.8%; Pred. No. 3,8e-147;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIFNLVTDLLQISLVAPMWVAVSVLPFWPLNSHFCALVSLTHLFAFASVN 120
DB 61 QLLQVTRNFIFNLVTDLLQISLVAPMWVAVSVLPFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
QY 181 LCSMTWGSPSYTTLSVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLSEVRKYD 240
DB 181 LCSMTWGSPSYTTLSVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLSEVRKYD 240
QY 241 CVENDEDEGAKEKEFEODESEFRROHGEVAKKGRMAKDGSLAKEGSGTSSSEV 300
DB 241 CVENDEDEGAKEKEFEODESEFRROHGEVAKKGRMAKDGSLAKEGSGTSSSEV 300

QY 301 RGESEVRESSVADSGMEGKSTKVEENSMKADKRTENOCSDLGEDMFEGBDI 360
DB 301 RGESEVRESSVADSGMEGKSTKVEENSMKADKRTENOCSDLGEDMFEGBDI 360
QY 361 NFSDDVAVVIPSLSPPSRNSNPPLPRCYCKAKAVYFIIFSVYSLGFCFLAV 420
DB 361 NFSDDVAVVIPSLSPPSRNSNPPLPRCYCKAKAVYFIIFSVYSLGFCFLAV 420
QY 421 LAVVVDVETQVQVWVITIIWLFLLQCCIHBYVYGVNKKTIKKEIDMLKKFCKEPPK 480
DB 421 LAVVVDVETQVQVWVITIIWLFLLQCCIHBYVYGVNKKTIKKEIDMLKKFCKEPPK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATRP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATRP 508

RESULT 2

Q5JSM8_HUMAN PRELIMINARY; PRT; 508 AA.
ID Q5JSM8_HUMAN PRELIMINARY; PRT; 508 AA.
AC Q5JSM8;
DT 10-MAY-2005 (TREMblrel. 30, Created)
DT 10-MAY-2005 (TREMblrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMblrel. 30, Last annotation update)
DE G-protein-coupled receptor, 101.
GN Name=GPCR101; ORFNames=NP11-308D16.5-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawlor S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL330879; CA14047.1; -; Genomic DNA.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln.; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B5 CRC64;

Query Match 99.9%; Score 2641; DB 2; Length 508;
Best Local Similarity 99.8%; Pred. No. 3,8e-147;
Matches 507; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVLRKP 60
DB 1 MTSTCTNSTRESNSHTCMPLSKMPSISLAHGIRSTVIVIFLAASFVGNIVLALVLRKP 60
QY 61 QLLQVTRNFIFNLVTDLLQISLVAPMWVAVSVLPFWPLNSHFCALVSLTHLFAFASVN 120
DB 61 QLLQVTRNFIFNLVTDLLQISLVAPMWVAVSVLPFWPLNSHFCALVSLTHLFAFASVN 120
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
QY 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
DB 121 TIVVSVDRYLSIIHPLSYPSKMTQRGYLLVGTWIVAILQSTPPLVGMGQAADFERN 180
QY 181 LCSMTWGSPSYTTLSVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLSEVRKYD 240
DB 181 LCSMTWGSPSYTTLSVSVFIVPLIWIACYSVVFCAARQHALLVNKKHSLSEVRKYD 240
QY 241 CVENDEDEGAKEKEFEODESEFRROHGEVAKKGRMAKDGSLAKEGSGTSSSEV 300
DB 241 CVENDEDEGAKEKEFEODESEFRROHGEVAKKGRMAKDGSLAKEGSGTSSSEV 300


```
QY 301 RSSEVRESSTVADSGMEKSGSTVEBNSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
DB 301 RSSEVRESSTVADSGMEKSGSTVEBNSMKADKGRTEVNOCSIDLGEDMEFGEDDI 360
QY 361 NFSEDDVEAVNIPEISLPSRRNSNSNPRLPCRYQCAAAVYFIIFSYLSIGPYCELA 420
DB 361 NFSEDDVEAVNIPEISLPSRRNSNSNPRLPCRYQCAAAVYFIIFSYLSIGPYCELA 420
QY 421 LAWVWDEVOVPOWVTTIIMLFLOCCIHPPVYGMHTIKREIOMDKKPFCKEKKPK 480
DB 421 LAWVWDEVOVPOWVTTIIMLFLOCCIHPPVYGMHTIKREIOMDKKPFCKEKKPK 480
QY 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
DB 481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508
481 EDSHPDLPGTEGTEGKIVPSYDSATFP 508

RESULT 3
O4RP59 TETNG PRELIMINARY; PRT; 229 AA.
ID O4RP59
AC O4RP59
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 1 SCAF15008, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00031265001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC EMBL, CAEB01015008; CAG09823.1; -; Genomic_DNA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 229
FT SEQUENCE 229 AA; 25449 MW; 6CEB5B9850A9AA6 CRC64;

Query Match 22.2%; Score 588; DB 2; Length 229;
Best Local Similarity 49.3%; Pred. No. 6; 9e-27;
Matches 113; Conservative 47; Mismatches 57; Indels 12; Gaps 3;
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```
QY 6 TNSRESNSSHTCMPLSKMPLSLAHGIRSTVLVFLAASFVGNIVLALVLRKPOLLOV 65
DB 11 TNNTD-----ARGVSTVDSVVMVIALILCSLFGNVVLLVFPKRQPLLHV 60
QY 66 TNRFFNLVLDLQISLVAPNVVATVDPLEPLNSHFTALVSLTHLFAFASVNTIVL 125
DB 61 ANRFVNLILLADLLQTVLWMPALAAVGVMPDLARLQALVLMHLFPAFAGVNTIIV 120
QY 126 SYDRVLSITHPLSYSPSKMORRGYLLVCTVVALVLTQSTPPLVYGCQAADFERNLCSMI 185
DB 121 SYDRVLSITHPLSYSPSKMORRGYLLVCTVVALVLTQSTPPLVYGCQAADFERNLCSMI 180
QY 186 WGSASVYTI--SVGSFIVPLIIVLACYSVFCAARQHALVYVRHS 233
DB 181 WSSLSYSIMVSTLSF-WLPVIMLCGMVVRARARQNALVHPYQYOS 228

RESULT 4
O4SUM2 TETNG PRELIMINARY; PRT; 200 AA.
ID O4SUM2
AC O4SUM2
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF13862, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00012395001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_Taxid=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Bismont C., Skalli Z., Catolico L., Poulain J., De Bernardinis V.,
RA Cruaud C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -! SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC EMBL, CAEB01013862; CAF95660.1; -; Genomic_DNA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1.2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON TER 200
FT SEQUENCE 200 AA; 22473 MW; 8DOA26D8F99489C CRC64;

Query Match 21.8%; Score 576; DB 2; Length 200;
Best Local Similarity 55.1%; Pred. No. 3e-26;
Matches 109; Conservative 39; Mismatches 48; Indels 2; Gaps 2;
```

```
QY 37 VLVFLLAASFGVGNIVLALVLRKPOLLOVTRNFNLLVTDLIQISLVAPVAVATSVPLF 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 LIALILCVSLFSGNVVLLVLFQRPOLLVHNFVNLILLADLLQTVLWMPFLAASVPGV 62
QY 97 WPLNSHCTALVSLTLHLFAFASVNTIVSVVDRLYSIIHPLSPSKMTQORGYLLXGTW 156
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 63 WPLDLRLCOALVNLHLFAFAGVNTIVSVVDRLYSIIHPLSPSKMTQORGYLLXGTW 122
QY 157 IVAILQSTPPLVGMGOAALFDERNALCSMIWGAASPSYTLI-SVVSFIVPLIVMIACYSV 215
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 VLSLIQSTPPLVGMGOAALFDERNALCSMIWGAASPSYTLI-SVVSFIVPLIVMIACYSV 181
QY 216 FCAARROHALVYNKRHS 233
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 182 FRAARROHALVYNKRHS 199
```

RESULT 5

```
Q90X46_BRARE PRELIMINARY; PRT; 526 AA.
ID Q90X46_BRARE PRELIMINARY; PRT; 526 AA.
AC Q90X46;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Novel protein similar to human G-protein coupled receptor R22.
GN Name=sl:rp1-2015.4; Synonyms=OTDARPO00001218;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lloyd D.;
RL Submitted (DEC-2004) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL550146; CAC94897.2; -; Genomic DNA.
DR Ensembl; ENSDARG0000000007; Danio rerio.
DR ZFIN; ZDB-GENE-030616-58; sl:rp1-2015.4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 526 AA; 58485 MW; CACE795D6385B3E CR664;
```

```
Query Match 14.8%; Score 392.5; DB 2; Length 526;
Best Local Similarity 23.6%; Pred. No. 4.9e-15;
Matches 110; Conservative 75; Mismatches 137; Indels 145; Gaps 10;

QY 7 NSTRSNSHTCMPLSKPISLAHGIIRSTVIVFLAASFGVGNIVLALVLRKPOLLOVTR 66
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 6 NGTAVANSTNGLDNGLM-----VLESVSIITIIAIIACLDNLVIVTLVYKPYLLPS 58
QY 67 NRIFFNLVTDLIQISLVAPVAVATSVPLFPLNSHFC--TALVSLTLHLFAFASVNTIVL 124
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 59 NKFVSLSSNNLLSLVLMPLFVASSVRDMMFGVWCMFTHLH--LVSSSMULTLGA 116
QY 125 VSVDRYSIIHPLSPSKMTQORGYLLXGTWIVAILQSTPPLVGMGOAALFDERNALCSM 184
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 IALDYIVVILYPMIYPMKITGNRAVLAIVYIMLHSLVGLPLFGMSPEFDRFKWCTIV 176
QY 185 IWSGSPSTIISVSVFIVPLIVMIACYSVVFCAARROHALVYNKRHSLEVRVADCVEN 244
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
```

```
Db 177 SMKEISTAFWWTWCCILPLVAMLVCGVIFVRAR----- 212
QY 245 EDERGAKEKEEFODESEFRRQHEGEVAKAEGRMKADGSLKAKGSGTSTSSSVEARGSE 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 -----IAKRVYCG----- 221
QY 305 EVRESSTYASDGMGKEGKSTKVEENSKADKGTENVQCSIDIDGEDDMERGEDDINSE 364
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 222 -----SVVVS-----QESSSQNNGRKNSVTSISSG----- 248
QY 365 DDEAVNIPESLPSRRN---SNSNPPLRCYCKAAKVFIRIIFSVLSLGPYCFGLAVL 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 -----SRKSLISGS-----QCKAFITLVVLTFLTTGCPYVVVIST 286
QY 422 AVWVDVETQVPOWYITIIIMLFPLQCCIHPPYGYMHTIKKEIQDM 468
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 287 BALGKNSVSPQ-VETIVSWLSFTSAVCHPILYGLMNTVAKELIGM 332
```

RESULT 6

```
Q5TGK0_HUMAN PRELIMINARY; PRT; 407 AA.
ID Q5TGK0_HUMAN PRELIMINARY; PRT; 407 AA.
AC Q5TGK0;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE G-protein-coupled receptor 161.
GN Name=GPRI61; ORFNames=RP4-745114.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Martin S.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
DR EMBL; AL033532; CA12624.1; -; Genomic DNA.
DR Ensembl; ENSG00000143147; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 407 AA; 45363 MW; 000788B85B8C1F21 CAC64;
```

```
Query Match 14.8%; Score 391; DB 2; Length 407;
Best Local Similarity 23.6%; Pred. No. 4.6e-15;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

QY 31 GIIRSTVIVFLAASFV--GNIVLALVLRKPOLLOVTRNFNLLVTDLIQISLVAPV 88
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 25 GVIIITQFAIVITTFVCLGNLVIVVITYKKSYSLLTSNKKVFSLLSNFLSLVLPFV 84
QY 89 VATSVPLFMPPLNSHCTALVSLTLHLFAFASVNTIVSVVDRLYSIIHPLSPSKMTQORRG 148
   |||||:|:~|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 85 VTSSIRRMINGVWCMNSALYLLISSASMLTGIVAIIDRYVAVLVPMYPMKITGNRA 144
QY 149 YLLVGTWIVAILQSTPPLVGMGOAALFDERNALCSMIWGAASPSYTLISVSVFIVPLIVM 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 VVALVYIMLHSLIGCLPLPLFGMSVVEFDEFKMVCVAAMHRRPGYTAFWQICALFPFLVM 204
QY 209 IACYSVVFCARROHALVYNKRHSLEVRVADCVENDEBGAKEKEEFQDSEFRRQHEG 268
   |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 205 LVCTGIFIRVAR-----VKARKVHCGTIVIVE-EDAQ----- 235
```

```
OY 269 EVKANEGRMEADKSLAKKEGSGTSSSEVARGSEEVRESSTVADSGMECKEGSTKYE 328
      : |||
      : |||
DB 236 ----RTGR-----KNSSTSTSSG-----250
OY 329 ENSMADKRTERTVNOCSIDLGEDMEFEGDDINFSEDVVEAVNIPESLPPSRNS-----383
DB 251 -----SRNNAFGVY 260
OY 384 -NSNPPLPRCYOCCAKAKVFIIFSYVLSIGPY-CFLAVLAVM--VDVEFOVPOVITII 439
      : |||
      : |||
DB 261 YGAN-----OQKALITLVVGAFMTVWGPVMTVIVASEBALMGKSSVSPSLFTMA-----309
OY 440 IWLFLQCCIHPPYVYGVMHTIKKEIQDM 468
      : |||
      : |||
DB 310 TWLSPASAVCHPLIVGLMKTKVTRKELLGM 338

RESULT 7
GP161 HUMAN
ID GP161 HUMAN STANDARD; PRT; 529 AA.
AC Q8N6U8; 075963;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable G-protein coupled receptor 161 (G-protein coupled receptor
RE2).
GN Name=GPRI61;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RC TISSUE=Brain;
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "Isolation of cDNA coding for G-protein coupled receptor RE2.";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Brain;
RA Raming K., Konzelmann S., Breer H.;
RT "Identification of a novel G-protein coupled receptor expressed in
RL distinct brain regions and a defined olfactory zone.";
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stampleton M., Soares M.B., Donald M.F., Caesvant T.L., Scheetz T.E.,
RA Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Franke C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodrigues A.C., Grimmwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
```

```
CC -!- ALTERNATIVE PRODUCTS;
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC Isoid=Q8N6U8-1; Sequence=Displayed;
CC Name=2;
CC Isoid=Q8N6U8-2; Sequence=VSP_010560, VSP_010561;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AY275468; AAP3300.1; -; mRNA.
CC EMBL; AF091890; AAC61598.1; -; mRNA.
CC EMBL; BC028163; AAH28163.1; -; mRNA.
CC Ensembl; ENSG00000143147; Homo sapiens.
CC HGNC; HGNC:23694; GPRI61.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC Pfam; PR00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_RHODOPSIN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
CC KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
CC Receptor; Transducer; Transmembrane.
CC -----
CC TOPO_DOM 1 30 Extracellular (Potential).
CC FT 31 51 1 (Potential).
CC FT TOPO_DOM 52 64 Cytoplasmic (Potential).
CC FT TRANSMEM 65 85 2 (Potential).
CC FT TOPO_DOM 86 92 Extracellular (Potential).
CC FT TRANSMEM 93 113 3 (Potential).
CC FT TOPO_DOM 114 143 Cytoplasmic (Potential).
CC FT TRANSMEM 144 164 4 (Potential).
CC FT TOPO_DOM 165 191 Extracellular (Potential).
CC FT TRANSMEM 192 212 5 (Potential).
CC FT TOPO_DOM 213 269 Cytoplasmic (Potential).
CC FT TRANSMEM 270 290 6 (Potential).
CC FT TOPO_DOM 291 306 Extracellular (Potential).
CC FT TRANSMEM 307 327 7 (Potential).
CC FT TOPO_DOM 328 529 Cytoplasmic (Potential).
CC FT CARBOHYD 4 4 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 15 15 N-linked (GlcNAc...) (Potential).
CC FT VARSPLIC 403 406 TDM -> NTRA (in isoform 2).
CC FT FTID VSP_010560.
CC FT VARSPLIC 407 529 Missing (in isoform 2).
CC FT FTID VSP_010561.
CC FT VARSPLIC 529 AA; 58559 MW; FC7D1AC0894DC3F3 CRC64;
CC SQ SEQUENCE

Query Match 14.8%; Score 391; DB 1; Length 529;
Best Local Similarity 23.6%; Pred. No. 66-15;
Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;

OY 31 GIIRSTVIVIFPLAAFFV--GNIVLALVLOKPKQLQVTRFIFNLVTDLQISVAPVW 88
      : |||
      : |||
DB 25 GVIITFOFIAIYITITFVCGNLVIYTYLKYKSYLTKNSKVPSTLTSNPLSVLVLPV 84
OY 89 VATSVPLFPLNHSFCTALVSLTHLPAPASVNTIVASVDRYLSIHPSPSKXTORRG 148
      : |||
      : |||
DB 85 VTSIRREIMFVGVNCFNSALLYLLISSASMTLGVIAIDRYAVLVPMVYPMKITGNRA 144
OY 149 YLLIGTAVVAILQSTPPYLGWGAAPFERNALGSMIGASSTYITLVSIVPLIYM 208
      : |||
      : |||
DB 145 VVALVYIWMHSLIGCLPPLFGMSVVEFEKMKCAAAHREGYTAFMQIWCALPPLFM 204
OY 209 IACYSVFPCARQHALLYNVRHSLVAVKDCVNEDEEGAKKEKFEODESEFRRQHG 268
      : |||
      : |||
DB 205 LVYCGFIRFVRV-----VYAKVHCITVIYE-EDAQ-----235
OY 269 EVKANEGRMEADKSLAKKEGSGTSSSEVARGSEEVRESSTVADSGMECKEGSTKYE 328
      : |||
      : |||
DB 236 ----RTGR-----KNSSTSTSSG-----250
```

QY 329 ENSKADKGRTEVNCSTIDLGEDDMEFEGDDINFESEDDVEAVNIPESLPSPRRNS----- 383
 Db 251 -----SRNAFGQGV 260
 QY 384 -NSNPPLRCYQCKAKAVYFIIFSYVLSGPy-CFLAVLAVM--VDVETQVPOQVITII 439
 Db 261 YSAN-----QCKALITILVLGAFMVTWGPYVNVVIASEALMGKSSVPSLETMA----- 309
 QY 440 IWLFLQCCIHPIYVGYVNHKTIKEIODM 468
 Db 310 TWLSFASAVCHPLIYGLMKNKTVRKELGM 338

RESULT 8
 O5TGK1 HUMAN PRELIMINARY; PRT; 529 AA.
 ID O5TGK1 HUMAN PRELIMINARY; PRT; 529 AA.
 AC O5TGK1
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DE G-protein-coupled receptor 161.
 GN Name=GPRI61; ORFNames=RP4-745114.2-002;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Martin S.;
 RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL; AL033533; CA122623.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 529 AA; 58559 MW; FC7D1AC0894DC3F3 CRC64;

Query Match 14.8%; Score 391; DB 2; Length 529;
 Best Local Similarity 23.6%; Pred. No. 66-15;
 Matches 106; Conservative 67; Mismatches 130; Indels 146; Gaps 11;
 QY 31 GIRSTVIVIFPLAASFV--GNIVLALVLRKPOLQVTRRFIENLITVDLQISLVAPV 88
 Db 25 GVIITQFAIIVITITFVCLGNIVITVLYKSYLLTNSKPFSLTNSFLSVLVPV 84
 QY 89 VATSVPLWPLNSHFCIALVSLTHLFAFASVNTIVLVSDRYLSIHPISYSPKXTORRG 148
 Db 85 VTSSIRREMIFGVWNCFSALTYLLISSASMLTIGVIALDRYAVVLPVYPMKITGNRA 144
 QY 149 YLLVGTWIVALTOSTPLPYGCGAFAFERNALCGMIMWASSYITLISVSTIVPLVM 208
 Db 145 VVALVYIMHSLTIGCLPPLFGMSVVEFBEKMWCVAAHREGEYTAFWQIMCALPFLVM 204
 QY 209 IACYVVECAARQHALLVNVRHSLLEVAVKDCVENEDDEGAKKEEFQDESEFRHQEG 268
 Db 205 LVTCYFIRVAR-----VAKRVHCTVIVIE-EDQ----- 235
 QY 269 EYKAGEGMEAKDGLKAKESGTGTSSEVSEARGSEEVRESSSTVASDGSMEKSGSTKYE 328
 Db 236 ----RTGR-----KNSSSTSSSG----- 250
 QY 329 ENSMADKGRTEVNCSTIDLGEDDMEFEGDDINFESEDDVEAVNIPESLPSPRRNS----- 383

Db 251 -----SRNAFGQGV 260
 QY 384 -NSNPPLRCYQCKAKAVYFIIFSYVLSGPy-CFLAVLAVM--VDVETQVPOQVITII 439
 Db 261 YSAN-----QCKALITILVLGAFMVTWGPYVNVVIASEALMGKSSVPSLETMA----- 309
 QY 440 IWLFLQCCIHPIYVGYVNHKTIKEIODM 468
 Db 310 TWLSFASAVCHPLIYGLMKNKTVRKELGM 338

RESULT 9
 Q4SOK3_TETNG PRELIMINARY; PRT; 535 AA.
 ID Q4SOK3_TETNG PRELIMINARY; PRT; 535 AA.
 AC Q4SOK3;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DE Chromosome 2 SCAR14781, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=STENG0025981001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorph; Tetraodoniformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dobas C., Segurens B.,
 RA Dastivie C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Catclicco L., Poulan J., De Bernardis V.,
 RA Crnaud C., Duprat S., Brottier P., Couancan J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Boeck S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Querlet F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolihus H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CA601014781; CAG05829.1; -; Genomic DNA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON TER 535
 SQ SEQUENCE 535 AA; 58074 MW; 5203973C7F10E884 CRC64;

Query Match 14.1%; Score 373; DB 2; Length 535;
 Best Local Similarity 23.0%; Pred. No. 6.9e-14;
 Matches 112; Conservative 72; Mismatches 136; Indels 168; Gaps 13;
 QY 13 NSSHTCMLP-SKMPISLHGIIRSVIVIFPLAASGVGIVLALVLRKPOLQVTRRFI 71
 Db 2 NTSRNCIVASGEGIALESVMAITVTL-----ACLSULLVATLYRRPYLLTSNKFV 57
 QY 72 NLLVTDLQISLVAPWVAVTSVPLFWPLNSHFCIALVSLTHLFAFASVNTIVLVSD-- 128
 Db 58 SLTSLNLLSVLVPFVAVSVREMLFGVWNCFTALTYLLISSASMLTIGALAIIDRSV 117
 QY 129 -----RYLSIHPISYSPKXTORRGYLLVGTWIVALTOSTP 165

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Db      118 FSPSSCGAATLWVLTSLVLTTRYAVVYPMIYPKIKGNRAVVAISYVWLHSLVGLP 177
Qy      166 PLYGAGQAFDERNALCSMIGWASPSYTLVSFVIFLYIMICYSVVPQAAHQHNL 225
Db      178 PLEGMSSSEFDDLKRTCVASMRBSPYTFMWIWCLLPPLCYWLACVYVIFVVAR----- 232
Qy      226 LYNVRHSHLSLEVAVKDC---VENEDEGAKEKEEPQDESEFRQHEGVEKAKEGMEARD 281
Db      233 -----MKARKVHCITVTVGPDDAGAG-----RSGR----- 258
Qy      262 GSLKAKESGTSTSESSVEARGSEEVRESSTVASDSGMEKESGTVKENSMAKADKGRTEV 341
Db      259 -----KNSSTSTS-----SNSG---RSLVVA-----GS----- 279
Qy      342 NCGSIDLGEDDMFEGEDDINFSEDDVEAVNIPESLPSPRRNSNSNPPLPRCYQCKRAKY 401
Db      280 -----OQKAFVTI 287
Qy      402 FIIFSVYLSLGPYC-FLAVLAVWVDEVQVPOWVITIIIMFLQCCIHPPVYGMYHKT 460
Db      288 LVVIGTFVITWKPYPYGVCTEALM--GGGSVAPGLETLVAMLSLCSAVCHPLIYGFWMKT 345
Qy      461 IKKEIQDM 468
Db      346 VKRELLGM 353

RESULT 10
ACM4_CHICK STANDARD; PRT; 490 AA.
ID P17200;
AC 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Muscarinic acetylcholine receptor M4.
GN Name=CHRM4;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=90153912; PubMed=2154460;
RA Tietje K.M., Goldman P.S., Nathanson N.M.;
RT "Cloning and functional analysis of a gene encoding a novel muscarinic
RT acetylcholine receptor expressed in chick heart and brain.";
RL J. Biol. Chem. 265:2828-2834(1990).
CC -!- FUNCTION: The muscarinic acetylcholine receptor mediates various
CC cellular responses, including inhibition of adenylylate cyclase,
CC breakdown of phosphoinositides and modulation of potassium
CC channels through the action of G proteins. Primary transducing
CC effect is inhibition of adenylylate cyclase. May couple to multiple
CC functional responses in cell lines.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in heart and brain.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC removed.
CC
CC EMBL; J05218; AAA48563.1; -; Genomic_DNA.
CC
CC DR PIR; A35546; A35546.
CC DR HSSP; P02699; 1BOY.
CC DR Ensembl; ENSGALG00000008365; Gallus gallus.
CC DR GO; 0016021; C:integral to membrane; IC.
CC DR GO; 0004981; F:muscarinic acetylcholine receptor activity; NAS.
CC DR GO; 0007194; P:negative regulation of adenylylate cyclase ac. .; NAS.
CC DR GO; 0003084; P:phosphoinositide metabolism; NAS.

```

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DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR001432; M4_receptor.
DR InterPro; IPR000995; M4AC_receptor.
DR PANTHER; PTHR19266:SF85; M4_receptor; 1.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR00541; MUSCARINICR.
DR PROSITE; PS00541; MUSCARINICR.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family;
KW Phosphorylation; Posttranslational modification; Receptor; Transducer;
KW Transmembrane.
FT TRANSMEM 1 42 Extracellular (Potential).
FT TOPO_DOM 43 64 1 (Potential).
FT TOPO_DOM 65 78 Cytoplasmic (Potential).
FT TRANSMEM 79 99 2 (Potential).
FT TOPO_DOM 100 116 Extracellular (Potential).
FT TRANSMEM 117 138 3 (Potential).
FT TOPO_DOM 139 158 Cytoplasmic (Potential).
FT TRANSMEM 159 181 4 (Potential).
FT TOPO_DOM 182 203 Extracellular (Potential).
FT TRANSMEM 204 226 5 (Potential).
FT TOPO_DOM 227 412 Cytoplasmic (Potential).
FT TRANSMEM 413 433 6 (Potential).
FT TOPO_DOM 434 447 Extracellular (Potential).
FT TRANSMEM 448 467 7 (Potential).
FT TOPO_DOM 468 490 Cytoplasmic (Potential).
FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 15 15 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 20 20 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
FT DISULFID 115 195 By similarity.
SQ SEQUENCE 490 AA; 54937 MW; 2CDFB5FATD2298E CRC64;

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Query Match 13.0%; Score 343.5; DB 1; Length 490;
 Best Local Similarity 23.7%; Pred. No. 3,4e-12;
 Matches 116; Conservative 94; Mismatches 176; Indels 103; Gaps 17;

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Qy 36 TVLVFLA-----ASFVGNIVLALVQKRPQLQTNRTIFNLVTLDDL-----QISL 83
Db 39 TVELVFIAIVTGLSLVTVVGNILVMSLTKVNRQQTANNVFLFSLACADLIIGVPSMWL 98
Qy 84 VAPVAVATSVPLFVFNLSHFTALVSLTLFAPASVNTIVLVSVRYSIIHPLSYPSQM 143
Db 99 YTVYIIKG---YVFLGAVVCDLMLADYVNSNABVMLLISFPRICVTKPLTPPAR 154
Qy 144 TORRGYLLYGTWIVAILQSTPPLYGW---GQAAFDERNALCSMIGWASPSYTLISVVS 199
Db 155 TTKMAGLMAAMWILSFLIMAPALIFWQIVGKRTVHERE--CYIQLSNPAVTFGTALA 212
Qy 200 FIVIPLYIMACYSVVPCARQAHLLVNRHSLER-----YVDCVNN 244
Db 213 AFVLPVIMTVIYIHISLSRSR-----VRHKKESRERKRGKSLSPKAPVYQNNNN 266
Qy 245 EDEGAKEKEEPQDESEFRQHEGVEKAKEGMEAKDGLKAKESGTSTSESSVEARGSE 304
Db 267 SKRAVEYKEERK-----GRV-----DQPSQATATGQOE-----KE 301
Qy 305 EVRESSTVASDSGMEKESGTVKENSMAKADKGRTEVNCQSIDLGEDDMFEGEDDINFSE 364
Db 302 TNESSSTVSMQTQDKP-TTEILPAGQGQSPAHPRVNPST-----KWSKIKIVTKQ 352
Qy 365 DVEAVNIPESLP-----PSRRN--SNSNP-LPRCY-----QCKAAKY 400
Db 353 TGTESVTALIEIVPAGASDHNLSNSRPNVARRFASIASQVKKRQMAAREKVVVT 412
Qy 401 FIIFSVYLSLGPYCFLAVLAVWVDEVQVPOWVITIIIMFLQCCIHPPVYGMYHKT 460
Db 413 FVAILLAPLITTPFNWVLIWTF--CETCVETWMSIGWLCYVNSTINPACVYALCMT 470
Qy 461 IKKEIQDM 469

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Db	471	FKKTFKHLL	479
RESULT 11			
ID	GP101 MOUSE	STANDARD;	PRT; 77 AA.
AC	080762;		
DT	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Probable G-protein coupled receptor 101 (Fragment).		
GN	Name=GP101;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
OC	Muroidea; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RA	[1]		
RP	Nucleotide sequence [LARGE SCALE MRNA].		
RX	MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;		
RA	Vassiliadis D.K., Hohmann U.G., Zeng H., Li F., Ranchalis J.E.,		
RA	Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,		
RA	Bergman J.E., Gaitanaris G.A.;		
RT	"The G protein-coupled receptor repertoires of human and mouse.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).		
CC	-1- FUNCTION: Orphan receptor.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	-----		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	-----		
DR	EMBL: AY255576; AAC85088.1; -, mRNA.		
DR	Ensembl: ENSMUSG00000036357; Mus musculus.		
DR	MG1; MG1:2685211; Gp101.		
DR	InterPro: IPR000276; GPCR_Rhodpsn.		
DR	Pfam: PF00001; 7tm.1; 1.		
DR	PRINTS: PR00237; GPCRHHODPSN.		
DR	PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.		
KM	G-protein coupled receptor; Receptor; Transducer; Transmembrane.		
FT	TOPO_DOM <1 9 Cytoplasmic (Potential).		
FT	TRANSMEM 10 30 4 (Potential).		
FT	TOPO_DOM 31 56 Extracellular (Potential).		
FT	TRANSMEM 57 77 5 (Potential).		
FT	DISULFID <1 42 By similarity.		
FT	NON_TER 1 1		
FT	NON_TER 77 77		
SO	SEQUENCE 77 AA; 8517 MW; C760758CB179D114 CRC64;		
Query Match 13.0%; Score 343; DB 1; Length 77;			
Best Local Similarity 81.6%; Pred. No.5.6e-13;			
Matches 62; Conservative 6; Mismatches 8; Indels 0; Gaps 0;			
Qy	141 SKMTORRGYLLIYGTVAIIQSTPEPLGWGQAARDEBNALCSMTWGSPEYTLISVSF 200		
Db	1 SKMTRRRRIYLLIYGTVAIAFLDSTPEPLGWGHAATDDNACNMTWGSAPATVIVSVSF 60		
Qy	201 IYIPLIWIACYSVVF 216		
Db	61 IYIPLGVWIACYSVVF 76		
RESULT 12			
ID	Q96RE8_HUMAN	PRT; 466 AA.	
AC	Q96RE8;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		
DE	Adrenergic receptor alpha-1a.		

GN Name=ADRA1A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Banerjee A.G.N., Aarti A.,
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This alpha-adrenergic receptor mediates its action by
 CC association with G-proteins that activate a phosphatidylinositol-
 CC calcium second messenger system. Its effect is mediated by G(q
 CC and G(11) proteins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 DR EMBL: AF395806; AAK77197.1; -, mRNA.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004937; F: alpha-adrenergic receptor activity; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007166; P: G-protein coupled receptor protein signaln. .; IEA.
 DR GO: GO:0007165; P: signal transduction; IEA.
 DR InterPro: IPR001004; A: receptorA1C.
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0557; ADRENRCGA1A.
 DR PROSITE: PRO0237; GPCR_RHODOPSN.
 DR PROSITE: PS00237; G PROTEIN RECP FL 1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 SQ SEQUENCE 466 AA; 51431 MW; 876CBFB35323B7A1 CRC64;

 Query Match 13.0%; Score 343; DB 2; Length 466;
 Best Local Similarity 21.6%; Pred. No. 3,56-12;
 Matches 106; Conservative 76; Mismatches 178; Indels 130; Gaps 10.

RESULT	13
OBUES_MOUSE	PRELIMINARY; PRT, 427 AA.
ID	OBUES_MOUSE
AC	OBUES;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:063005ON06 product:cdrenegic receptor, alpha 1a, ALPHA
DE	1A-ADRENOCORTEX, full insert sequence.
GN	Name=Adra1a;
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
LN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RT	Carninci P., Hayashizaki Y.;
RL	"High-efficiency full-length cDNA cloning.";
RL	Meth. Enzymol. 303:19-44(1999).
LN	[2]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kankawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batraiov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brenneisen M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Guernicini S., Hill D., Hofmann W., Hume D.A., Kamya M., Lee N.H.,
RA	Lyons P., Marchionni L., Maehima T., Mazzarelli U., Mombertis P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA	Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
LN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RA	The FANTOM Consortium,
RA	"the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs.";
RL	Nature 420:563-573(2002).
LN	[4]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA	Carninci P., Shibata Y., Hayatsu N., Sugihara Y., Shibata K., Itoh M.,
RA	Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";
RL	Genome Res. 10:1617-1630(2000).
LN	[5]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA	Kono H., Akiyama J., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kankawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batraiov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brenneisen M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Guernicini S., Hill D., Hofmann W., Hume D.A., Kamya M., Lee N.H.,
RA	Lyons P., Marchionni L., Maehima T., Mazzarelli U., Mombertis P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA	Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
LN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Saeki N., Carninci P.,
RA	Kono H., Akiyama J., Nishi K., Kiyosawa H., Kondo S., Yamada I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kankawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batraiov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Resole G., Quackenbush J.,
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brenneisen M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Guernicini S., Hill D., Hofmann W., Hume D.A., Kamya M., Lee N.H.,
RA	Lyons P., Marchionni L., Maehima T., Mazzarelli U., Mombertis P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA	Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohitsuki S.,
RA	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
RL	Nature 409:685-690(2001).
LN	[3]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=C57BL/6J; TISSUE=Kidney;
RX	MEBLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA	Shibata K., Itoh M., Aiz

RA	Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,	
RA	Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,	
RA	Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,	
RT	"RIKEN integrated sequence analysis (RISA) system-384-format	
RT	sequencing pipeline with 384 multiscapillary sequencer."	
RL	Genome Res. 10:1757-1771 (2000).	
RN	[6]	
RP	NUCLEOTIDE SEQUENCE	
RC	STRAIN-C57BL/6J; TISSUE=Kidney;	
RA	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,	
RA	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,	
RA	Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,	
RA	Horii F., Imocani K., Ishii Y., Itoh S., Keada I., Kasukawa T.,	
RA	Karoch H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,	
RA	Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,	
RA	Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,	
RA	Saito R., Saitoh K., Sakai K., Sakai K., Sakazume N., Sano H.,	
RA	Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,	
RA	Tagawa A., Takahashi F., Takaku-Kabira S., Takeda Y., Tanaka T.,	
RA	Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,	
RL	Submitted (APR-2002) to the EMBL/Genbank/DBD databases.	
CC	-1- FUNCTION: This alpha-adrenergic receptor mediates its action by	
CC	association with G proteins that activate a phosphatidylinositol-	
CC	calcium second messenger system. Its effect is mediated by G(q)	
CC	and G(11) proteins (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.	
DR	EMBL; AK085653; BAC39495.1; -; mRNA.	
DR	MGI; MGI:104773; Adra1a.	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0008217; P:regulation of blood pressure; IMP.	
DR	InterPro; IPR001276; GPCR_Rhodopsn.	
DR	InterPro; IPR000011; 7tm_1; 1.	
DR	PRINTS; PR00587; ADRENORCCADP.	
DR	PRINTS; PR00237; GPCRHHODOPS.	
DR	PROSITE; PS00237; G PROTEIN RECP_F1_1; 1.	
DR	PROSITE; PS00262; G PROTEIN RECP_F1_2; 1.	
KW	G-protein coupled receptor; Receptor; Transducer; Transmembrane.	
SQ	SEQUENCE 427 Aa; 47516 Mw; 38105DaD5FA09317 CRC64;	
Query Match	12.9%; Score 341; DB 2; Length 427;	
Best Local Similarity	22.7%; Pred. No. 4-2e-12;	
Matches 115; Conservative	75; Mismatches 183; Indels 134; Gaps	13
QY	7 NSTRESSNSHTCMPISKMPISLANCIISTVLVFLAASFPVGNIVLAVLRKPOLQYT	66
DB	7 NASEGSNCNCTH--PPAQNISKKA--ILDGVLIGGLIIGVGNIIVLIVISVCHRHLSVT	61
QY	NRFLFNLLVTDLLOLSIVAPWVAIVTSVLPFPLINSHFCTALVSLNHLPAFASVNTIVLS	126
DB	62 HYIYVNLAVADLLTSTVLPSFSAIFELIGYAWFGKRVFVNIAADVLCCTASIMGLCTIS	121
QY	127 VDRYLSIHPLSYDSKMTQRGGLYLVTGTVAIALQSTPPYLGWQQAIFDERNALCSMIW	186
DB	122 IDRYIGVGYPLRPYIVTQRRGVALLCVWMLSVISIGPLFGMRQQA--PEDETIQCI--	178
QY	187 GASPSYITLVSFVFLPILVIMACISYVFCARQRQALLYNVKRHSLEVRKDCVENBD	246
DB	179 NEEPPGYVLFSAIGSEFVYPLITIIILWYCVVYVAKR-----ESRG	217
QY	247 EGAKEKKEPQDESFFRRQHGSEVYAKGKRMKADKQSLKAKEGSGTSESSVEARGSEBV	306
DB	218 LKSGLKTDKSDSEOVTLRIHKRNPV-----EGS-GVSSA-----	251
QY	307 RBSSTVASDGSMEKKEGSGTKEVENSMAKDKGRTEVNNQCSIDLGEEDMFEGBDINFSBD	366
DB	252 -----KQKT-----KQKT-----HFSVRLKFSRK	268
QY	367 VEAVNVIPESLPSPRRNSNPNPLPQCYCKAKAKYIFIIIFSYVLSLGGYCFPLATLAAYWD	426
DB	269 -----KAKTLGIVGGFVLQWLPF--FLWMPIGSFF	298


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QY 427 VETQVPMVITITITLFLQCCIHRYVYGVNMAKTIKKELQDMLKKFCKEKPCKEDS--- 483
DQ 299 ENFKRPETVFKIVFVLGYLNSCINPIIYPCSSQEFKKAFOVNLRIQCLRRSSGHALGY 358
OY 484 --HPDLPTGEGTEGKI-VPSYDSATF 507
DB 359 TLHPESQAVEGQHRGMVRIIPVGSGETF 385

RESULT 14
Q8BV77 MOUSE PRELIMINARY; PRT: 466 AA.
ID Q8BV77.1
AC Q8BV77.1
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched
DE library, clone:A330054N1 product:adrennergic receptor, alpha 1a, ALPHA
DE 1A-ADRENOCEPTOR, full insert sequence.
GN Name=Adra1a;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OK NCBI_taxid=10090;
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493974; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Steinhilber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake U., Boffelli D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohno S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20493974; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).

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RN [5]
RC NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi U., Aizawa K., Akiyama T., Aikawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai U., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: This alpha-adrennergic receptor mediates its action by
CC association with G proteins that activate a phosphatidylinositol-
CC calcium second messenger system. Its effect is mediated by G(q)
CC and G(11) proteins (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL: AK079357; BAC37694.1; -; mRNA.
CC ENSEMBL: ENSMUSG00000045875; Mus musculus.
DR MGI: MGI:104773; Adra1a.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR GO: GO:0008217; P:regulation of blood pressure; IMP.
DR InterPro: IPR001004; A_receptor1A.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00557; ADRENRGALAR.
DR PRINTS: PR00237; GPCRHDOPSN.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 466 AA; 51744 MW; BCSFE5C67E885795 CRC64;

Query Match 12.9%; Score 341; DB 2; Length 466;
Best Local Similarity 22.7%; Pred. No. 4.6e-12;
Matches 115; Conservative 75; Mismatches 183; Indels 134; Gaps 13;

QY 7 NSTRESNSHTCMPLSKMPISLHGIIRSTVLVFLASPVGNITLALVLRKPOLLOVT 66
DB 7 NASEGSNCTH--PQAQNIKSKA--ILGVLGGILIRGVNITLVISVACHRLHLSVT 61
QY 67 NRIFNVLVTLDTLQISLVAPEVNVATSVLPPLNSHFTALVSLTHLPAFASVNTIVLV 126
DB 62 HYIIVNLVAVDLLLTSTLPSAIFELIIGVAFGVFCINWAAVDVLCCTASIMLCIIS 121
QY 127 VDRVLSIILPLSYSPKMTQGRGVLLYGTGTVAILQSPPLPYGQGAFAFDSNALCSMIM 186
DB 122 IDRYIGVSPPLRPIYVYQKRGVALLCVMLSLVTSIGPLFGMRQA--PEDRTICQL-- 178
QY 187 GASPEYTLISVSPFIVPLIWMACYSVFCAARQHALLVNKKHSLSEVVKOCVENED 246
DB 179 NEEPEYVLFALSGSYVFLTLILVMYGVVAVAK-----ESRG 217
QY 247 EBGAKKEEFODESFRQHGEGEVAKGKREADGSLAKEGSGTGESSEVYARGSEEV 306
DB 218 LKSGIKTKDSSEQVTLIRHKRVPA-----EGS-GVSSA----- 251

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Oy 307 RESSTVADSGSMGKSGSTKRVENSNAKDKGRTEVNOQSIDGDEDDMERGEDDINSEDD 366
Db 252 -----KNKT-----HFSVRLKTSRKB 268
Oy 367 VEAVNIPESLPSPRRNSNSNPPLPCRCYCKAAKAVITIIIFSYVLSGPICFLAVALVWD 426
Db 269 -----KAAKTGIVGCGFVLCWLPF-FLVMPISGFF 298
Oy 427 VETQVQWVITIIIMLFPCOCCHIPVYGVGMHTIKGEIOMDKKPFCEKPKKEDS---- 483
Db 299 PNFKEPEYFKIVFMGLYNSCINPFIITCCSSOEFFKAFQVNLICLRROSSKHALGY 358
Oy 484 --HPDIPGTEGTEGKI-VPSSYDSATP 507
Db 359 TLHPPSQAVEGQHRGVMRIPVSGGERTF 385

RESULT 15
SH1A_HUMAN
ID SH1A_HUMAN STANDARD; PRT; 422 AA.
AC P08908; O6LA87;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 13-SEP-2005 (rel. 48, Last annotation update)
DE 5-hydroxytryptamine 1A receptor (5-HT-1A) (Serotonin receptor 1A) (5-HT1A) (G-21).
GN Name=HTR1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=87315369; PubMed=3041227; DOI=10.1038/329075a0;
RA Koblika B.K., Friele T., Collins S., Yang-Feng T.L., Koblika T.S., Francke U., Lefkowitz R.J., Caron M.G.;
RT "An intronless gene encoding a potential member of the family of receptors coupled to guanine nucleotide regulatory proteins.";
RL Nature 329:75-79(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Saltzman A.G., Morse B., Felder S.;
RT Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver project.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RA Puhl H.U., Iikeda S.R., Aronstam R.S.;
RT "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schaeetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Miliady S.J., Bosack S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahney J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Rauterfeld Y.S.N., Krzywicki M.J., Skalska U., Smailus D.B., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 1-9.
RX MEDLINE=92115564; PubMed=1766875;
RA Parks C.L., Chang L.S., Shenk T.;
RT "A polymerase chain reaction mediated by a single primer: cloning of genomic sequences adjacent to a serotonin receptor protein coding region.";
RL Nucleic Acids Res. 19:7155-7160(1991).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 200-365.
RX MEDLINE=93329096; PubMed=8393041;
RA Aune T.M., McGrath K.M., Sarf T., Bombara M.P., Kelley K.A.;
RT "Expression of SH1A receptors on activated human T cells. Regulation of cyclic AMP levels and T cell proliferation by 5-hydroxytryptamine.";
RL J. Immunol. 151:1175-1183(1993).
RN [8]
RP FUNCTION.
RX MEDLINE=88334700; PubMed=3138543; DOI=10.1038/335358a0;
RA Farin A., Raymond J.R., Lohse M.L., Koblika B.K., Caron M.G., Lefkowitz R.J.;
RT "The genomic clone G-21 which resembles a beta-adrenergic receptor sequence encodes the 5-HT1A receptor.";
RL Nature 335:358-360(1988).
RN [9]
RP VARIANTS SER-22 AND VAL-28.
RX MEDLINE=95275307; PubMed=7755630;
RA Nakai B., Nielsen D.A., Linnoila M., Goldman D.;
RT "Two naturally occurring amino acid substitutions in the human 5-HT1A receptor: glycine 22 to serine 22 and isoleucine 28 to valine 28.";
RL Biochem. Biophys. Res. Commun. 210:530-536(1995).
RN [10]
RP VARIANTS LEU-16 AND ASP-273.
RX MEDLINE=98425601; PubMed=9754630;
RA DOI=10.1002/(SICI)1096-8628(19980907)81:5<434::AID-AJMG13>3.0.CO;2-D;
RA Kawamishi Y., Harada S., Tachikawa H., Okubo T., Shiratsuki H.;
RT "Novel mutations in the promoter and coding region of the human 5-HT1A receptor gene and association analysis in schizophrenia.";
RL Am. J. Med. Genet. 81:434-439(1998).
CC -1- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate cyclase activity.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC EMBL; M28269; AAA36440.1; -; Genomic DNA.
CC EMBL; X13556; CA431908.1; -; Genomic DNA.
CC EMBL; X57829; CA40962.1; -; Genomic DNA.
CC EMBL; M83181; AAA66493.1; -; Genomic DNA.
CC EMBL; AB041403; BAA94488.1; -; Genomic DNA.
CC EMBL; BC069159; AAH69159.1; -; mRNA.
CC EMBL; AF498978; AAM21125.1; -; mRNA.
CC EMBL; Z11168; AA47560.1; -; Genomic DNA.
CC PIR; I38209; I38209.
CC HSSP; P08913; 1H1L.
CC Ensembl; ENSG00000178394; Homo sapiens.
CC HGNC; HGNC:5286; HTR1A.
CC MIM; 109760; -.

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DR GO: GO:0005887; C:Integral to plasma membrane; TAS.
DR GO: GO:0004993; F:serotonin receptor activity; TAS.
DR GO: GO:0007610; P:behavior; TAS.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaln. . .; TAS.
DR GO: GO:0008284; P:positive regulation of cell proliferation; TAS.
DR InterPro: IPR000610; SH1A_receptor.
DR InterPro: IPR002231; SHT_receptor.
DR InterPro: IPR002761; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00512; SH1A_receptor; 1.
DR PRINTS: PR01101; 5HT1ARECEPTR.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Multigene family;
KW Polymorphism; Receptor; Transducer; Transmembrane.
FT TOPO_DOM 1 36 Extracellular (Potential).
FT TRANSMEM 37 62 1 (Potential).
FT TOPO_DOM 63 73 Cytoplasmic (Potential).
FT TRANSMEM 74 98 2 (Potential).
FT TOPO_DOM 99 109 Extracellular (Potential).
FT TRANSMEM 110 132 3 (Potential).
FT TOPO_DOM 133 152 Cytoplasmic (Potential).
FT TRANSMEM 153 178 4 (Potential).
FT TOPO_DOM 179 191 Extracellular (Potential).
FT TRANSMEM 192 217 5 (Potential).
FT TOPO_DOM 218 345 Cytoplasmic (Potential).
FT TRANSMEM 346 367 6 (Potential).
FT TOPO_DOM 368 378 Extracellular (Potential).
FT TRANSMEM 379 403 7 (Potential).
FT TOPO_DOM 404 422 Cytoplasmic (Potential).
FT CARBOHYD 10 10 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 11 11 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 24 24 N-linked (GlcNAc . .) (Potential).
FT DISULFID 109 187 By similarity.
FT VARIANT 16 16 P -> L (1n dbSNP:1800041).
FT VARIANT 16 16 /FTid=VAR_003446.
FT VARIANT 22 22 G -> S (1n dbSNP:1799920).
FT VARIANT 22 22 I -> V (1n dbSNP:1799921).
FT VARIANT 28 28 /FTid=VAR_011826.
FT VARIANT 184 184 P -> L (1n dbSNP:1800043).
FT VARIANT 220 220 R -> L (1n dbSNP:1800044).
FT VARIANT 220 220 /FTid=VAR_011829.
FT VARIANT 273 273 G -> D (1n dbSNP:1800042).
FT CONFLICT 152 154 RAA -> PR (1n Ref. 1).
FT CONFLICT 172 172 M -> I (1n Ref. 1).
FT CONFLICT 200 202 TFG -> RPR (1n Ref. 7).
FT CONFLICT 228 228 K -> R (1n Ref. 7).
FT CONFLICT 244 244 A -> AA (1n Ref. 7).
FT CONFLICT 355 355 I -> T (1n Ref. 7).
FT CONFLICT 363 365 IVA -> MKP (1n Ref. 7).
FT CONFLICT 418 418 K -> N (1n Ref. 1).
SQ SEQUENCE 422 AA; 46107 MW; 762664FCF62CFD8F CRC64;
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Query Match 12.9%; Score 340.5; DB 1; Length 422;

Best local Similarity 22.0%; Pred. No. 4,4e-12; Matches 101; Conservative 92; Mismatches 190; Indels 77; Gaps 9;

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OY 144 TORRGVLLXGTWIVAILLOSTPPLPGWGQAAPDERNALCSMTWGASPTTILSVSFIY 203
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DB 149 TPRRAAALISLTWLGFLISIPMLGWRP--EDRSDDPACTISKDHGYTIYSTFGAFYI 206
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OY 204 PLIVMIACYSVFCAPARRQHALLVNKRHSLEIVKDCVENEDGAKKEEFODESEFR 263
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DB 207 PLLMLVLVYGRIFRAAR-----FRIKRTVKVEKGTGADTRHGASPAPOPK 251
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OY 264 RQHEGEVYAKKGRM--EKQDSL-----KAKGSTGTSESSVEARGSEVNESSVTASDG 316
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DB 252 KSVNGESGRNRWRIGVESKAGALCANGAVNQDGAALLEIVEH----- 296
   :::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 317 SMEKEGSTKVEENSMKADKRTVENOCSDLDGEDMEFGEEDINFSIEDVEAVNIPESL 376
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Search completed: December 3, 2005, 06:36:43
Job time : 176.873 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 04:47:24 ; Search time 5052 Seconds
(without alignments)
5715.850 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSSTRESNSHTCMP.....GTEGTEKIVPSYDSTPEP 508

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 segs, 2842172563 residues

Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :

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3: gb_env:*
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15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
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3	2644	100.0	1527	6	AX497863	AX497863 Sequence

4	2644	100.0	1580	6	AX497909	AX497909 Sequence
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8	2641	99.9	1527	6	C0736967	C0736967 Sequence
9	2641	99.9	1527	6	AR679058	AR679058 Sequence
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11	2641	99.9	1527	6	AX230165	AX230165 Sequence
12	2641	99.9	1527	6	AX355868	AX355868 Sequence
13	2641	99.9	1527	6	AX497907	AX497907 Sequence
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21	2641	99.9	1820	6	AX355867	AX355867 Sequence
22	2641	99.9	2781	6	AR679128	AR679128 Sequence
23	2641	99.9	2781	6	AX148262	AX148262 Sequence
24	2641	99.9	7524	6	AX543323	AX543323 Sequence
25	2641	99.9	140628	14	AC016468	AC016468 Homo sapi
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28	2637	99.7	1659	6	AX497906	AX497906 Sequence
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38	2021	76.4	1530	6	AX286523	AX286523 Sequence
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ALIGNMENTS

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LOCUS	BD173594				
DEFINITION	Novel G protein-coupled receptor protein and DNA thereof.				
ACCESSION	BD173594				
VERSION	BD173594.1 GI:28414925				
KEYWORDS	WO 02059304-A/1.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1524)				
AUTHORS	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.				
TITLE	Novel G protein-coupled receptor protein and DNA thereof				
JOURNAL	Patent: WO 02059304-A 1 01-AUG-2002; TAKEDA CHEMICAL INDUSTRIES LTD, MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA				
COMMENT	OS Homo sapiens (human) PN WO 02059304-A/1 PE 22-JAN-2002 WO 2002JP0000405 PR 23-JAN-2001 JP 01P 015050.30-MAR-2001 JP 01P 102560 PI MASANORI MIWA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC C12N15/12, C12P21/02, C07K14/705, C07K16/28, A61K45/00, A61P25/00, PC A61P29/00, PC A61P9/00, A61P35/00, A61P37/00, A61P1/00, G01N33/566, PC				

GOIN33/50, GOIN33/15	PC CC Key	Novel G protein-coupled receptor protein and DNA thereof FH
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		/db_xref="taxon:9606"
ORIGIN		
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Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	6	Gaps: 0
US-10-712-615-2 (1-508) x BD173594 (1-1524)		
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QY	21 LeuSerLysMetProTLeuSerLeuAlaHisGlyTilLeuArgSerThrValLeuValIle	40
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QY	41 PheLeuAlaAlaSerPheValGlyAsnIleValIleValLeuAlaLeuAlaGlnArgLysPro	60
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QY	61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln	80
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QY	81 IleSerLeuValAlaProTrrValValAlaThrSerValProLeuPheTrrProLeuAsn	100
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QY	101 SerHisPheCySerThrAlaLeuValSerLeuThrHisIleuPheAlaPheAlaSerValAsn	120
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QY	161 LeuGlnSerThrProProLeuTyrGlyTrrPrrGlyGlnAlaIlePheAspGluArgAsnAla	180
Db	481 CTGCAAGACATCTCTCATCTTACGGCTGGGGGCGAGGCTCCCTTTATGAGCCCAATGCT	540
QY	181 LeuCySerMetIleTrrPrrGlyAlaSerProSerTyrThrIleuSerValIleSerPhe	200
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Db	781	GAGTTTGCCGCCCGCAGCATGAAAGGTGAGGTCAAGGCCAAGAGAGGGCAGAAATGGAAAGCCAG	840
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Db	841	GACGGCAGCCCGAAAGGGCCAAAGAAAGAAAGACGGGGGACAGTGAAGATGATGTAGAGGCC	900
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Db	901	AGGGCCAGCGAGAGAGGTCAAGAGAGCAGCAGCGGTGCCAGCGCAGCAGCATGAGAGGT	960
Oy	321	LYsGluGlySerThrLYsValGluGluAaSerMetLYsAlaAspLYsGlyAaRgThrGlu	340
Db	961	AAGBAGGCGACACCAAAAGTTGAGAGAAACAGCATGAAAGGCACAAAGGGTCGCACAGAG	1020
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Oy	421	LeuAlaValTPsValAspValGluThrGluValProGlnTrpValIleThrIleIleIle	440
Db	1261	CTGGCCGGTGGGGAGTGTGAAGAACCCAGAGTACCCAGTGGGTGATCACCATATATATC	1320
Oy	441	TrpLeuPhePheLeuGlnCYsCYsAlaIleAspTYrValTYrGlyTYrMetHisLYsThr	460
Db	1321	TGGCTTTTCTTCTCTGCAGTGTGTGATCACCCTCATGTCTATGTGCTACATGCACAGACC	1380
Oy	461	IleIleLYsGluIleGlnAspMetLeuLYsAspPheCYsLYsGluLYsProProLYs	480
Db	1381	ATTAAGAAAGAAATCCAGACATGCTGAAGAAAGTTCTTCGCAAGAAAGCCCGCGAA	1440
Oy	481	GluAspSerHisProAspLeuProGlyTYrGluGlyGlyThrGluGlyValIleValPro	500
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Db	1501	TCCTACGATCTGCTACTTTTCTCT	1524
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BD095705			
LOCUS			
DEFINITION			
Novel guanosine triphosphate-bound protein-coupled receptors and			
genes encoding them, and their production and use.			
ACCESSION			
BD095705			
VERSION			
BD095705.1 GI:22641293			
KEYWORDS			
MO 0148188-A/17.			
SOURCE			
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ORGANISM			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Homnidae; Homo.			
REFERENCE			
1 (bases 1 to 1527)			
Matsumoto, S., Oda, T., Saito, Y., Noriyuki, Morikawa, Yoshida, K.,			
Suwa, M., Sugiyama, T., Kishimoto, T., Kanzaki, K., Yasuda, S. and			
Inoue, Y.			
TITLE			
Novel guanosine triphosphate-bound protein-coupled receptors and			
genes encoding them, and their production and use			

JOURNAL Patent: WO 0148188-A 17 05-JUL-2001;
HELIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO
SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU
SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO
YASUDA, YOSHIHISA INOUE
COMMENT OS Homo sapiens (human)
PN WO 0148188-A/17
PD 05-JUL-2001
PF 28-DEC-2000 WO 2000JP009408
PR 28-DEC-1999 JP 99P 375152,31-MAR-2000 JP 00P 101339 PI
SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI
MORIKAWA, KENJI YOSHIDA,
PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI
KANZAKI,
PI SHINICHIRO YASUDA, YOSHIHISA INOUE
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC
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G01N33/15,
PC G01N33/50
CC Novel guanosine triphosphate-bound protein-coupled receptors
CC and genes
CC encoding them, and their production and use
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FT source 1..1527
FT Location/Qualifiers
FT /organism='Homo sapiens (human)'.
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DB 361 ACCATTGTCTTGGTGTGAGTGCATCGCTACTGTCCATCAACCTCTCTCTACCG 420
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DB 1501 TCCTACGATTCGCTACTTTTCT 1524

RESULT 3
AX497863 1527 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 1 from Patent WO0240670.
DEFINITION AX497863
ACCESSION AX497863.1 GI:23342970
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS 1
TITLE Battaglini, P., Feder, J., Mintler, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
A novel human g-protein coupled receptor, hgrprym8, expressed
highly in brain
JOURNAL Patent: WO 0240670-A 1 23-MAY-2002;
Bristol-Myers Squibb Company (US)
FEATURES
SOURCE 1..1527
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 3,81e-207 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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DB 61 CTCCTCAAAATGCCATCAGCTGCGCCACGGCATCATCGCTCAACCGTGTGCTTATC 120
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LOCUS AX497909
DEFINITION Sequence 47 from Patent WO0240670.
ACCESSION AX497909

VERSION AX497909.1 GI:23342984
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
AUTHORS Battaglini, P., Feder, J., Muntler, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
TITLE A novel human g-protein coupled receptor, hgrprbm8, expressed
highly in brain
JOURNAL Patent: WO 0240670-A 47 23-MAY-2002;
Bristol-Myers Squibb Company (US)
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VERSION AL356783.20 GI:14456213
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ORGANISM Homo sapiens
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REFERENCE
AUTHORS      Homindae; Homo.
TITLE        Heath, P.
JOURNAL      Direct Submission
              Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire
              CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
              requests: clonerequest@sanger.ac.uk
              On Jun 14, 2001 this sequence version replaced gi:14329943.

COMMENT
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Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
-----
Project Information
Center project name: DB13L21
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Summary Statistics
Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; L08752; 10% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Dye-terminator: Big Dye; 64% of reads
Consensus quality: 173062 bases at least Q40
Consensus quality: 174012 bases at least Q30
Consensus quality: 174525 bases at least Q20
Insert size: 17485; sum-of-contigs
Quality coverage: 5.89x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 102859: contig of 102859 bp in length
* 102860 102955: gap of 100 bp
* 102956 126878: contig of 23919 bp in length
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* 126979 132924: contig of 5946 bp in length
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* 136362 136461: gap of 100 bp
* 142243 142244: contig of 5782 bp in length
* 142244 142343: gap of 100 bp
* 142344 150640: contig of 8297 bp in length
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ACCESSION	BD173595.1			
VERSION	BD173595.1			
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	Homidae; Homo.			
REFERENCE	1 (bases 1 to 1524)			
AUTHORS	Miwa,M., Ito,T., Shintani,Y. and Miyajima,N.			
TITLE	Novel G protein-coupled receptor protein and DNA thereof			
JOURNAL	Patent: WO 02059304-A 2 01-AUG-2002;			
	TAKEEDA CHEMICAL INDUSTRIES LTD,MASANORI MIWA,TAKASHI ITO, YASUSHI			
	SHINTANI, NOBUYUKI MIYAJIMA			
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ACCESSION BD144320
VERSION BD144320.1 GI:27850078
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Homnidae; Homo.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Hage,T., Takeda,S. and Miyake,N.
TITLE Novel G-protein coupled receptors
JOURNAL Patent: JP 2002112793-A 45 16-APR-2002;
COMMENT JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002112793-A/45
PD 16-APR-2002

PF 09-FEB-2001 JP 2001034434
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Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
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Db 1501 TCCTACGATTCGCTACTTTTCT 1524

RESULT 8
CQ736967 1527 bp DNA linear PAT 03-FEB-2004
LOCUS CQ736967
DEFINITION Sequence 22901 from Patent WO2068579.
ACCESSION CQ736967
VERSION CQ736967.1 GI:42334039
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 22901 06-SEP-2002;
PE Corporation (US)
FEATURES
source 1..1527
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 6 71e-207 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x CQ736967 (1-1527)
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Db 1 ATGACGTCCACCTGACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValaLeuValIle 40
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QY 41 PheLeuAlaIleSerPheValaGluAsnIleValaLeuValaLeuGluArgLysPro 60
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QY 61 GlnLeuLeuGlnValaThrAsnArgPheIlePheAsnLeuValaThrAspLeuGln 80
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QY 121 ThrIleValaLeuValaSerValaAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db 361 ACCATTGTGAGTGTCAAGTGAATCCCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 420
QY 141 SerLysMetThrGlnArgArgGlyIleLeuLeuLeuTyrGlyThrTrpIleValaIle 160
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QY 201 IleValaIleProLeuIleValaMetIleAlaCysTyrSerValaIlePheCysAlaIleArg 220
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QY 241 CysValIGluAsnGluAspGluGluGluValAGluLylsLysGluLupheGlnAspGluSer 260

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Pred. No.:      6,716-207          Length:      1527
Score:          2641.00           Matches:      507
Percent Similarity: 100.00%       Conservative: 1
Best Local Similarity: 99.80%     Mismatches: 0
Query Match:     99.89%           Indels:      0
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QY      21 LeuSerIlyMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
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DB      181 CAGCTGCTGCAAGTACCAACCGTTTATCTTTAACTCTCTGCACCGACCTGCTGACG 240

QY      81 IleSerLeuValAlaProTrrValValAlaThrSerValProLeuPheTrrProLeuAsn 100
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QY      101 SerHisPheCysThrAlaLeuValSerLeuThrHisIleuPheAlaPheAlaSerValAsn 120
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DB      361 ACCATTGCTGTGTGTGTCAATGATGTGCTACTTGTCTCATATCAACCCCTCTCTTACCG 420

QY      141 SerIlyMetThrGlnArgArgIlyTrrIleuLeuLeuTyrGlyThrTrrIleValAlaIle 160
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DB      481 CTGCAGAGACACTCTTCACATCTTACGCGCTGGGCGCAGGCTGCTTGTATATGACCCAAATGCT 540

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QY      241 CysValIleGlnAsnGlnAspGlnIlyGlnIlyAlaGlnIlyValGlnIlyPheGlnAspGlnSer 260
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QY      261 GluPheArgArgGlnHisGlnIlyGlnValIlyAsnAlaIlyGlnIlyArgMetGlnAlaIlyS 280
DB      781 CAGTTTCCGCGCCACGATGAAGTGAAGTCAAGGCGCCAAAGAGGCGCAATGAAACCAAG 840

QY      281 ArgGlySerLeuIlyAlaIlySglnIlySerThrGlyThrSerGlnSerSerValGlnAla 300

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Qy 321 LysGluGlySerThrIleValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAAGCGACGACCAAGTTGAGAGAACAGCATGAGGACAGACAAAGGTTCCACAGAG 1020
Qy 341 ValAsnGlnCysSerIleLeuAspLeuGlyValAspAspMetGluPheGlyValAspAspIle 360
Db 1021 GTCACACGAGCGACATGACTTGGGGTGAAGACATGAGATTTGGTGAAGACGACATC 1080
Qy 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProPheSerArg 380
Db 1081 AATTTGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
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RESULT 10
AX148174 1527 bp DNA linear PAT 08-JUN-2001
LOCUS AX148174
DEFINITION Sequence 15 from Patent WO0136471.
ACCESSION AX148174
VERSION AX148174.1 GI:14347080
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE
AUTHORS Chen, R., Dang, H.T. and Lowitz, K.P.
TITLES Endogenous and non-endogenous versions of human g protein-coupled
JOURNAL receptors
PATENT: WO 0136471-A 15 25-MAY-2001;
ARENA Pharmaceuticals, Inc. (US)
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Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
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Db 421 TCCAGATATACCAAGGCGCGGTTACTGCTCTCTATAGCACTCGAATTGGGCAATC 480
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Db 1501 TCTTACGATTCTGCTTCTTTCT 1524

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LOCUS AX230165 Sequence 52 from Patent WO0162797.
DEFINITION AX230165
ACCESSION AX230165 GI:15592183
VERSION AX230165.1
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homnidae; Homo.
REFERENCE 1
AUTHORS Vogeli, G., Wood, L.S., Parodi, L.A. and Lind, P.
TITLE Novel g protein-coupled receptors
JOURNAL Patent: WO 0162797-A 52 30-AUG-2001;
PHARMACIA & UPJOHN COMPANY (US)
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ORIGIN
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Pred. No.: 6,71e-207 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
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US-10-712-615-2 (1-508) x AX230165 (1-1527)

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QY 461 ILeIlyIlysgIuIleGlnAspMetLeuIlyIlyAspPheCysIlysgIuIlyProIlyAs 480
Db 1381 ATTAAGAGGAATCCAGACATGCTGAAGAAGTTCTTGCAGAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValPro 500
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RESULT 12
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LOCUS DERIVATION AX355868
ACCESSION AX355868
VERSION AX355868.1 GI:18620521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS Ramakrishnan,S.
TITLE Regulation of human_g(a)1a2adrenergic receptor-like G
JOURNAL protein-coupled receptor
Patent: WO 0188126-A 2 22-NOV-2001;
Bayer Aktiengesellschaft (DE)
FEATURES
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ORIGIN
Alignment Scores:
Pred. No.: 6,71e-207 length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
Gaps: 0
US-10-712-615-2 (1-508) x AX355868 (1-1527)

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QY 301 ArgGlySerGluGlnValArgGluSerSerThrValIleSerAspGlySerMetGluGly 320
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AX497907 1527 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 45 from Patent WO0240670.
ACCESSION AX497907
VERSION AX497907.1 GI:23342982
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
AUTHORS 1 Battaglinio, P., Feder, J., Muntier, G., Nelson, T., Ramanathan, C.,
Westphal, R., Cacace, A., Barber, L., Hawken, D. and Kornacker, M.
TITLE A novel human g-protein coupled receptor, hgrbny8, expressed
highly in brain
JOURNAL Patient: WO 0240670-A 45 23-MAY-2002;
Bristol-Myers Squibb Company (US)
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Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
Gaps: 0
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QY 121 ThrIleValIleuValSerValAspArgTYrleuSerIleIleIleIleIleIleIleIle 140
Db 361 ACCATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 141 SerIleuSerTrpGlnArgArgIleTYrIleuLeuLeuTYrIleIleValAlaIle 160
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RESULT 14

AX543321 1527 bp DNA linear PAT 23-NOV-2002

LOCUS Sequence 1 from Patent WO02059151.

DEFINITION AX543321

ACCESSION AX543321

VERSION AX543321.1 GI:25276744

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Li, Z., Cravchik, A., Milshina, N., Wei, M.H., Ketchum, K.A., di Francesco, V., and Beasley, E.M.

TITLE Isolated human g-protein coupled receptors, nucleic acid molecules encoding human gpcr proteins, and uses thereof

JOURNAL Patent: WO 02059151-A 1 01-AUG-2002; PE Corporation (NY) (US)

FEATURES

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location/Qualifiers

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ORIGIN

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Pred. No.: 6,71e-207 Length: 1527

Score: 2641.00 Matches: 507

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.80% Mismatches: 0

Query Match: 99.89% Indels: 0

DB: Gaps: 0

US-10-712-615-2 (1-508) x AX543321 (1-1527)

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ACCESSION AX549297
VERSION AX549297.1 GI:25813959
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Burner, G.C., Roush, C.L. and Brown, J.P.
AUTHORS Antigenic peptides, such as for G protein-coupled receptors
TITLE (GPCRs), antibodies thereto, and systems for identifying such
JOURNAL antigenic peptides
LifeSpan Biosciences, Inc. (US)
Patent: WO 02061087-A 582 08-AUG-2002;
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Location/Qualifiers
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Pred. No.: 6.71e-207 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservatave: 1
Best Local Similarity: 99.80% Mismatches: 0
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US-10-712-615-2 (1-508) x AX549297 (1-1527)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

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Post-processing: Minimum Match 0%

Maximum Match 100%
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-DEV_TIMEBOUT=120 -WARN_TIMEBOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: /cg2n_6/ptodata/1/ina/RE.COMB.seq:*
9: /cg2n_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2641	99.9	1537	3	US-10-314-048A-15
2	2641	99.9	2781	3	US-10-314-048A-103
3	2636	99.7	1537	3	US-10-314-048A-91
4	391.5	14.8	1382	3	US-09-364-425B-22
5	389	14.7	1584	2	US-08-748-485-2
6	389	14.7	1584	2	US-09-016-434-284
7	371	14.0	2481	2	US-08-467-568-1
8	371	14.0	2481	2	US-09-030-582-1
9	368	13.9	2481	6	PCT-US94-09051-1

10	338.5	12.8	1639	2	US-08-334-698-5	Sequence 5, Appl1
11	338.5	12.8	1639	2	US-08-228-932-5	Sequence 5, Appl1
12	338.5	12.8	1639	2	US-08-468-933-5	Sequence 5, Appl1
13	338.5	12.8	1639	2	US-08-406-855A-5	Sequence 5, Appl1
14	338.5	12.8	1639	2	US-08-722-190-5	Sequence 5, Appl1
15	338.5	12.8	1639	2	US-08-244-354-5	Sequence 5, Appl1
16	338.5	12.8	1639	3	US-09-206-899-5	Sequence 5, Appl1
17	338.5	12.8	1639	3	US-09-444-783-5	Sequence 5, Appl1
18	338.5	12.8	1639	3	US-09-688-415-5	Sequence 5, Appl1
19	338.5	12.8	1639	3	US-09-444-783-5	Sequence 5, Appl1
20	338.5	12.8	1639	6	PCT-US95-04203-5	Sequence 5, Appl1
21	338.5	12.8	1997	2	US-08-722-001-27	Sequence 27, Appl1
22	333.5	12.6	2004	2	US-08-722-001-11	Sequence 11, Appl1
23	333.5	12.6	2290	3	US-09-016-434-1368	Sequence 1368, Ap
24	333.5	12.6	2536	3	US-09-919-039-5	Sequence 5, Appl1
25	325	12.3	1579	3	US-09-016-434-1243	Sequence 1243, Ap
26	324	12.3	1666	3	US-09-826-509-424	Sequence 424, App
27	314.5	11.9	1621	2	US-08-722-001-13	Sequence 13, Appl1
28	314.5	11.9	1776	2	US-08-722-001-29	Sequence 29, Appl1
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30	314.5	11.9	2140	2	US-08-334-698-1	Sequence 1, Appl1
31	314.5	11.9	2140	2	US-08-228-932-1	Sequence 1, Appl1
32	314.5	11.9	2140	2	US-08-468-933-1	Sequence 1, Appl1
33	314.5	11.9	2140	2	US-08-406-855A-1	Sequence 1, Appl1
34	314.5	11.9	2140	2	US-08-722-190-1	Sequence 1, Appl1
35	314.5	11.9	2140	3	US-08-244-354-1	Sequence 1, Appl1
36	314.5	11.9	2140	3	US-09-206-899-1	Sequence 1, Appl1
37	314.5	11.9	2140	3	US-09-444-783-1	Sequence 1, Appl1
38	314.5	11.9	2140	3	US-09-688-415-1	Sequence 1, Appl1
39	314.5	11.9	2140	3	US-09-444-783-1	Sequence 1, Appl1
40	314.5	11.9	2140	6	PCT-US95-04203-1	Sequence 1, Appl1
41	309.5	11.7	1601	2	US-08-722-001-7	Sequence 7, Appl1
42	304.5	11.5	3335	2	US-07-676-174A-1	Sequence 1, Appl1
43	300.5	11.4	1987	2	US-08-722-001-26	Sequence 26, Appl1
44	293	11.1	1440	3	US-09-826-509-518	Sequence 518, App
45	287	10.9	2108	3	US-09-032-742-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-314-048A-15
; Sequence 15, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unetec, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Hong T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Law, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22 US6.CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13


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; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-048A-15

Alignment Scores:
Pred. No.: 3,726-278 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: Gaps: 0

US-10-712-615-2 (1-508) x US-10-314-048A-15 (1-1527)

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QY 21 LeuSerLyMetProIIeSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCAAAATGCCATCAGCTGGCCGCGCATCATCGCTCAACCGTCTGTTATC 120
QY 41 PheLeuAlaIaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLyPro 60
DB 121 TTCCTCGCGCGCTTTTGTGTGGCAACATAGTGGCGCTAGTGTGCGAGCGCAAGCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTGCAGAGTGCACCAACCGTTTATCTTAACTCTCTGTCACCGACCTGTCAG 240
QY 81 IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsn 100
DB 241 ATTGGCTGTGGCCCCCTGGGGTGGGACCTCTGCTCTCTCTCTGCGCCCTCAAC 300
QY 101 SerHisPheCyethrAlaLeuValSerLeuThrHisIleLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTCTGCACGGCCCTGGTTAGCCTCACCCACTGTTGCCCTTGGCCAGCGTCAAC 360
QY 121 ThrIleValLeuValSerValAsnArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGGCTGTGGTGCATGATGCTACTTGTCTCATCATCACCTCTCTCTCAACCG 420
QY 141 SerLyMetThrGlnArgArgIlyTyrLeuLeuLeuLeuTyrThrTriIleValAlaIle 160
DB 421 TTCAGATGACCCAGGCGCGGGTTACCTGCTCTTATGGCACTGGATGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
DB 481 CTGGAGAGACCTCTCCACTCAACGGCTGGGGCCAGGCTGCTTTGATAGGCGCATGCT 540
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QY 201 IleValIleProLeuIleValMetIleAlaCyTyrSerSerValValPheCyAsnAlaArg 220
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QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIlyAsArgHisSerLeuGlnValArgValIlyAsp 240
DB 661 AGGCAAGCATGCTCTGTGTACATGTCAAGACACACAGCTTGGAGTGGAGTCAAGGAC 720
QY 241 CyValIlyAsnGluAspGluGluGlyAlaGlyIlyValIlyGluIlePheGlnAspGlySer 260
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QY 261 GluPheArgArgGlnHisGluGlyValIlyValIlyValIlyGluGlyArgMetGluAlaIly 280
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QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluIly 320
DB 901 AGGGCACCGAGAGGTGAGAGAGAGACGACGCGGTGGCCAGCAGACGACATGGAGGT 960
QY 321 LySGluGlySerThrLyValGlyIlyAsnSerMetLyAlaAspLyGlyArgThrGlu 340
DB 961 AAGGAAGCACACCAAAAGTTGAGAGAAACAGCATGAAGGACGACCAAGGTCGACAG 1020
QY 341 ValAsnGlnCySerTyrAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCATGACGATGACTGGGTGMAATGACATGAGGATTTGGAGACACATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCACTGAGATGACGTGAGGACATGAACATCCCGAGAGCTTCCACCATGCTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCyTyrGlnCyIlyAlaIlyVal 400
DB 1141 CGTAACACCAACAGAACCTCTCTGCGCAGGTGCTTCACTGCAAAAGCTGTAAGTGT 1200
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGlyProTyrCyPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTCTCTCTATGTGCTATCCCTGGGGCCCTACTCTTTTATGCAATC 1260
QY 421 LeuAlaValTyrValAspValGlyThrGlnValProGlnTyrPvalIleThrIleIle 440
DB 1261 CTGGCGGTGGTGGAGTGAAGAACCCAGGTACCCAGTGGTGAATCAATATATCATC 1320
QY 441 TyrLeuPhePheLeuGlnCyCyIleIleAspProTyrValTyrGlyTyrMetHisIlyThr 460
DB 1321 TGGCTTTCTCTCTGCACTGCTGATCCACCCCTATGTCTATGCTACATGACACAGACC 1380
QY 461 IleLySlyGlyIleGlnAspMetLeuIlyAspPheCyIlyGlyIlyAspProLyAs 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAAATTTCTTCCAAAGAAACCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyTyrGluGlyIlyThrGluIlyIleValPro 500
DB 1441 GAAGATACCCACCCAGACCTGCCGGAACAGAGGTGGAGTGAAGGCAAGATTGTCTCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TTCTACGATTCTGCTACTTTTCT 1524

RESULT 2
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; Sequence 103, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unet, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314, 048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096, 511
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/ PRIOR FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: 09/995,543
/ PRIOR FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: 60/399,917
/ PRIOR FILING DATE: 2002-07-29
/ PRIOR APPLICATION NUMBER: 60/404,761
/ PRIOR FILING DATE: 2002-08-19
/ PRIOR APPLICATION NUMBER: 60/410,747
/ PRIOR FILING DATE: 2002-09-13
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 103
/ LENGTH: 2781
/ TYPE: DNA
/ ORGANISM: Homo Sapiens and Rat
US-10-314-048A-103

Alignment Scores:
Pred. No.:          9,97e-278      Length:      2781
Score:             2641.00         Matches:      507
Percent Similarity: 100.00%        Conservative: 1
Best Local Similarity: 99.80%      Mismatches:  0
Query Match:       99.89%          Indels:       0
DB:                3              Gaps:         0

US-10-712-615-2 (1-508) x US-10-314-048A-103 (1-2781)

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QY      21 LeuSerLyMetProLieserLeuAlaHISGLYIleIleArgSerThrValIleuValIle 40
DB      61 CTCTCCAAATGCCATCTACGCTGCGCCACGAGATATCCGCTCAACCGTGTGTTATC 120
QY      41 PheLeuAlaAlaSerPheValGlyAsnIleValIleuAlaLeuValIleuGlnArgPro 60
DB      121 TTCCTGCGCGCTCTTTCGCGGCAACATGAGTCTGCGCTAGTGTGCGACGCAAGCCG 180
QY      61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAsnLeuGln 80
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QY      101 SerHisPheCyThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB      301 AGGCACTTCTGACGCGCCCTGTAGCTCAACCACTGTTGCTTCGCGCAAGTCAC 360
QY      121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB      361 ACCATTGTGTGGTGTGACGTGATCTCTATTCATCATTCACCTCTCTCTCCACCC 420
QY      141 SerLyMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB      421 TCCAAATGACCCAGGCGCGGCTTACCTGCTCTATGACCTTGAGATTGGCCATC 480
QY      161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAsnProGluAsnAla 180
DB      481 CTCGACAGGACCTCTCACTCACTGAGGTGGGCGGACGCTCTTATGAGGCCAATGCT 540
QY      181 LeuCySerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValValSerPhe 200
DB      541 CTCTGCTCCATGTATCTGGGGGGGCGAGCCCAAGCTACATCTCAAGCGTGTCTTCC 600
QY      201 IleValIleProLeuIleValMetIleAlaCysTrpSerValValPheCysAlaIleArg 220
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QY      221 ArgGlnHisAlaLeuLeuTyrAsnValLysArgHisSerLeuGluValArgValLysAsp 240
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DB      721 TGTGTGACAAATGAGATATAGAGGAGGACGACGAGAAAGAGAGAGTTCAGATGAGAGT 780
QY      261 GluPheArgArgGlnHisGluGlyGluValLysAlaLysGluGlyValArgMetGluAlaLys 280
DB      781 GAGTTTCGCGCCAGCATGAAAGGTGAGTCAAGGCGCAAGGAGGCGAGATGGAAGCCAA 840
QY      281 AspGlySerLeuLeuValLysGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB      841 GACGCGAGCTGAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY      301 ArgGlySerGluGluValArgLusSerThrValAlaSerAspGlySerMetGluGly 320
DB      901 AGGGCGAGCGAGGAGGTCAAGAGACACAGGTGGCCAGCGACGACATGAGAGGT 960
QY      321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB      961 AAGGAAGCAGACCAAAAGTTGAGGAGAACAGATGAAGGACAGACAAAGGCTCGCACAG 1020
QY      341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB      1021 GTCAACCACTGACGATTCGATGGGTGAAGATGACATGAGATTGGTGAAGCAGCATC 1080
QY      361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB      1081 AATTGATGAGGATGACGTCCAGGCGATGAAATCCCGAGAGCTCCCAACCAAGTCCG 1140
QY      381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysLysAlaAlaLysVal 400
DB      1141 CGTACAGCAACAGCAACCTCTCTGCGCAGGTGTACAGTCAAGCAACTGCTAAAGTC 1200
QY      401 IlePheIleIlePheSerTyrValLeuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB      1201 ATCTCATCATCATTTTCTCTATGCTATCCCTGCGGCGCCCTCACTGCTTTTAAAGCAGTC 1260
QY      421 LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle 440
DB      1261 CTGGCGGTGGGTGATGTCGAAACCCAGGTACCCCAAGGTGGTATACCAATATCATC 1320
QY      441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB      1321 TGGCTTTTCTTCTGAGAGTGTGCATCCACCCCTAATGCTATAGGCATCAACCAAGACC 1380
QY      461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
DB      1381 ATTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTCTGCAAGGAAAGCCCCGAAA 1440
QY      481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
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QY      501 SerTyrAspSerAlaThrPhePro 508
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RESULT 3
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/ Sequence 91, Application US/10314048A
/ Patent No. 6902902
/ GENERAL INFORMATION:
/ APPLICANT: Unect, David J.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Richman, Jeremy
/ APPLICANT: Connolly, Daniel
/ APPLICANT: Dang, Huang T.
/ APPLICANT: Choi, Bryan
/ APPLICANT: Leonard, James
/ APPLICANT: Hakak, Yaron
/ APPLICANT: Liaw, Chen
/ APPLICANT: Lowitz, Kevin P.
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```

; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22, US6, CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 09/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 91
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-314-048A-91

Alignment Scores:
Pred. No.: 1,316-277 Length: 1527
Score: 2636.00 Matches: 506
Percent Similarity: 99.80% Conservative: 1
Best Local Similarity: 99.61% Mismatches: 1
Query Match: 99.70% Indels: 0
Gaps: 0

US-10-712-615-2 (1-508) x US-10-314-048A-91 (1-1527)

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Db 1 ATGAGTCCACCTGACCAACAGCAGCGCGAGAGTAAACAGCAGCAGCAGTGCATGCC 60
QY 21 LeuSerLysMetProGluSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
Db 61 CTCCTCAAAATGCCATCAAGCTGCGCCAGGCGCATCATCTCCATCAACCTGCTGTTATC 120
QY 41 PheLeuAlaIaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
Db 121 TTCCTCGCGCGCTTTTGGTGGCAACATGATGCTGGCGCTAGTGTGACGAGCAAGCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuLeuGln 80
Db 181 CAGCTGCTGACAGTACCAACCGTTTATCTTTAACTCTCTGTCACCTGCTGACCTGCTG 240
QY 81 IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsn 100
Db 241 ATTGGCTGTCGCGCCCTGGGTGGTGGCCACTCTGTCCTCTCTTCTGGCCCTTCACAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
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QY 121 ThrIleValLeuValSerValAspArgTrpLeuSerIleIleHisProLeuSerTrpPro 140
Db 361 ACCATTTGCTGGTGTCACTGATGCTGCTTATCATCATCATCACCTCTCTCTTCAACCG 420
QY 141 SerLysMetThrGluArgArgLysTrpLeuLeuLeuLeuTrpThrTrpIleValAlaIle 160
Db 421 TCCAAAGATGACCCAGCGCGCGGTTAACCCTCTCTATGGCACTTGAGATTGTGGCATTC 480
QY 161 LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAlaAlaPheAspGluArgAsnAla 180
Db 481 CTGCAAGAGACACTCTCACTCAACGGCTGGGCGAGGCTGCTTTGATAGGCAATGCT 540
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTrpThrIleLeuSerValIleSerPhe 200
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Db 541 CTCCTGCTCATGATGGGGGACCAAGCCCAAGCTCACTATTTCTAGCGGTGTCCTTC 600
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Db 601 ATCGCATTCATCATGATGTCATGATGCTGCTGCTACTCCGGTGTCTTGTCAGCCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTrpAsnValIleArgHisSerLeuGlnValIaArgValIleAsp 240
Db 661 AGGCAGCATGCTGCTGCTTACATGTCATCAAGACACACCTTGGAAGTCCGAGTCAAGGAC 720
QY 241 CysValGluAsnGluAspGluGluGlyAlaGlyLysValGluIlePheGluAspGluSer 260
Db 721 TGTGTGAGAAATGAGATGAAAGAGGAGACAGAGAAAGAGAGAGTTCAGAGATGAGT 780
QY 261 GluPheArgArgGlnHisGlyGlyValIleValIleValIleValIleValIleValIle 280
Db 781 CAGTTTCCCGCCCGCAGCATGAAGGTGAGTCAAGCCAGGAGGAGGAGGAGATGAAACCAAG 840
QY 281 AspGlySerLeuLysAlaLysGluLysSerThrGlyThrSerGluSerSerValGluAla 300
Db 841 CACGCGACCTGAGAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
QY 301 ArgGlySerGluGluValIaArgGluSerSerThrValIaSerAspGluSerMetGluGly 320
Db 901 AGGGCAGCAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 960
QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
Db 961 AAGGAAGCAGACACCAAGTTGAGAGAAACAGCATGAAGGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValAsnGlnCysSerTrpAspLeuGlyLysAspAspMetGluPheGlyGluAspAspIle 360
Db 1021 GTCAACCATGTCAGATGATGCTGGTGTGAATGATCATGAGAGAGAGAGAGAGAGAGAG 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAlaHisIleProGluSerLeuProSerArg 380
Db 1081 AATTTCAGTGAAGATGAGTCAAGAGAGTGAACATCCCGAGAGAGCTCCACCATGCTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTrpGlnCysValAlaAlaLysVal 400
Db 1141 COTACACAGCAACAGCAACCTCTCTGCGAGTCTACAGTGCAGAGAGAGAGAGAGAGAG 1200
QY 401 IlePheIleIleIlePheSerTrpValLeuSerLeuGlyProTrpCysPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTCTCTCATATGCTATCCCTGGGGCCCTACTGCTTTTACAGATC 1260
QY 421 LeuAlaValIleTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIle 440
Db 1261 CTGGCCGTGTGGTGAATGTCGAACCCAGGATACCCAGTGGTGAATCAACATAATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTrpValIleTrpGlyTrpMetHisLysThr 460
Db 1321 TGGCTTTTCTTCTGCAATGCTGATCCACCCCTATGTCATATGCTATGCAACAGAAC 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1381 ATTAAGAAAGAAATCAAGAGACATGCTGAAGAAATCTTCTGCAAGAAAGAGAGAGAG 1440
QY 481 GluAspSerHisAspAspLeuProGlyThrGluGlyValIleValIleValIleValIle 500
Db 1441 GAAAGATGACCAACAGAGCTGCGGAGACAGAGGGTGGGACTGAAGAGGAGAGATTGCT 1500
QY 501 SerTrpAspSerAlaThrPhePro 508
Db 1501 TCTTACGATTCGCTACTTTTCT 1524

RESULT 4
US-09-364-425B-22
; Sequence 22, Application US/09364425B
; Patent No. 6653086
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
```



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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITTH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 284:
SEQUENCE CHARACTERISTICS:
LENGTH: 1584 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT06
CLONE: 1722180
US-09-016-434-284

Alignment Scores:
Pred. No.: 3, 71e-32 Length: 1584
Score: 389.00 Matches: 110
Percent Similarity: 38.82% Conservative: 74
Best Local Similarity: 23.21% Mismatches: 142
Query Match: 14.71% Indels: 148
Gaps: 12
DB: 3

US-10-712-615-2 (1-508) x US-09-016-434-284 (1-1584)
QY 9 ThrArgGluSerAsnSerSerHisThrCys--MetProLeuSerLysMetProIleSer 27
DB 164 ACCATGAGCTCAACTCTCCCTCAGCTGACGAGAGAGCTGAGTATCTCACTGAGGG 223
QY 28 LeuAla-----HisGlyIleIleIleArgSerThrValLeuValIleIleLeuAlaIleSer 45
DB 224 GAGGGTGGCGAAGGGGGCGTCATCACTCCAGCTTCACTCCCATCTTGCATCACCATT 283
QY 46 PheVal-----GlyAsnIleValLeuAlaLeuValIleGlnArgLysProGlnLeuLeu 63
DB 284 TTTCCTGCTGCTGGAAACCTGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 343
QY 64 GlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGlnIleSerLeu 83
DB 344 ACCCTAGCAACAAAGTTCCTTCAAGCTGACTCTGCTCAACTTCTGCTGCTGCTGCTG 403
QY 84 ValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsnSerHisPhe 103
DB 404 GTGCTGCTTTTGTGTGTGACGAGCTCCATCCGAGGAGAAATGATCTTTGTGTGATGTGG 463
QY 104 CysThrAlaLeuValSerLeuThrHisLeuPheAlaSerValaenThrIleVal 123

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DB 464 TCGAATTCTCTGCTCTCTCTCACTGCTGATCAGCTGCTGCGACAGATGTAACCTCGGG 523
QY 124 LeuValSerValAspArgThrLeuSerIleIleHisProLeuSerLysMet 143
DB 524 GTCATTTGCATCGACCGCTACTATGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
QY 144 ThrGlnArgArgGlyTyreLeuLeuValThrIlePheValAlaIleLeuGlnSer 163
DB 584 ACAGGAGACCGGGCTGTATGACATTCGTCATCATGCTGCTTCACTCGCTCATCGGCTCG 643
QY 164 ThrProLeuValTyreGlyThrGlyGlnAlaAlaPheAspGlnArgAsnAlaLeuCysSer 183
DB 644 CTGCCACCTCTTTGTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703
QY 184 MetIleThrGlyAlaSerProSerThrThrIleLeuSerValValSerPheIleValIle 203
DB 704 GCTGCTGGACCGGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
QY 204 ProLeuIleValMetIleAlaCysTyreSerValAlaPheCysAlaAlaArgArgGlnHis 223
DB 764 CCTTTCTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
QY 224 AlaLeuLeuTyraAsnValIleArgHisSerLeuGlnValArgValIleAspCysValGlu 243
DB 814 ----- 814
QY 244 AsnGluAspGluGluGlyAlaGluValIleGluGluPheGlnAspGluSerGluPheArg 263
DB 814 ----- 814
QY 264 ArgGlnHisGluGlyGluValIleValIleValIleValIleValIleValIleValIle 283
DB 815 -----GTCAAGGCAAGC----- 826
QY 284 LeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGlnAlaArgGlySer 303
DB 827 ---AAGGTCACTGTGTCACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
QY 304 GlnGluValArgGluSerSerThrValAlaAlaSerAspGlySerMetClnIlysgGluGly 323
DB 881 -----GTCCGAAAGAACTCCAGCACCTCCCTCTTCA----- 916
QY 324 SerThrIleValIleGluIleAsnSerMetLysAlaAspLysGlyArgThrGluValaGln 343
DB 916 ----- 916
QY 344 CysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIleAsnPheSer 363
DB 916 ----- 916
QY 364 GluAspAspValGluAlaValaenIleProGluSerLeuProProSerArgArgAsnSer 383
DB 917 -----GGCGACGAGGAGAAATGCC 924
QY 384 -----AsnSerAsnProProLeuProArgCysArgGlnCysLysAla 397
DB 935 TTTCAGGGTGTGCTACTCGGCAC-----CAGTCCAAAGCC 973
QY 398 AlaLysValIlePheIleIleIlePheSerTyraValLeuSerLeuGlyProTyr---Cys 416
DB 974 CTCATCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033
QY 417 PheLeuAlaValaLeuAlaValIlePheValIleValIleValIleValIleValIleVal 434
DB 1034 GTCATGCTCTGTAGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1093
QY 435 ValIleThrIleIleIleThrPhePheLeuGlnCysCysIleHisProTyraValTyr 454
DB 1094 GCC-----ACATGCTGCTGCTTTCGACAGGCTGTCTGCCACCCCTGATCTAT 1141
QY 455 GlyTyraMetHisLeuThrIleLysValGluIleGlnAspMet 468

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Db 1142 GGACTCTGGACACAGCACTTCCGAAGAACTACTGGGATG 1183

RESULT 7

US-08-467-568-1

Sequence 1, Application US/08467568

Patent No. 5817477

GENERAL INFORMATION:

APPLICANT: SOPPET, DANIEL R

TITLE OF INVENTION: ADRENERGIC RECEPTOR

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Giffillan, Cecchi,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: NJ

COUNTRY: USA

ZIP: 07068-1739

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,568

FILING DATE: 06-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Periaro, Gregory D

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-324

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2481 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 101..1687

US-08-467-568-1

Alignment Scores:

Pred. No.: 7,176-30

Score: 371.00

Percent Similarity: 37.53%

Best Local Similarity: 23.06%

Query Match: 14.03%

DB: 2

US-10-712-615-2 (1-508) x US-08-467-568-1 (1-2481)

QY 6 ThrAsnSerThrArgGlu-----SerAsnSerSerHisThrCysMetPro 20

Db 140 ACTAATCTCACTGAGAGGAGGAGGTGGCGAAGGGCGCTATCATCACCGAGTTTCATCGCCA 199

QY 21 LeuSerLysMetProLLeSerLeuAlaHisGlyIleIleIleArgSerThrValIleuValIle 40

Db 200 TCATTGTCTACCA----- 214

QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValIleuAlaLeuValIleuGlnArgLysPro 60

Db 215 TTTTGTCTGCC-----TGGGAAACCTGGTCATCTGTGTCACCTTGTAACAAGATCC 268

QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80

Db 269 TACCTCCTCACCCCTGACGAACAAGTTCTGCTTACGCTCACTCTGTCCAACTTCCTGCTG 328

QY 81 IleSerLeuValAlaProIleValAlaIleThrSerValProLeuPheIleProLeuAsn 100

Db 329 TCCGTGTGTGTCGCTCTTTGTGTGTGACGAGCTTCATCCCGAGGAATGATCTTGTGT 388

QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120

Db 389 GTAGTGCTGCAACTTCTGTGCTGCTCTCTTACCTGCGTGAAGAGCTGTGCCAGATGCTA 448

QY 121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140

Db 449 ACCCTCGGGGATGATGCGATGAGCATGAGCTTATGCTGTCCGTATGCCATCGCTGTACCCC 508

QY 141 SerLysMetThrGlnArgArgGlyTyrIleuLeuLeuTyrGlyThrTrpIleValAlaIle 160

Db 509 ATGAAGATCAGAGGAGACCGGAGCTGTGATGGACATTGTCTACATCTGCTTACCTGCTC 568

QY 161 LeuGlnSerThrProLeuTyrGlyTyrGlyGlnAlaAlaPheAspArgLysAsnAla 180

Db 569 ATCGGCTGCTGCGACCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 628

QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200

Db 629 ATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 688

QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaIleArg 220

Db 689 GCCCTTTCCCTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 748

QY 221 ArgGlnIleAlaLeuLeuTyrAsnValIleLysArgHisSerLeuGlnValArgValIleAsp 240

Db 749 -----GTCAAGCAGACGAGGAGGACCTGTGAGCACTGTCTC 784

QY 241 CysValGluAsnGluAspGluGluGlyValaGluValGluGluPheGlnAspGluSer 260

Db 785 ATCTGTGAG--GAGGATGCTCAG----- 805

QY 261 GluPheArgArgGlnHisGluGlyGluValIleLysAlaLysGluGlyArgMetGluAlaLys 280

Db 806 -----AGACCCGGAGG----- 817

QY 281 AspGlySerLeuLysAlaLysGluGlySerThrGlyThrSerGluSerValGluAla 300

Db 818 -----AAGATCCAGACACTCTCACTCTCTTCA----- 847

QY 301 ArgGlySerGluValArgGluSerSerThrValAlaAspArgLysSerMetGluGly 320

Db 847 ----- 847

QY 321 LysGluGlySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340

Db 848 -----GGGAGG----- 853

QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360

Db 853 ----- 853

QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380

Db 854 -----AGG 856

QY 381 ArgAsnSer-----AsnSerAsnProProLeuProArgCysThrGln 394

Db 857 AGGAATGCTTTCAGGGGTGTGTCTACTCGGCAAC-----CAG 895

QY 395 CysLysAlaAlaLysValIlePheIleIleIlePheSerTyrValIleSerLeuGlyPro 414

Db 896 TCCAAAGCCCTCATACCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 955

QY 415 Tyr---CysPheLeuAlaValIleuAlaValIlePhe-----ValAspValGluThrGlnVal 431

Db 956 TACATGATGTGTGATGCTGTGAGGCTCTGTGGGGAAGAACTCCGTCTCCCGAGAGCTG 1015

QY 432 ProGlnIleProValIleThrIleIleIleThrLeuPhePheLeuGlnCysValIleHisPro 451

QY 389 LeuProArgCysTyrGlnCysValAlaAlaValIlePheIleIleIlePheSerTyr 408
DB 893 -----CAGTGCMAAGCCCTCATCATCATCTGGTCTCGGTCCTTC 937
QY 409 ValLeuSerLeuGlyProTyr---CysPheLeuAlaValLeuAlaValTP-----Val 425
DB 938 ATGGTACCTGGGGCCCTACATGCTTGTCATGCTCTGAGGCCCTCTGGGGGAAAGC 997
QY 426 AspValGluThrGlnValProGlnTPValIleThrIleIleIleTPLeuPheLeu 445
DB 998 TCCGTCTCCCGGAGCTGGAGACTTGAGCC-----ACATGGCTGTCTTGGC 1045
QY 446 GlnCysCysIleHisProTyrValTyrGlyTyrMetHisLeuThrIleLysGluIle 465
DB 1046 AGCGCTGTCTGGCAACCCCTGATCTATGACTCTGGAACAGACAGTTCGAAGAAGCTA 1105
QY 466 GlnAspMet 468
DB 1106 CTGGGCATG 1114
RESULT 10
US-08-334-698-5
Sequence 5, Application US/08334698
Patent No. 5556753
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ. ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYROTHERICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 126..1523
OTHER INFORMATION:
US-08-334-698-5
Alignment Scores: 1.29e-26 Length: 1639
Pred. No.:

Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 167
Query Match: 12.80% Indels: 131
DB: 2 Gaps: 11
US-10-712-615-2 (1-508) x US-08-334-698-5 (1-1639)
QY 8 SerThrArgGluSerAsnSerSerHisThrCysMetProLeuSerLysMetProIleSer 27
DB 138 TCGGAAAGAGCTTCCAGACAGCTTCAAGTCCAGCCCAACCG-----CCGGACCGGGAAC 191
QY 28 LeuAlaHisGlyIleIleLeuArgSerThrValLeuValIlePheLeuAlaIleAspPheVal 47
DB 192 ATTTCAGAGGACATCTGTCTCGGGGTAGATCTTGAGGGGAGCTCATTTCTTTCGGGGGTGCTG 251
QY 48 GlyAlaIleValLeuAlaLeuValLeuGlnArgLysProGlnLeuGlnValThrAsn 67
DB 252 GGTAACTCTAGTAGTCTCTCCGAGCCTGTCAACCGACCTGCATCACTCACTGACGAC 311
QY 68 ArgPheIlePheAsnLeuLeuValThrAspLeuLeuGlnIleSerLeuValAlaProTP 87
DB 312 TACTACATCTGAACCTGAGCGGTGGCGGACCTCTGCTACCTTCAAGTCTGCTCCCTTC 371
QY 88 ValValAlaIleThrSerValProLeuPheTPProLeuAsnSerHisPheCysThrAlaLeu 107
DB 372 TCCGCATCTTGAGAGTCTTAGGCTAGCTAGGCTTCCGAGGCTTCTTCCGAACATCTGG 431
QY 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValIleThrIleValLeuValSerVal 127
DB 432 GCGGAGTGGATGTGCTGTGTGCAACCGGCTCATCATCATGAGCTGTGATCATCTTCATC 491
QY 128 AspArgTyrLeuSerIleIleHisProLeuSerTyrProSerLysMetThrGlnArg 147
DB 492 GACCGCTACATGCGGCTGAGCTTACCGGCTGCGCTACCAACATGCTTCAACCAAGAGAG 551
QY 148 GlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIleLeuGlnSerThrProProLeu 167
DB 552 GGTTCATGCGCTGTGCTGTGCGTGGCGCATCTCCCTGTATATCATTTGAGACCCCTG 611
QY 168 TyrGlyTyrGlyGlnAlaAlaPheAspGluAspAsnAlaLeuCysSerMetIleTyrGly 187
DB 612 TTCGGCTGAGAGCGCGGCC---CCCGAGGACGAGACCATCTGCCAGATC-----AAC 662
QY 188 AlaSerProSerTyrThrIleLeuSerValIleSerPheIleValIleProLeuIleVal 207
DB 663 GAGGAGCGGCGTACGTCTTCTTACGCGTGGGCTCTTCTTACCTCTTGGGCCATC 722
QY 208 MetIleAlaCysTyrSerValAlaPheCysAlaAlaArgArgGlnHisAlaLeuLeuTyr 227
DB 723 ATCTGCTCATGTACTGCGCGCTTACGTCGTGGCCAAAGG----- 764
QY 228 AsnValIlyAspArgHisSerLeuGlnValAlaValIlyAspCysValGluAsnGlnAspGlu 247
DB 765 -----GAGAGCGGCGGCTC 779
QY 248 GluGluAlaGluLysLeuGluLysPheGlnAspGluSerGluPheArgArgGlnHisGlu 267
DB 780 AAGTGTGCTTCAAGACGACAGTCCGAGCTGCGCAAGTACGCTCCGATCTCCATCGG 839
QY 268 GlyGluValIlyAlaLysGluGluLysArgMetGluAlaLysAspGlySerLeuLysAlaLys 287
DB 840 AAAAAGCGCCCGGCA----- 854
QY 288 GluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySerGluGluValArg 307
DB 855 ---GGAGGAGCGGAGTGGCAGCGCCCAAGACCAAGACCACTTCTCACTGAGGCTC--- 908
QY 308 GluSerSerThrValAlaSerAspGlySerMetGluGlyLysGluGlySerThrLysVal 327
DB 908 ----- 908
QY 328 GluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnGlnCysSerIleAsp 347

Db 908 ----- 908
Qy 348 LeuGlyGluAspAspMetGluPheGlyGluAspAspIleAspPheSerGlyAspAspVal 367
Db 909 -----CTCAAGTTCTCCCGGAGAG---- 929
Qy 368 GluAlaValAsnIleProGluSerLeuProSerArgArgAsnSerAsnSerAsnPro 387
Db 929 ----- 929
Qy 388 ProLeuProArgCysTyrgInCysAlaValAlaValIlePheIleIleIlePheSer 407
Db 930 -----AAAGCGGCAAAACGCTGGCGATGCTGCTGCGCTGC 965
Qy 408 TyrValLeuSerLeuGlyProTyrCysPheLeuAlaValIleValIleValIleAspVal 427
Db 966 TTCGTCCTCTGCTGCTGCTGCTTTT---TTCCTTAGTCATGCCATTTGGCTTTCTCCCT 1022
Qy 428 GluThrGlnValProGlnTTrpValIleThrIleIleIleIleIleIleIlePhePheGlnCys 447
Db 1023 GATTTCAGCCCTCGAAACAGTTTAAATAGATTTTGGCTCGATATCTAAACAGC 1082
Qy 448 CysIleLeuProTyrValTyrGlyTyrMetIleIleIleIleIleIleIleIleIleIleIleIle 467
Db 1083 TGCATCAACCCCATCATATACCCATGCTCCAGCCAAAGATTCAAAAGCCCTTTCAGAT 1142
Qy 468 MetLeuLys---LysPhePheCysLysGluLysProPheGlu-----Asp 482
Db 1143 GCTTTGAGAATTCAGTGTCTGCGAAGAGAGTCTCCAAACAGCCCTGGGCTACAC 1202
Qy 483 SerHisProAspLeuProGlyThrGlyGlyThrGlyGlyLysIle---ValProSer 501
Db 1203 CTGCACCGCCGACGAGCCGTGGAAGGCAACAGAGCATGTGCGCATCCCGCG 1262
Qy 502 TyrAspSerAlaThrPhe 507
Db 1263 GGATCAAGAGAGACCTTC 1280
RESULT 11
US-08-228-932-5
Sequence 5, Application US/08228932
Patent No. 5578611
GENERAL INFORMATION:
APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
Theresa A. Branche, John M. Weizel and Paul R. Harris
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JBW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 664-0525
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-228-932-5

Alignment Scores:
Pred. No.: 1,29e-26 Length: 1639
Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
DB: 2 Gaps: 11

US-10-712-615-2 (1-508) x US-08-228-932-5 (1-1639)
Qy 8 SerThrArgGluSerAsnSerSerHisThrCysMetProLeuSerLysMetProIleSer 27
Db 138 TCGGGAATGCTGTCGACAGCTCCACACTGCACCCACCG-----CCGGCACCGGTGAC 191
Qy 28 LeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleSerPheVal 47
Db 192 ATTTCAAGGCACTGCTGCTGGGATATCTTGGGGGCGCTCATTTCTTGGGGTGTG 251
Qy 48 GlyAsnIleValIleAlaLeuValLeuGlnArgLysProGlnLeuLeuGlnValThrAsn 67
Db 252 GGTAAACATCTTAGATTCCTCTCCGTACCGCTGCACCGACACCTGCACCTACGTACGAC 311
Qy 68 ArgPheIlePheAsnLeuLeuValIleThrAspLeuGlnIleSerLeuValAlaProTyr 87
Db 312 TACTACATGTCACACTGCGGTGGCGGACCTCTGTCACCTGCACCGGTGCTGCTGCTTC 371
Qy 88 ValValAlaThrSerValProLeuPheThrProLeuAsnSerHisPheCysThrAlaLeu 107
Db 372 TCCGCCATCTTCAGAGTCTTAGGCTACGAGCTTGGCAGAGTCTTGGACATCTGG 431
Qy 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValAsnThrIleValIleValSerVal 127
Db 432 GCGGACGTGATGCTGCTGCTGCGACCGCGTTCATCATAGGCGCTCTGCATCTCCATC 491
Qy 128 AspArgTyrLeuSerIleIleHisProLeuSerTyrProSerLysMetThrGlnArgArg 147
Db 492 GACCGCTACATCGGCTGAGCTACCCCGCTGGCGTACCAACATCATGTCACCGAGGAGG 551
Qy 148 GlyTyrLeuLeuLeuTyrGlyThrTrrIleValAlaIleLeuGlnSerThrProLeu 167
Db 552 GGTCTCATGGCTGCTGCTGCTGCGTACCTCTCCCTCATATCTTGGAGACCTTG 611
Qy 168 TyrGlyTrrGlyGlnAlaAlaPheAspGluArgAsnAlaLeuCysSerMetIleTrrGly 187
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Db 723 ATCCGTGATGTACTGCGCGGTCTACGTGTCGCGCAAGAG----- 764
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Qy      208 MetIleAlaCyTySerValValPheCyValAlaIaArgArgIleIleAlaLeuLeuTy 227
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Qy      248 GluGluAlaGluIyLeuGluIupheGluAspGluSerGluPheArgGluIleGlu 267
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Qy      268 GluGluValIyValIleLysGluGluIyArgMetGluAlaLysAspGlySerLeuLysAlaLys 287
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Qy      288 GluGlySerThyThrSerGluSerSerValGluAlaArgGlySerGluValArg 307
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Qy      308 GluSerSerThValAlaIaSerAspIySerMetGluGlyLysGluGlySerThyIyVal 327
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Qy      368 GluAlaValAlaIleProGluIleuSerProProSerArgArgAsnSerAsnSerAsnPro 387
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Db      930 -----AAAGCGGCCAAACCGCTGGCATCGTGTGCGCTGC 965
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Qy      448 CyValIleHisProTyTrgValIyTrgIyTrgMetHisLysThrIleLysLysGluIleGlnAsp 467
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Qy      468 MetLeuLys---LysPhePheCyLysGluLysProProLysGlu-----Asp 482
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Qy      483 SerHisProAspLeuProGlyThrgLysGlyIyThrgLysIyLysIle---ValProSer 501
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; Sequence 5, Application US/08406855A
; Patent No. 5861309
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08406, 855A
; FILING DATE: 21-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28, 678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPM/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1639 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 126..1523
; OTHER INFORMATION:
; US-08-406-855A-5
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Alignment Scores:
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Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
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Oy	428	GlnThrGlnValProGlnTTrpValaIleThrIleIleIleIleIlePheLeuPheLeuGlnCys	447
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/ Sequence 5, Application US/08722190
/ Patent No. 5990128
/ GENERAL INFORMATION:
/ APPLICANT: Charles Gluchowski, Carlos C. Porray, George
/ APPLICANT: Chiu, Theresa A. Branchek, John M. Wetzel and Paul R. Hartig
/ TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: COOPER & DUNHAM LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.24
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/722,190
/ FILING DATE: 4-APR-1995
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPW/AGL
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1639 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: N
/ ANTI-SENSE: N
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 126..1523
/ OTHER INFORMATION:
US-08-722-190-5

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Pred. No.: 1,29e-26 Length: 1639
Score: 338.50 Matches: 108
Percent Similarity: 37.15% Conservative: 80
Best Local Similarity: 21.34% Mismatches: 187
Query Match: 12.80% Indels: 131
DB: 2 Gaps: 11

US-10-712-615-2 (1-508) x US-08-722-190-5 (1-1639)
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GenCore version 5.1.6
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Run on: December 10, 2005, 06:42:34 ; Search time 778 Seconds

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Perfect score: 2644

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Total number of hits satisfying chosen parameters: 19587084

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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

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6	2644	100.0	2241	9	US-10-505-486-233
7	2644	100.0	4718	6	US-10-293-983-8
8	2641	99.9	1527	3	US-09-791-932-52

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10	2641	99.9	1527	5	US-10-094-417-5	Sequence 5, Appl1
11	2641	99.9	1527	5	US-10-225-567A-582	Sequence 582, App
12	2641	99.9	1527	6	US-10-345-332-1	Sequence 1, Appl1
13	2641	99.9	1527	6	US-10-321-807-15	Sequence 15, Appl
14	2641	99.9	1527	6	US-10-276-242-2	Sequence 2, Appl1
15	2641	99.9	1527	7	US-10-436-715-13	Sequence 13, Appl
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22	2641	99.9	1527	10	US-11-086-846-5	Sequence 5, Appl1
23	2641	99.9	1527	10	US-11-086-846-5	Sequence 925, App
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25	2641	99.9	2781	6	US-10-321-807-103	Sequence 103, App
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29	2641	99.9	2781	9	US-10-930-662-103	Sequence 1087, Ap
30	2641	99.9	3024	6	US-10-017-161-1087	Sequence 3, Appl1
31	2641	99.9	7524	6	US-10-345-332-3	Sequence 44, Appl
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38	2636	99.7	1527	7	US-10-314-048A-91	Sequence 46, Appl
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ALIGNMENTS

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; Sequence 1, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNAKNER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPFRMY8.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPFRMY8.
; FILE REFERENCE: D0047NP
; CURRENT FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-11-14
; PRIOR FILING DATE: 2001-09-04
; PRIOR FILING DATE: 2001-07-27
; PRIOR FILING DATE: 2001-02-14
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1527

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QY 121 ThrIleValIleuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGCTTGGTGTGACGTGATCGCTACTTGTCCATCATCAACCTCTCTCTTACCCG 420
QY 141 SerIleMetThrGlnArgArgIleTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 421 TCCAAATGACCCAGCGCCGCGGTACTGCTCTCTCATAGGCACTGATTTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaIlePheAspGluAsnAla 180
DB 481 CTGCACAGACCTCTCCACTCTACGGGTGGGGCCAGGCTCTTGTGATGGCCAAAGCT 540
QY 181 LeuCysSerMetIleTyrGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 541 CTCCTGCTCATGATCTGGGGGGCCAGCCCAAGCTACACTTCTCAGCGGTGCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaAlaArg 220
DB 601 ATCGTCATTCACATGATTCATGATGCTGCTACTCCGTGGTGTCTGTGACAGCCGG 660
QY 221 ArgGlnHisIleAlaLeuLeuTyrAsnValIleArgHisSerLeuGluValAlaGlyValAsp 240
DB 661 AGGCAGATGCTCTGCTGTACATGTCACATGTCACAGCACTGGAAAGTGCACAGTCAAG 720
QY 241 CysValGluAsnGluAspGluGluGlyValAlaGlyIleValIleValIleValIleValIle 260
DB 721 TGTGTGAGAAATGAGATGAGAGAGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGlyValValIleValIleValIleValIleValIleValIle 280
DB 781 GAGTTTCGCGCCAGCATGAAAGGTGAGTCAAGGCCAAGAGGCGCAAAATGGAAGCCAG 840
QY 281 AspGlySerLeuValAlaGlyGluGlySerThrGlyThrSerGluSerSerValGluVal 300
DB 841 GACGGCGAGCTGAAAGGCAAGAGAAAGCAAGGAGCAAGTGAAGTGAAGAGCC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGGCGAGAGAGGTCAAGAGAGAGCAAGCTGGCCAGCGACGACAGATGAGAGGT 960
QY 321 IysGluGlySerThrIleValGluGluAsnSerMetIleValAlaAspIleGlyArgThrGlu 340

DB 961 AAGAAAGCAGCACCAAGTTGAGAGAAACAGCATGAAGGACAGCAAGGTCGCACAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCAATGACGACATTGACTTGGGTGAAGATGATGAGTGGTGAAGACGATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTAGAGATACGTCGAGGACATGAAACATCCGAGAGCTCCCAACCAATCATC 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysAlaValAlaVal 400
DB 1141 CGTAAAGCAACAGCAACCTCTCTGCGCAGGTGTACAGTGAAGCAAGCTGTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValIleuSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTATCATCTATTTCTCTTATGAGCTATCCCTGGGCGCTACTGCTTTTAAAGATC 1260
QY 421 LeuAlaValTrpValAspValGluThrGlnValProGlnTrpValIleThrIleIleIle 440
DB 1261 CTGGCGGTGGGTGATGTGAAACCAAGTACCCCAAGTGGGTGATCAACATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValIleTyrGlyTyrMetHisIleThr 460
DB 1321 TGGCTTTTCTCTGACAGCTGTCATCAACCCCTATGTCTATGTGCTAATGCAAGACC 1380
QY 461 IleIleValGluIleGlnAspMetLeuValIleValPheCysIleValIleValIleValIle 480
DB 1381 ATTAAGAGGAATTCAGAGCATGTGAAGATTTCTGCAAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIleValIlePro 500
DB 1441 GAGATAGACCAACCAACCTGCGGGAACAGAGAGGTGGAGCTGAAGCAAGATTGTCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCCTACGATTCCTCTACTTTTCT 1524

RESULT 3

US-10-712-615-1
Sequence 1, Application US/10712615
Publication No. US20040214317A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPMYB, EXPRESSED
TITLE OF INVENTION: HIGLY IN BRAIN
FILE REFERENCE: D0047A-CIP
CURRENT APPLICATION NUMBER: US/10/712,615
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: U.S. 09/992,238
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: U.S. 60/248,285
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: U.S. 60/268,581
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: U.S. 60/308,285
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: U.S. 60/317,166
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-712-615-1

Alignment Scores:

Pred. No.: 3,82e-284 Length: 1527
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

DB: 8 Gaps: 0
US-10-712-615-2 (1-508) x US-10-712-615-1 (1-1527)
QY 1 MetThrsSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGAGCTGCACCTGCAGCAACGACGCGCGAGATTAACAGACGACACGCTGATGCC 60
QY 21 LeuSerIysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCCTCAAAATGCCATCAGCTGCAGCCAGGCATCATCTCCGTCAACGCTGCTGATTATC 120
QY 41 PheLeuAlaAlaSerPheValGlyValenIleValleAlaValleLeuGlnArgIysPro 60
DB 121 TTCCTGCGCGCTCTTTCGTGCGCAACATAGTGTGGCGCTAGTGTGGAGGCGAAGCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGCTGCTGCAGGTATACCAACGCTTTTATCTTAACTCTCTGTCACCGACCTGCTGAC 240
QY 81 IleSerLeuValAlaProTrrpValValAlaThrSerValProLeuPheTrrpProLeuAsn 100
DB 241 ATTGCTGTGTGGCCCCCTGGGTGGGCGACCTGTGTCCTCTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTCTGCAGCGCCCTGGTTAGCCCTCACCCACCTGTTCCTGCGCCAGCTCAAC 360
QY 121 ThrIleValleLeuValSerValAspArgTrrLeuSerIleIleHisProLeuSerTrrPro 140
DB 361 ACCATTGCTTGGTGTGCTGAGTGAATGCTTATCTGTCAATCATCAACCTCTCTCCATCCG 420
QY 141 SerIysMetThrGlnArgArgGlyTrrLeuLeuLeuTrrGlyTrrTrrIleValAlaIle 160
DB 421 TCCAGATGACCCAGCGCGCGGTTAACCTGCTCTCTATGACCACTGGATGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTrrGlyTrrpGlyGlnAlaAlaPheAspGlnArgAsnAla 180
DB 481 CTGCGAGACACTCTCTCACTTACGCGTGGGCGCGGCTCTTTGATGAGCGCATGT 540
QY 181 LeuCysSerMetIleTrrpGlyValaSerProSerTrrThrIleLeuSerValAlaSerPhe 200
DB 541 CTCCTCTCATATATCTGGGGGCGACGCCAGCTACACTATCTCAAGCGTGTGCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTrrSerSerValAlaPheCysAlaAlaArg 220
DB 601 ATCGCATTCACCTGATGTCAATGATTGCTCTACTCGGTGTGTGTGTGTGTGTGTGTGT 660
QY 221 ArgGlnHisAlaLeuLeuTrrAsnValIlysaArgHisSerLeuGlnValArgValIlysaAsp 240
DB 661 AGGCGAGCATGTCTCTGTACAAATGTCAAGACACAGCTTGAAGTGGAGTCAAGGAC 720
QY 241 CysValIleGluAsnGluAspGluGluGlyAlaGluIlysaIlysaGluIlysaIlysaIlysa 260
DB 721 TGTGTGGAATATGAGATCAAGAGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 GluPheArgArgGlnHisGluGlyGluValIlysaIlysaIlysaIlysaIlysaIlysa 280
DB 781 GAGTTTCCCGCCAGCATGAAGTGAAGTCAAGGCCAAGAGAGGCGCAATGAGAACCAAG 840
QY 281 AspGlySerLeuLeuValAlaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysa 300
DB 841 GACGGCAGCTGTAAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysa 320
DB 901 AGGGCAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGlySerThrIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysaIlysa 340
DB 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 341 ValaGlnCysSerIleAspLeuGlyIlysaAspMetGluPheGlyIlysaAspIle 360

DB 1021 GTCAACCGCTGCAGCTTGAATTTGGGTGAGATGACATGAGCTTGGTGAAGACACATC 1080
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProSerArg 380
DB 1081 AATTTCACTGAGATGAGCTGAGAGAGAGTGAACATCCCGAGAGAGCTCCACCGAGTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTrrGlnCysGlyValAlaIlysaVal 400
DB 1141 CGTAACAGCAACAGCAACCTCTCTGCGAGGTGTACAGTGTCAAGGCTGTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTrrValLeuSerLeuGlyProTrrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTCTCTTAATGCTATCTCTGGGCGCTTACTGCTTTTTCAGCTC 1260
QY 421 LeuAlaValTrrpValAspValGluThrGlnValProGlnTrrpValIleThrIleIle 440
DB 1261 CTGGCGGTGTGGGTGAGATGTGAACCCAGGTATCCCGAGTGGGTGATCACCATATATC 1320
QY 441 TrrLeuPhePheLeuGlnCysCysIleHisProTrrValIlysaIlysaIlysaIlysa 460
DB 1321 TGGCTTTCTTCTGTGAGTGTGATCCACCCCTATGTCTTATGCTATCATACAAAGCC 1380
QY 461 IleLysIlysaGluIleGluAspMetLeuLysAspPheCysIlysaGluLysProProLys 480
DB 1381 ATTAAAGAGAAATCCAGACATGCTGAAGAACTTTCTTCAAGAAAACCCCCGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyIlysaIlysaPro 500
DB 1441 GAAGTATACCAACCCAGACTGCGGAGAACAGAGGTGGAGCTGAAGGCAATGTCTCCT 1500
QY 501 SerTrrAspSerAlaThrPhePro 508
DB 1501 TCCTAAGATTCTGCTAATTTTCT 1524
RESULT 4
US-09-992-238-47
; Sequence 47, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAKKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-47
Alignment Scores: 4,04e-284 Length: 1580
Pred. No.: 1

Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-712-615-2 (1-508) x US-09-992-238-47 (1-1580)

QY 1 MetThSerThCySerThzAsnSerThrArgGluSerAsnSerSerThrCysMetPro 20
DB 32 ATGAGCTCCACCTGACCAACAGCAGCCGAGAGTAACAGCAGCCACGTCATGCC 91
QY 21 LeuSerLyMetProLLeuSerLeuAhiSGIYIleIeaArgSerThrValLeuVal 40
DB 92 CTCTCCAAATATCCCATCAGCTCGGCCACGGCATCATCCGCTCAACCTGCTGGTTATC 151
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLyPro 60
DB 152 TTCCTGCGCCCTCTTCTGCGCAACATAGTGGCGCTAGTGTGGAGCGCAAGCCG 211
QY 61 GlnLeuLeuGlnValThzAsnArgPheIlePheAsnLeuValThzAsnLeuGln 80
DB 212 CAGCTGCTGACAGTACCAACCGTTTATCTTAACTCTCTGTCACGACCTGCTGAG 271
QY 81 IleSerLeuValAlaProTrpValValAlaIthnSerValProLeuPheTrpProLeuAsn 100
DB 272 ATTTGCTGCTGGCCCCCTGGGTGGTGCCACCTGCTGCTCTCTTCTGGCCCCCTCAAC 331
QY 101 SerThIlePheCySerThrAlaLeuValSerLeuThrIleLeuPheAlaPheAlaSerValIle 120
DB 332 AGCCACTTCTGCACGGCCCTGTGTAGCCCTCACCCACTGTTCGCTTCCGCGCCAGCTCAAC 391
QY 121 ThrIleValLeuValSerValAspArgTrpLeuSerIleIleIleIleProLeuSerTrpPro 140
DB 332 ACCATTGCTTGTGTGTCAGTGAATGCGTACTGTGCTCATATCACTCTCTCTCAACCG 451
QY 141 SerLyMetThrGlnArgArgLyTrpLeuLeuLeuValGlyThrTrpIleValAlaIle 160
DB 452 TCCAAAGATGACCCAGGCGCGGTTACCTGCTCTTATGGGACCTGGATTGGGCATC 511
QY 161 LeuGlnSerThrProProLeuTrpGlyTrpGlyGlnAlaIlePheAspGluArgAsnAla 180
DB 512 CTGCGAGAGACTCTCCACTTCAACGGCTGGGCGCAGGCTGCTTGTATAGCGCATGCT 571
QY 181 LeuCySerMetIleTrpGlyValAspProSerTrpThrIleLeuSerValIleSerPhe 200
DB 572 CTCTGCTCATATCTGGGGGGCGAGCCCAAGCTACACTATCTCAAGCTGGGTCTTC 631
QY 201 IleValIleProLeuIleValMetIleAlaCyTrpSerValValPheCysAlaAlaArg 220
DB 632 ATCGTCATTCCACTGATTTGTCAATGATGCTGCTGCTACTCCGTGTGTCTGTCAAGCCGG 691
QY 221 ArgGlnIleAlaLeuLeuTrpAsnValIlyBatGhiIleSerLeuGluValArgValIlyAsp 240
DB 692 AGGCGAGCATGCTCTGCTGTCATATGTCACAGACACAGCTTGAAGTGAGATCAAGAGAC 751
QY 241 CysValGluAsnGluAspGluGluGlyAlaGlyValIlyValGluGluPheGlnAspGluSer 260
DB 752 TGTGTGAAATGAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 811
QY 261 GluPheArgArgGlnIleGluGlyGluValIlyAlaIlyArgMetGluAlaIly 280
DB 812 GAGTTTCCGCGCAGCATGAGTGAAGTCAAGGCCAAGAGAGGCGCATGAGCAAG 871
QY 281 AspGlySerLeuIlyAlaIlyGluGlySerThrGlyThrSerGluSerSerValGluAla 300
DB 872 GACGGAGGCTCAAGGCTCAAGAGCAAGCAAGGAGCAAGCAAGTGAAGTGAAGGCC 931
QY 301 ArgGlySerGluGluValArgIlySerSerThrValIleSerAspGlySerMetGluGly 320
DB 932 AGGGGAGGAGGAGGAGTCAAGAGGAGCAAGCGGTGGCCAGCGCAGCATGAGGAGGT 991
QY 321 LysGluGlySerThrLyValGluGluAsnSerMetLyAlaAspLyAsGlyArgThrGlu 340

DB 992 AAGGAGGAGGAGCAAAAGTTGAGAGAAACAGCAAGAGGCGAGACAGGCTGCACAGAG 1051
QY 341 ValaGlnIlySerSerIleAspLeuGlyGluAspMetGluPheGlyGluAspAspIle 360
DB 1052 GTCAACAGTGGAGCATTTGACTTGGGTGAAGTGAATGAGATTTGGTGAACAGCATC 1111
QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerIleProProSerArg 380
DB 1112 AATTTCAGTGAAGAGTGAAGTGAAGGAGTGAACATCCGGAGAGCTCCACCATGCT 1171
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTrpGlnCysLeuAlaAlaIlyVal 400
DB 1172 CATAACAGCAAGCAACCTCTCTGCGCAGGTGCTCAAGTGAAGCTCTAAAGTG 1231
QY 401 IlePheIleIleIlePheSerTrpValLeuSerLeuGlyProTrpCysPheLeuAlaVal 420
DB 1232 ATCTTCATCATATTTCTCTATATGTATCTCGGGGCTCTACTGCTTTTATCAGTTC 1291
QY 421 LeuAlaValATrPValAspValGluTrpGlnValProGlnTrpValIleThrIleIleIle 440
DB 1292 CTGGCCGTGTGGGTGATGTGAAACCAAGTACCCAGTGGGTGATCACCATATCATC 1351
QY 441 TrpLeuPhePheLeuGlnCysCysIleIleIleIleIleIleIleIleIleIleIleIle 460
DB 1352 TGGCTTTCTTCTCTCAGGTGTCATCAACCCCTATGTATGCTATGCTATGACAAAGCC 1411
QY 461 IleLyLyGluIleGluAspMetLeuLyLySerPhePheCysValGluLySerProLy 480
DB 1412 ATTAAGAAAGAAATCAGAGCATGTCTGAAGAAATCTTCTGTGAAGAAAGCCCGGAAA 1471
QY 481 GluAspSerIleProAspLeuProGlyTrpGluGlyGlyThnGluGlyIlySerIleValPro 500
DB 1472 GAAGATAGCCACCCAGACTGCCCCGAAACAGAGGAGTGGAGTGAAGGCAAGTTGTCT 1531
QY 501 SerTrpAspSerAlaThrPhePro 508
DB 1532 TCCTACGATTCGTACTTTCTCT 1555

RESULT 5
US-10-712-615-47
; Sequence 47, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBM78, EXPRESSED
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-712-615-47

Alignment Scores:
Pred. No.: 4,04e-284 Length: 1580
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0


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QY 21 LeuSerIyMeCProIIeSerIeuAlaHISGIYIleIeArGSeThrValIeuValIle 40
DB 61 CTCTCCAAATATGCCCATAGCCCTGGCCCGGCGCATCATCGCTCAACCGTGGTATTC 120
QY 41 PheIeuAlaIaSerPheValGIyaenIIeValIeuAlaIeuValIeuGlnArgIySPRO 60
DB 121 TTCCTGCGCGCTTTGCTGGCAACATAGTCTGGCTAGTGTGGACGCGCAAGCCG 180
QY 61 GlnIeuGlnValThraSnaArgPheIIePheAsnIeuValThraSpleuGln 80
DB 181 CAGCTGCTGAGGTGACCAACCTTTATCTTTAACTCTCTCTCAACCTGCTGCGAG 240
QY 81 IISerIeuValIaProItrPValValaIaThraSerValProIeubheTrPProIeuaAn 100
DB 241 ATTTGGCTGCTGGCCCCCTGGGGTGGGCACTCTGTGCTCTCTTCTTGGCCCCCTCAAC 300
QY 101 SerIiPheCyGThraIaIeuValSerIeuThraIaIeuPheAlaPheAlaSerValaAn 120
DB 301 AGCCACTTCTGACAGCGCCCTGTGTAGCTCACCCACCTGCTTCCCTTCCGCAAGCTCAAC 360
QY 121 ThrIleValIeuValSerValaAspArgIyIleuSerIleIeHISProIeuserIyPro 140
DB 361 ACCATTGCTTGGTGTGACGTGATCGCTACTGTTCATCCATCCACCTCTCTCTAACC 420
QY 141 SerIySmeCThraGlnArgArgIyIyIleuIeuIeuIyIyThraTrpIleValaIaIle 160
DB 421 TCCAGATATGCCAGCGCGCGGTTACGTGCTCTCTAAGGACCTGGATTGTGGCCATC 480
QY 161 IeuGlnSerThraProIeuserIyIyIyTrpGIyGlnAlaIaPheAspGIuArgaAnaIa 180
DB 481 CTGCGAGAGCACTCTCCACTACGCGTGGGCGCAGGCTGCTTGTATGAGCCCATGTCT 540
QY 181 LeuCySseMeIleTrpGIyIaIaSerProSeTrIyThraIeuserValIaIaSerPhe 200
DB 541 CTCTGCTCATGATCTGGGGGGGCGCACCCCGCTACACTATTTCCAGCGGGTCTTCT 600
QY 201 IleValIISerProIeuserIeValMeIleAlaCySTrSerValaIaPheCySAlaIaIaArg 220
DB 601 ATCGTCATTCCACTGATTTGCATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 221 ArgGlnHISAlaIeuIeuIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 240
DB 661 AGCGACATGCTCTGCTGTAACAATGCAAGAGACACAGCTTGCAAGTGCAGTCAAGGAC 720
QY 241 CySValGIuAsnGIuAspGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 260
DB 721 TGTGTGGAAGATGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 261 GIuPheArgArgGlnHISGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 280
DB 781 GAGTTTCGCGCGCAGCATGAGGTGAGTCAAGGCCAAGAGGCGCAAGATGCAAGCCAG 840
QY 281 AspGIySerIeuIyAlaIyGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 300
DB 841 GACGCGAGCTGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900
QY 301 ArgGIySerGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 320
DB 901 AGGCGAGAGGAGAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 960
QY 321 IySGIuGIySerThraIySValGIuGIuAsnSerMeIyIaIaAspIySGIyArgTrGIu 340
DB 961 AAGGAAGCAGACCAAAAGTTGAGAGAACAGCATGAAGCAGACAAAGGTCACAGAGAG 1020
QY 341 ValIaenGlnCySserIleAspIeuGIyIuAspAspMeCIIuPheGIyIuAspAspIle 360
DB 1021 GTCGAACAGTGCAGCACTTGGCTGGAAGATGATGAGAGTGTGTGAAGACGACATC 1080
QY 361 AsnPhSerGIuAspAspValGIuGIuAlaAsnIleProGIuSerIeuProProSerArg 380
DB 1081 AATTTAGTGAAGATACGTGAGGAGAGTGAACATCCCGAGAGCTCCCAACCACTGCT 1140
QY 381 ArgAsnSerAsnSerAsnProIeuserIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 400

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DB 1141 CGTAAACAGCAAGCAACCTCTCTGCGCAGAGTGTACAGTGCAGAACTGTAAAGTG 1200
QY 401 IIPheIleIleIIpPheSerIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 420
DB 1201 ATTTTCATCATCATATTTCTCTTAATGTCTATCTCTGGGCCCCCTACTGCTTTTAAAGATC 1260
QY 421 LeuAlaValIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 440
DB 1261 CTGGCGGTGGGTGGATGTGCAAAACCAAGATCCCAAGTGGGTATGACCAATATCATC 1320
QY 441 TrpIeuPhePheIeuGlnCySIIeHISProIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 460
DB 1321 TGGCTTTTCTCTGAGTGTGATCCATCCACCCCTATGTCTATGAGCTACATGCAAGACC 1380
QY 461 IlyIyIyGIuIIeGIuAspMeIeuIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 480
DB 1381 ATTAAGAAAGAAATCCAGACATGCTGAAGAGTTCTTGTGAAGAAAGCCCGGAAA 1440
QY 481 GIuAspSerIaProAspIeuProGIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 500
DB 1441 GAAGATAGCCACCCAGACCTGCCCCGGAACAGAGGTGGACTGAAGCAAGATTGTCTCT 1500
QY 501 SerIyAspSerAlaThraPhePro 508
DB 1501 TCTACGATTTCTGTAATTTCTCT 1524

RESULT 7
US-10-293-983-8
; Sequence 8, Application US/10293983
; Publication No. US2003014998A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Blatcher, Maria
; APPLICANT: Paulsen, Janet
; APPLICANT: Bates, Brian G
; TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Therefor
; FILE REFERENCE: AM100476
; CURRENT APPLICATION NUMBER: US/10/293,983
; CURRENT FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 4718
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: (332)..(1858)
; OTHER INFORMATION:
US-10-293-983-8

Alignment Scores:
Pred. No.: 2,43e-283 Length: 4718
Score: 2644.00 Matches: 508
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-712-615-2 (1-508) x US-10-293-983-8 (1-4718)
QY 1 MetThraSerThraCyGThraSnaSerThraArgGIuSerIaAsnSerSerIaThraCySMeCPro 20
DB 332 ATGAGCTCCACCTGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 391
QY 21 LeuSerIyMeCProIIeSerIeuAlaHISGIYIleIeArGSeThrValIeuValIle 40
DB 392 CTCTCCAAATATGCCCATAGCCCTGGCCCGGCGCATCATCTGCTCAACCTGCTGTTATC 451
QY 41 PheIeuAlaIaSerPheValGIyaenIIeValIeuAlaIeuValIeuGlnArgIySPRO 60
DB 452 TTCCTGCGCGCTTTCTGCTGCAACATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511

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QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
Db 512 CAGTGTGAGAGTGAACCGTATTATCTTAACCTCTCGTCAACGACCTGCTGAG 571
QY 81 IleSerLeuValAlaProTyrValAlaThrSerValProLeuPheTyrProLeuAsn 100
Db 572 ATTGGCTGTGGCCCTGGGGTGGTGGCCCTGTGGCTCTTCTTGGGCCCTCAAC 631
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
Db 632 AGCCACTTGTGACCGGCTGTGAGTACCTCAACCTCTTGGCTTGGCCAGCTCAAC 691
QY 121 ThrIleValLeuValSerValAsnArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
Db 692 ACCATTGCTTGTGTGAGTGTGATCGCTTGTGCATCATCAACCTCTCTCTACCCG 751
QY 141 SerIleMetThrGlnArgArgTyrTyrLeuLeuLeuTyrGlyThrTyrIleValAlaIle 160
Db 752 TCCAAAGATGACCCAGCGCGGTTACCTGCTCTATGGGACCTGGATTGTGGCCATC 811
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrGlyGlnAlaAlaPheAspGluArgAsnAla 180
Db 812 CTGCAAGACATCTCTCCACTTACCGCTGGGCGCAGGCTGCTTGTGATGAGCCATGCT 871
QY 181 LeuCysSerMetIleTyrGlyValaSerProSerTyrThrIleLeuSerValIleSerPhe 200
Db 872 CTCTGCTCATGATCTGGGGGCGCCAGCCCACTACATTAATCTCAGCTGTGCTTCC 931
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerSerValValPheCysAlaAlaArg 220
Db 932 ATCGTCATTCCACTATTGTGATGATGATGCTCTCTCTGCTGTGCTGTGCTGTGCTGTG 991
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIlyAsArgHisSerLeuGlnValArgValIlyAsp 240
Db 992 AGGCAGCATGCTCTCTGTCACATGTCAAGACACACAGCTTGGAACTGGCAATCAAGAC 1051
QY 241 CysValGluAsnGluAspGluGluGlyAlaGluIlyValGluIlyPheGlnAspGluSer 260
Db 1052 TGTGTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1111
QY 261 GluPheArgArgGlnHisGluGluIlyValIlyValIlyValIlyValIlyValIlyVal 280
Db 1112 GAGTTTCCGCGCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1171
QY 281 AspGlySerLeuIlyAlaIlyValGluGluGluGluGluGluGluGluGluGluGluGlu 300
Db 1172 GACGGCAGCTGAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
QY 301 ArgGlySerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
Db 1232 AGGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1291
QY 321 LysGluGluGluSerThrIlyValGluGluAsnSerMetIlyValAspIlyValArgThrGlu 340
Db 1292 AAGGAAGGAGAGACCAAGTTGAGAGACACACATGAAAGGAGAGACCAAGGAGAGAG 1351
QY 341 ValaGlnGluCysSerIleAspLeuGluGluAspAspMetGluPheGluGluAspIle 360
Db 1352 GTCAACCAAGTGAAGATTTGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1411
QY 361 AsnPheSerGluAspAspValGluAlaValaAsnIleProGluSerLeuProProSerArg 380
Db 1412 AATTTCAGTGAAGATGACGTGAGAGAGAGATCCCGAGAGAGCTCCCAACCAAGTCT 1471
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCysTyrGlnCysIlyValAlaIlyVal 400
Db 1472 CGTAAACAGCAACCAACCTCTCTGCGCAGGTGTCTACAGTGAACCAACCTCTAAAGG 1531
QY 401 IlePheIleIleIlePheSerTyrValLeuSerLeuGluProTyrCysPheLeuAlaVal 420
Db 1532 ATCTTCATCATATTTTCTCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATGAGCATC 1591

QY 421 LeuAlaValTyrPValAspValGluThrGlnValProGlnTyrValIleThrIleIleIle 440
Db 1592 CTGGCCGTGTGGTGGAGTGTGAACCCAGGTACCCAGTGGGTGATCACCATAATCATTC 1651
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGlyTyrMetHisGlyThr 460
Db 1652 TGGCTTTCCTTCGCAATGCTGCAATCCACCTTATGTCTATGGCTTACATCAAGAAC 1711
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProProLys 480
Db 1712 ATTAAGAAAGAAATCCAGAGATGCTGAAGAAAGTTCTTCTGCAAGAAAGCCCCGAAA 1771
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyIlyThrGluGlyLysIleValPro 500
Db 1772 GAAGATACCCACCAAGACCTCCCGGAACAGAGGTGGATGGAAGGCAAGATTGCTCCT 1831
QY 501 SerTyrAspSerAlaThrPhePro 508
Db 1832 TCTTAGATTCGCTACTTTTCT 1855

RESULT 8
US-09-791-932-52
; Sequence 52, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayser, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Ruff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1 G Protein-coupled Receptors Cross-Referen
; FILE REFERENCE: 00325 US1
; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-791-932-52

Alignment Scores:

Pred. No.: 8,266-284 Length: 1527
 Score: 2641.00 Matches: 507
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.80% Mismatches: 0
 Query Match: 99.89% Indels: 0
 DIs: 3 Gaps: 0

US-10-712-615-2 (1-508) x US-09-791-932-52 (1-1527)

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QY 1 MetThrSerThrCySerThraSerThraArgGluSerAsnSerSerHisThrCyMetPro 20
Db 1 ATGACCTCCACCGCCGACCAACAGCAGCGCGAGAGTAACAGCAGCCACGTCATGCCC 60

QY 21 LeuSerIleMetProIleSerIleuAlaHisGlyTlleIleArgSerThrValLeuValIle 40
Db 61 CTCTCCAAATATGCGATCAGCCTGGCCCAAGGCATATCCGCTCAACCGTGTGTATATC 120

QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValIleuAlaLeuValIleuGlnArgIlePro 60
Db 121 TTCCTGCGCGCCCTTTTCGTGCGCAACATAGTCTGCGCTAGTGTGCGACGCCAAGCCG 180

QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
Db 181 CAGCTGCTCAGAGTGACCAACCGTTTATCTTAACCTCCTCGTCAACGACTGTGCGAG 240

QY 81 IleSerIleuValAlaProTTPValIValAlaThrSerValProLeuPheTTPProLeuAn 100
Db 241 ATTTGCTGCTGGGCCCCCTGGGTGGTGGCCACTGTGTGCTCTCTTGGCCCCCTCAAC 300

QY 101 SerHisPheCySerThraIleuValSerLeuThrHisIleuPheAlaPheAlaSerValAsn 120
Db 301 AGCCACTTTCGACAGCGCCCTGGTTAGCTTACCACTCACTGTTCCCTTCCGCAACGCTAAC 360

QY 121 ThrIleValIleuValSerValAspArgIleLeuSerIleIleHisProLeuSerIlePro 140
Db 361 ACCATTGTGCTGGTGCAGTGATGCTTCTTCCATCATCAACCTCTCTCTCAACCG 420

QY 141 SerIleMetThrGlnArgArgIleYrLeuLeuLeuLeuYrGlyThrTTPIleValAlaIle 160
Db 421 TCCAAATATGACCAAGCGCGCGGTATCCTGCTCTATGGCACCCTGGAATTTGGGCCATC 480

QY 161 LeuGlnSerThrProProLeuYrGlyTTPGlyGlnAlaAlaPheAspGluAspAsnAla 180
Db 481 CTGCAAGACCTCTCTCACTCTAGCGCTGGGCGCAGGCTGCTTTATGAGCCAAATGCT 540

QY 181 LeuCySerMetIleTTPGlyAlaSerProSerIleThrIleuSerValIleSerPhe 200
Db 541 CTCTGCTCATGATCTGGGGGGGCCAGCCCAAGCTACATATTCTCAAGCGTGTCTTCT 600

QY 201 IleValIleProLeuIleValIleMetIleAlaCySerIleSerValIalPheCyAlaAlaArg 220
Db 601 ATCGTATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660

QY 221 ArgGlnHisAlaLeuLeuYrAsnValIleValArgHisSerIleuGlnValArgValIleAsp 240
Db 661 AGGACACATGCTTGTCTGTAACATGTCAGAGACACAGCTTGGAGAGTGGAGACAGAGAC 720

QY 241 CyValIleGluAsnGluAspGluGluGlyAlaGluIleValSerGluIleuPheGlnAspGluSer 260
Db 721 TGTGTGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGAT 780

QY 261 GluPheArgArgGlnHisGluGluGlyIleValIleValIleValIleValIleValIleVal 280
Db 781 GAGTTTCGCGCCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840

QY 281 AspGluSerIleuValIleValSerGluIleValIleValIleValIleValIleValIleVal 300
Db 841 GACGGCAGCTGAGAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

QY 301 ArgGlySerGluGluValArgIleuSerSerThrValIleAlaSerAspGluSerMetGluGly 320
  
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Db 901 AGGGCGAGGAGAGAGGTCTCAGAGAGAGCAGCAGGTGGCCAGCGACGCGAGCATGAGGGGT 960
QY 321 LVSGIUGLISerThrIleValIleGluIleuAsnSerMetIleValAlaAspIleGlyArgThrGlu 340
Db 961 AAGAGAGGAGAGCAGCAAGATTTAGAGACACAGATGAAAGGACAGACAGAGGTGCCACAGAG 1020
QY 341 ValAsnGlnCySerIleAspLeuGlyIleuAspAspMetGluPheGlyIleuAspAspIle 360
Db 1021 GTCAACCATGAGCATTTGATCTTGGGTGAAATGATGATGATGATGATGATGATGATGATG 1080
QY 361 AsnPheSerGluAspAspValIleValIleValIleProGluSerIleuProProSerArg 380
Db 1081 AATTTCATGAGAGATGACCTTCAGAGGAGGAGATCCCGAGAGAGCTTCCACCACTGCTGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProArgCySerGlnCyIleValIleValIleVal 400
Db 1141 CGTAACAGACAGACAGCAACCTCTCTGCGCAGGTGTATCAAGTGGCAAGCTCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerIleValIleuSerIleuGlyProIleCySerPheLeuAlaVal 420
Db 1201 ATCTTCATCATCATTTTCTCTATGTGCTATCCCTGGGGCCCTTACTGCTTTTATGCAAGTC 1260
QY 421 LeuAlaValIleValIleAspValIleGluThrGlnValProGlnTTPValIleThrIleIle 440
Db 1261 CTGGCCGTGTGGGTGATGTCCAAACCCAGTACCCCAAGTGGGTGATCAACATATATCATC 1320
QY 441 TTPLeuPhePheLeuGlnIleCySerIleHisProIleValIleValIleValIleValIle 460
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QY 461 IleValIleGluIleGlnAspMetLeuValIleValIlePhePheCySerIleValIlePro 480
Db 1381 ATTAAGAGAGAAATCCAGACATGCTGAAGAGTCTTCTGCAAGAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyIleValIleValIleValIleVal 500
Db 1441 GAAGATAGCACCAGACCTGCCCCGAAACAGAGGGGTGAGATGAAAGCAAGATTGTCCCT 1500
QY 501 SerIleAspSerAlaIleThrPhePro 508
Db 1501 TCTTACGATTCGTCTACTTTTCT 1524

RESULT 9
US-09-992-238-45
; Sequence 45, Application US/09992238
; Publication No. US2003005444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; FILE REFERENCES: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patentin Ver. 2.1
  
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1527)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR36
US-10-094-417-5

Alignment Scores:
Pred. No.: 8,266-284 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 5 Gaps: 0

US-10-712-615-2 (1-508) x US-10-094-417-5 (1-1527)

QY 1 MetThrSerThCysThrAsnSerThArgGluSerAsnSerSerHisThrCysMetPro 20
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QY 21 LeuSerIleMetProIleSerLeuAlaHisGlyIleIleArgSerThrValIleuValIle 40
DB 61 CTCTCAAAATAGCCATCAGCCCTGCGCCACGSCATATCCGCTCAACCGCTGCTTATC 120
QY 41 PheLeuAlaIleSerPheValGlyAsnIleValIleuAlaIleuValIleuGlnArgIlePro 60
DB 121 TTCCTCGCGCCCTCTTCCTCGGCAACATAGTGTGCGCTAGTGTGGACGCGCAAGCCG 180
QY 61 GlnIleuGlnValIleThrAsnArgPheIlePheAsnIleuValIleThrAsnIleuGln 80
DB 181 CAGCTGCTCAGGTGACCAACGTTTATCTTTAACCTCTGTCACCACTGTCGACAG 240
QY 81 IleSerIleuValAlaProIleValIleAlaThrSerValProIleuPheIleProIleuAla 100
DB 241 ATTGCGCTGTGGCCCCCTGGGTGGTGGCCACCTCTGTGCTCTTCTTGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaIleuValIleSerIleuHisIleuPheAlaPheAlaSerValIle 120
DB 301 ACCCACTTGTGACGCGCCCTGTGTTAGCTCACCCACCTGTTCCCTTCCGCGACGCTCAAC 360
QY 121 ThrIleValIleuValSerValAspArgIleIleuSerIleIleHisProIleuSerIlePro 140
DB 361 ACCATGTGTGTGTGTCAGTGAATCGCTACTGTTCATCATCAACCTCTCTCAACCGG 420
QY 141 SerIleMetThrGlnArgArgIleGlyIleIleuIleuIleuIleuIleuIleuIleuIleu 160
DB 421 TCCAGATGATACCCAGGCGCGCGCTTACCTGCTCTCTATGSCACCTGGATTGGGSCATC 480
QY 161 LeuGlnSerThrProProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 180
DB 481 CTGCAGAGACATCTCTCACCTCTACGCGTGGGSCAGGCTGCTTATGAGCGCATGTGCT 540
QY 181 LeuCysSerMetIleIleIleIleValIleSerProSerIleuIleuIleuIleuIleuIleu 200
DB 541 CTCTGCTCATATATCGGGGGGCGACCCACCTCAATCAATCTCAGCGTGGTGTCTTCC 600
QY 201 IleValIleProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 220
DB 601 ATCGCATTCCTCACTATGTCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
QY 221 ArgGlnHisAlaIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
DB 661 AGGAGCATGCTCTGTGTAACAATGTCAAGAGACACAGCTTGAAGTGGAGAGTCAAGAGC 720
QY 241 CysValGluAsnGluAsnGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 260
DB 721 TGTGTGGAAGATGAGATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 261 GluPheArgArgGlnHisGluGluGluGluValIleValIleGlyGluGluIleArgMetGluAlaIle 280
DB 781 GAGTTTCGCGCGACAGATGAGGTGAGGTCAAGGCCAAGAGGAGGAGAGAGAGAGAGAGAG 840
QY 281 AspGlySerIleuIleuValIleGluGluGluSerThrGlyThrSerGluSerSerValGluAla 300
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DB 841 GACGGAGCCCTGAAGGCCAAGAGAGACACGGGGACCAAGTAGTGTAGAGGCC 900
QY 301 ArgGlySerGluGluValIleArgIleSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGGACGAGAGAGAGGTTCAGAGAGACACGCTGGCCACGACGACGACGACGACGACGACG 960
QY 321 IysGluGlySerThrIleValIleGluIleuAsnSerMetIleValIleAspIleGlyIleArgIle 340
DB 961 AAGGAGGACGACACCAAGTGTGAGGAGACATGATGAAGACAGACAGAGAGGAGGTGACAGAG 1020
QY 341 ValIleGlnIleCysSerIleAsnIleuGlyIleuAspAspMetGluPheGlyIleuAspAspIle 360
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QY 381 ArgAsnSerAsnSerAsnProProIleuProArgCysIleGlnCysIleValIleValIleVal 400
DB 1141 CGTAACAGCAACAGCAACCTCTCTGCGCAGGTGTACCAATGCAAACTGCTTAAGAGT 1200
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DB 1201 ATCTTCATCATCATTTTCTCTATGCTATGCTGCGGCGCTTACTGCTTTTATGACAGT 1260
QY 421 LeuAlaIleValIleValIleAspValGluIleuIleuIleuIleuIleuIleuIleuIleu 440
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QY 441 TrpLeuPhePheIleuGlnCysIleHisProIleValIleGlyIleIleIleIleIleIleIle 460
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QY 461 IleIleIleIleGluIleIleIleAsnMetIleuIleIlePhePheCysIleGluIleProIle 480
DB 1381 ATTAAGAAAGAAATCCAGGACATGCTGAAGAAGTCTTCTGCAAGAGAAAGCCCGGAAA 1440
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DB 1501 TCTTAGATTCGTACTTCTTCT 1524

RESULT 11
US-10-225-567A-582
; Sequence 582, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 582
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-582

Alignment Scores: 8,266-284 Length: 1527
Pred. No.: 2641.00 Matches: 507
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Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 5 Gaps: 0
US-10-712-615-2 (1-508) x US-10-225-567A-582 (1-1527)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGAGTGCACCTGACCAACAGCAGCGCGAGAGTAACAGCAGCAGCAGCAGTGC 60
QY 21 LeuSerLysMetProLleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCCTCAAAATGCTCATGAGCTGGCCCAAGCATCTCCATCCGCTCAACCGTGTGATTC 120
QY 41 PheLeuAlaAlaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLysPro 60
DB 121 TTCCTGCGCGCTCTTTCGTGCGCAACATAGTGTGCGCGCTGAGTGTGCGCGCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuGln 80
DB 181 CAGCTGTGACGAGTACCAACCGTTTATCTTAACCTCTGTCACCGACCTGTCGAG 240
QY 81 IleSerLeuValAlaProThrValValAlaThrSerValProLeuPheThrProLeuAsn 100
DB 241 ATTGCTGTGCGCCCTGCGGTGGTGGCCACTGTGCTGCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTGTGACGCGCCCTGTGTAGCTCAACCACTGTTGCGCTTCCCGCAGCTCAAC 360
QY 121 ThrIleValIleuValSerValAspArgLysLeuSerIleIleHisProLeuSerTyPro 140
DB 361 ACCATTGTCTGTGTCAGTGTGATGCTGATCTGCTCATCATCACCCTCTCTCAACCG 420
QY 141 SerLysMetThrGlnArgArgLysLysLeuLeuValLysLysIleValIle 160
DB 421 TCCAAAGATGACCCAGCGCGGTACCTGCTCTCTTAAGGACCTGGATGTGCGCATC 480
QY 161 LeuGlnSerThrProProLeuValLysLysIleValIleValAlaPheAspGluArgAsnAla 180
DB 481 CTGCAAGACACTCTCCACTCAAGCTGCGCGCCAGCTGCTTTGATGAGCGCATGCT 540
QY 181 LeuCysSerMetIleTTPGlyValaSerProSerTyThrIleLeuSerValIleSerPhe 200
DB 541 CTCTCTCATGATCTGCGGCGCGCCAGCCCACTCACTATCTCAGCGTGTGTCCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrsSerValValPheValAlaAlaArg 220
DB 601 ATCGTCATTCCACTGATTGTCAATGATGCTGCTCACTCCGTGTGTCTGTGCAAGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyrsAsnValLysArgHisSerLeuGlnValArgValLysAsp 240
DB 661 AGCGACATGCTCTCTCTGACATGTCAGAGACACAGCTTGGAAAGTGGAGTCAAGAC 720
QY 241 CysValGluAsnGluAspGluGluValaGluLysLysGluLysGluLysPheGlnAspGluSer 260
DB 721 TGTGTGGAATGATGAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGTTCAGATGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGluValValValValValValValValValValValVal 280
DB 781 GAGTTCCTCCCGCACATGATGAGTGAAGTCAAGGCGCAAGAGAGAGAGAGAGAGAGAG 840
QY 281 AspGlySerLeuValAlaValGluGluGluSerThrGlyThrSerGluSerSerValGluAla 300
DB 841 GACGCAAGCTTAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 301 ArgGlySerGluGluValArgLysSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGCGCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 321 LysGluGlySerThrLysValGluGluLysAsnSerMetLysAlaAspLysGlyArgThrGlu 340

DB 961 AAGAGGACAGCACCAGAACTTGAGAGAAACGATGAAGGACAGACAGGTCGACAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyGluAspAspIle 360
DB 1021 GTCAACCAAGTGCAGATTGATCTTGAGTGAAGATGATGATGATGATGATGATGATGATG 1080
QY 361 AsnPheSerGluAspAspValGluValAlaAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTCACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 381 ArgAsnSerAsnSerAspProProLeuProArgCysTyrsGlnCysLysAlaAlaLysVal 400
DB 1141 GCTAACAGCAACAGCAACCTCTCTGCGCGGTCTACAGTGTCAAGTGTCTTAAGTGTG 1200
QY 401 IlePheIleIleIlePheSerTyrsValLeuSerLeuGlyProTyrsCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTTCTCTTAAGTGTATCCCTGGGGGCTTACTGCTTTTATGCACTC 1260
QY 421 LeuAlaValITPValAspValGluThrGlnValProGlnTPValIleThrIleIleIle 440
DB 1261 CTGCGCGGTGTGATGTGAAACCCAGGTACCCCGAGTGTGATCATCATATATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyrsValTyrsLysTyrsMetHisLysThr 460
DB 1321 TGGCTTTCTTCTGCACTGCTGATCCACCTCATGCTATGCTATGCTATGCTATGCTATG 1380
QY 461 IleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProLys 480
DB 1381 ATTAAGAAGAAATCCAGACATGCTGAAAGATTTCTTCTCAAGAAACCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyTyrsGluGlyTyrsThrGluGlyLysIleValPro 500
DB 1441 GAAGATACCAACCCAGACCTCCCGGAAACAGAGGTGTGATGTAAGGCAAGATTTGCT 1500
QY 501 SerTyrsSerAlaThrPhePro 508
DB 1501 TCTTACGATTCGCTACTTTTCT 1524

RESULT 12
US-10-345-332-1
; Sequence 1, Application US/10345332
; Publication No. US20030129705A1
; GENERAL INFORMATION:
; APPLICANT: LI et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1000754CON
; CURRENT APPLICATION NUMBER: US/10/345,332
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/769,741
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/205,166
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/638,018
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-345-332-1

Alignment Scores:
Pred. No.: 8,266-284 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0
US-10-712-615-2 (1-508) x US-10-345-332-1 (1-1527)

QY 1 MetThrSerThrCysThrAsnSerThrArgGluSerAsnSerSerHisThrCysMetPro 20
DB 1 ATGAGCTCCACCGCGACCAAGCAGCGCGAGATGACAGCAGCCAGCTGACGCC 60
QY 21 LeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuValIle 40
DB 61 CTCTCCAAATGCGCATCAGCCCTGGGCCCGGCATATCCGCTCAACCGGTGGTTATC 120
QY 41 PheLeuAlaIleSerPheValIleGlyAsnIleValLeuAlaLeuValLeuGlnAspPro 60
DB 121 TTCCTGCGCGCTCTTTCGTGGCAACATAGTCTGCGTAGTGTGCAAGCCGCAAGCCG 180
QY 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGln 80
DB 181 CAGCTCTGAGGTGACCAACGTTTATCTTTTAACTCTGCTGACCAAGCCTGCTGAG 240
QY 81 IleSerLeuValAlaProTrpValValAlaThrSerValProLeuPheTrpProLeuAsn 100
DB 241 ATTTCCCTGCTGGCCCCCTGGGTGGTGGCCACCTGTGCTCTCTTCTGGCCCCCTCAAC 300
QY 101 SerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAlaPheAlaSerValAsn 120
DB 301 AGCCACTTCTGACAGGCGCTGTAGCTTACCCACCTGTGCTTCCGCAAGCTCAC 360
QY 121 ThrIleValIleLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro 140
DB 361 ACCATTGTGTGTGTGTCAGTGCATGCTCTTCCATCATCATCACTCTCTCTCAACCCG 420
QY 141 SerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValAlaIle 160
DB 421 TCCAAAGATGACCCAGCGCGCGGTACCTGCTCTCTCATGAGCACTGAGATTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyrGlyTyrTrpGlyGlnAlaIlePheAspGluAspGlnAla 180
DB 481 CTGCACAGACCTCTCCTCACTACGAGCTGGGCGCAGCGCTGCTTTATGAGCCCAATGCT 540
QY 181 LeuCysSerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTTCATGATCTGGGGGGCGCAGCCCGCATCACTTCTCAGCGTGTCTTCTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCysTyrSerValIlePheCysAlaAlaArg 220
DB 601 ATCGTCATTCCACTGATTCATGATGCTGCTGCTACCTGCTGCTGCTTCTGACGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyrAsnValIleValHisSerLeuGlnValAlaArgValIleAsp 240
DB 661 AGGACACATGCTCTGTGATCAATGTCACAGACACAGCTTGGAAAGTCAAGTCAAGGAC 720
QY 241 CysValIleAsnGluAspGluGluGlyAlaGluIleLysGluIlePheGlnAspGluSer 260
DB 721 TGTGTGGAATAATGAGATGAGAGGAGCAGAGCAGAGAAAGAGAGTTCCAGATGAGAGT 780
QY 261 GluPheArgArgGlnHisGluGlyGlyValValLysGluIleValArgMetGluAlaLys 280
DB 781 GAGTTTCCGCGCAGCATGAGGTGAGTCAAGGCCAAGGAGGCAAGATGAGCAAGCCAG 840
QY 281 AspGlySerLeuLeuValLysGluGlySerThrGlyThrSerGluSerValIleGluAla 300
DB 841 GAGGAGAGCTGAGAGCCAGAGAGAGAGACACGAGGACCGTAGAGTATGAGAGGCC 900
QY 301 ArgGluSerGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGAGAGCGAGAGAGTCAAGAGAGACAGACGCTGCGCCAGCAGCAGCAGTGAAGGT 960
QY 321 LysGluGlySerThrLysValIleGluGluAsnSerMetLysAlaAspLysGlyArgThrGlu 340
DB 961 AAGGAAGGAGCAGCAAGTGTGAGAGAACAGCATGAGGCAACAAGGTTGCCACAGAG 1020
QY 341 ValAsnGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyValAspAspIle 360
DB 1021 GTCAACCAAGTGAAGCATTTGAGGTGAGAGATGACATGAGATTGTGTAAGACGACATC 1080

QY 361 AsnPheSerGluAspAspValIleValAlaValIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTGAAGATGACGTGAGGAGAGTGAACATCCCGAGAGGCTCCACCCAGTGGT 1140
QY 381 ArgAsnSerAsnSerAsnProProLeuProAlaGlyGlyTrpGlnCysValAlaLysVal 400
DB 1141 CGTAACAGACAGCAACCTCTCTGCGCAGGTGTACAGTGCACAAAGCTCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyrValIleSerLeuGlyProTyrCysPheLeuAlaVal 420
DB 1201 ATCTTCATCATCATTTTCTCTATGTGCTATGCTCTGAGGACCTTACCTTTTATGACATC 1260
QY 421 LeuAlaValTrpValAspValIleValTrpGlnValProGlnTrpValIleThrIleIle 440
DB 1261 CTGGCCGTGTGGGTGATGTCCAAACCCAGTACCACCACTGGGTATCACTTAATCATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleIleHisProTyrValTyrGlyTyrMetHisLysThr 460
DB 1321 TGGCTTTTCTCTGCAAGTGTGATCCACCCCTATGTCTATGCTACATGACAAAGAC 1380
QY 461 IleLysLysGluIleGluAspMetLeuLysLysPheCysLysGluLysProProLys 480
DB 1381 ATTACAGAGAAATCCAGACATCTGTGAGAAAGTTCTTGTCAAGAAAGCCCGGAA 1440
QY 481 GluAspSerHisProAspLeuProGlyThrGluGlyGlyThrGluGlyLysIleValPro 500
DB 1441 GAAGATAGCCACCAAGACCTGCGCGGAAACAGAGGGGTGGAGCTGAAGGCAAGATTGTCCCT 1500
QY 501 SerTyrAspSerAlaThrPhePro 508
DB 1501 TCTACGATTCTGCTACTTTTCT 1524
RESULT 13
US-10-321-807-15
; Sequence 15, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hong T.
; APPLICANT: Dang, Hung T.
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; CURRENT FILING DATE: 2002-12-15
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-321-807-15

Alignment Scores:

Pred. No.:	8,266-284	Length:	1527
Score:	2641.00	Matches:	507
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.80%	Mismatches:	0
Query Match:	99.89%	Indels:	0
DB:	6	Gaps:	0

US-10-712-615-2 (1-508) x US-10-321-807-15 (1-1527)

QY	1	HeuTrSerSerThCyThrAnSerThrArgGluSerAsnSerSerhTrhTrCyMetPro	20
Db	1	ATGAGCTCCACCTGGACCAACGACGGCCGAGATGACAGACGCCACGTCATCTCC	60
QY	21	LeuSerLyMetProIleSerLeuAlaHhIsglyTleIleArgSerThrValLeuValIle	40
Db	61	CTCTCCAAAAATCCCATCAGCTGGCCACGGCATCATCGCTCAACCCGTGGTATTTC	120
QY	41	PheLeuAlaIaIaSerPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLyPro	60
Db	121	TTCTCTGGCGCTCTTTCTGTCGGACAAATAGTCTGGCGTAACTGTTCAGCCAAAGCCG	180
QY	61	GlnLeuLeuGlnValThrxAnArgPheIlePheAsnLeuLeuValThrxPheLeuGln	80
Db	181	CAGCTGTGACAGTGCACCAACGGTATTATCTTTAACTCTCGTCAACGACTGTGCAG	240
QY	81	IleSerLeuValAlaProTrpValValaIaIaThrSerValProIleuPheTrpProLeuAsn	100
Db	241	ATTTCGCTCGGGCCCCCTGGGTGGGGCACTCTGTGCTCTCTCTGGCCCCCTCAC	300
QY	101	SerHisPheCyThrAlaLeuValSerLeuThHisLeuPheAlaPheAlaSerValAsn	120
Db	301	AGCCACTTCTGCACGGCCCTGGTTAGCTTCAACCACCTGTGGCTTTCGCCACGTCAC	360
QY	121	ThrIleValLeuValSerValAspArgTyrLeuSerIleIleHisProLeuSerTyrPro	140
Db	361	ACCATGTTCGTGGTGCATGGATGCCTACTTGTTCATCATCCACCCTCTCTCTACCCG	420
QY	141	SerLyMetThGlnArgArgGlyTyrLeuLeuLeuTyrGlyThrTrpIleValaIle	160
Db	421	TCCAAGATGACCCACGGCGCGGTAACTCGTCTCTTAAGCACCTGGATTGGGCGATC	480
QY	161	LeuGlnSerThProProLeuTyrGlyTyrGlyAlaIaIaPheAspGluArgAsnAla	180
Db	481	CTGCAGACACCTCTCTCACTACGGCTGGGGCCAGGCTGCTTGAATAGCCCATGCT	540
QY	181	LeuCySerMetIleTrpGlyAlaSerProSerTyrThrIleLeuSerValIaSerPhe	200
Db	541	CTCTCTCATATGATCGGGGGGCCACCCACAGCTAACATTTCTCAGCGGTGCTCTTC	600
QY	201	IleValIleProLeuIleValMetIleAlaCyTySerValIaPheCyAspAlaIaArg	220
Db	601	ATCGCATTCCTCATGTTGTCAATGATGCTGCTACTCCGTGGTGTCTGTGCAGCCCGG	660
QY	221	ArgGlnHisAlaLeuLeuTyrAsnValIyAspHisSerLeuGlnValaArgValIyAsp	240
Db	661	AGGCAGCATGCTCTGTGTACAATGTCAAGACACAGCTTGGAAGTGGCAGTCAAGAC	720
QY	241	CysValIleGluArgGlnAspGluGluGlyAlaIaGlyLeuLyArgGluLeuPheGlnAspGluSer	260
Db	721	TGTGTGGAGAAAGAGATGAGAGGAGACAGACAGAAAGAGAGATTCCAGATGTAGACT	780
QY	261	GluPheArgArgGlnHisGluGluGlyValIyValaIyGluGluLyrPheMetGluAlaIyS	280
Db	781	GAGTTTCGGCCGACGATGAAGGTGTGGTCAAGGCCCAAGGAGGCCAGAAATGGAAGCCAG	840
QY	281	AspGlySerLeuLysAlaIyArgGluGlySerThGlyThrSerGluSerSerValGluAla	300
Db	841	GACGGCAGGCTGAAGGCCAAGGAAGGAAGACCGGGGACCAGTAGATGATGTAGAGCC	900
QY	301	ArgGlySerGluGluValaArgGluSerSerThValaIaSerAspGlySerMetGluGly	320

Db	901	AGGGGCGACGAGGAGTCTCAGAGAGAGCAGCAGGTGGCCAGCGACGGCAGCATGGAGGGT	960
Qy	321	LygSLuGLySerThrLyValGLuGLuAsnSerMetLySAlaApLyGLyAlaGThrGLu	340
Db	961	AAAGGAAGCGACGCCAAAGTTGAGAGAAACGCGATGAAAGCGACAAGGGGTGCGACAAAG	1020
Qy	341	ValAsnGLyCysSerIleAspLeuGLyGLuAspAspMetGLuPheGLyGLuAspAspIle	360
Db	1021	GTCAACCAAGTCAGACATTGACTTGGGTGAAAGATACATGGAGTTGGTGAAGACGACATTC	1080
Qy	361	AsnPheSerGLuAspAspValGLuAlaValAsnIleProGLuSerLeuProProSerArg	380
Db	1081	AATTTCAGTGAAGATGACGTGAGGCGAGTGAAATCCCGAGAGACCTCCACCCAGTCGT	1140
Qy	381	ArgAsnSerAsnSerAsnProProLeuProArgCysArgTyrGLyCysLySAlaAlaLyVal	400
Db	1141	CGTAAACGCAACAGCAACCTCTCTCCAGGAGTCAACGATCCAAAGCTGTAAAGATG	1200
Qy	401	IlePheIleIleIlePheSerTyrValLeuSerLeuGLyProTyrCysPheLeuAlaVal	420
Db	1201	ATCTTCATCATCATTTCTCTCTAATGTGCTATCCCTGGGGGCCCTACCTGTTTTHAGCACT	1260
Qy	421	LeuAlaValTyrValAspValGLuThrGlnValProGlnTyrValIleThrIleIleIle	440
Db	1261	CTGGCCCTGTGGGTGATGTGAAACCAGAGTACCCAGATGGTGATCACCATATATATCTC	1320
Qy	441	ThrLeuPhePheLeuGlnCysCysIleHisProTyrValTyrGLyTyrMetHisLysPhe	460
Db	1321	TGGCTTTTCTTCCTGCAGCTGCTGATCACCCTCATGTCTAATGGCTCATGCACAAAGACC	1380
Qy	461	IleLysLySGLuIleGlnAspMetLeuLysLysPhePheCysLySGLuLysProProLys	480
Db	1381	ATTAAAGAGGAATCCAGACATGCTGTAAGAAAGTTCTTCTGCAAGGAAGAAACCCCCGAA	1440
Qy	481	GluAspSerHisProAspLeuProGLyThrGlnGLyGLyThrGlnGLyLysIleValPro	500
Db	1441	GAAAGATGACCCACCCAGACCTGCCCGGAAACAGAGGTGGAGCTGAAGGCMAAGATTGTCCCT	1500
Qy	501	SerTyrAspSerAlaThrPhePro	508
Db	1501	TCTCAAGATTCCTGCTACTTTTCTT	1524

RESULT 14

US-10-276-243-2
; Sequence 2, Application US/10276243
; Publication No. US20030187219A1

; GENERAL INFORMATION:

APPLICANT: Bayer AG

1; TITLE OF INVENTION: REGULATION OF HUMAN α 1A ADRENERGIC RECEPTOR-LIKE

TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR

FILE REFERENCE: Lj0062 Foreign Countries

CURRENT APPLICATION NUMBER: 0

CONCERN: 00/10/2003
CURRENT FILING DATE: 2003-11-14

! CORKEN1 FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: US 60/204,145

PRIOR FILING DATE: 2000-05-15 ;

PRIOR APPLICATION NUMBER: L

PRIOR FILING DATE: 2000-12-

NUMBER OF SEC

SOFTWARE, DATA

SOE INCOME: FALL

! SEQ ID NO 2

! LENGTH: 1527

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;      TYPE: DNA
;      ORGANISM: Homo sapiens
US-10-276-243-2
Alignment Scores:

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Pred. No.:	8,266-284	Length:	1527
Score:	2641.00	Matches:	507
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.80%	Mismatches:	0
Query Match:	99.89%	Indels:	0
DB:	6	Gaps:	0

US-10-712-615-2 (1-508) x US-10-276-243-2 (1-1527)

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QY 1 MetThSerThCyThraSenSerThArGluSerAmsSerSerHisThrCysMetPro 20
DB 1 ATGACGTCCACCTGGACCAACAGACGCGGAGAGTAAAGCAAGCCACAGCTGCATGCCCC 60
QY 21 LeuSerLywMeProIleSerLeuAlaHisGlyIleIleArgSerThrValIleValIle 40
DB 61 CTCCTCAAAATGCGCATCAGCCCTGGCCACGGCATCATCCGCTCAACCCGTGCTGTTATC 120
QY 41 PheLeuAlaIleSerPheValIleGluAenIleValIleValIleValIleValIleValIle 60
DB 121 TTCCTGCGCGCTCTTTCGTGGCAACATAGTCTGGCGCTAGTGTTCGAGCCCAAGCCG 180
QY 61 GluLeuLeuGlnValThraAenArgPheIlePheAmsLeuValThraPheLeuGln 80
DB 181 CAGCTCTGCAGGTGACCAACCGTTTATCTTTAACTCTCTGTCACGACCTGCTGCGAG 240
QY 81 IleSerLeuValAlaProIleValAlaIleThrSerValProLeuPheIleProLeuAen 100
DB 241 ATTTCCCTCGTGCGCCCTGGTGGTGGCCACCTCTGTGCTCTTCTGCGCCCTCAAC 300
QY 101 SerHisPheCyThrThraLeuValSerLeuThraIleuPheAlaPheAlaSerValAen 120
DB 301 AGCACCTTCTGCAGCGCCCTGTGTAGCTTCAACCACCTGTTCGCTTGGCAGCGTCAC 360
QY 121 ThrIleValIleuValSerValAspArgTyLeuSerIleIleHisProLeuSerTyPro 140
DB 361 ACCATTGTGTGTGTGTCAGTGATCGCTACTTCTCATCATCAACCTCTCTCTCTACCG 420
QY 141 SerLywMetThrGlnArgArgIlyTyLeuLeuLeuTyGlyThrTrpIleValAlaIle 160
DB 421 TCCAAAGATGACCCAGCGCGCGGTACGTCTCTCTATGACGACCTGGATGTGGCCATC 480
QY 161 LeuGlnSerThrProProLeuTyTyGlyTyGlyGlnAlaIlePheAspGluAenAla 180
DB 481 CTGCAGACGACCTCTCACTCACTGAGGTGGGGCCAGGCTGCCCTTGTATGAGCCCAATGCT 540
QY 181 LeuCySerMetIleTyrGlyAlaSerProSerTyThrIleLeuSerValIleSerPhe 200
DB 541 CTCTGCTCCATGATCTGTGGGGGCCAGCCCAAGCTACACTTCTCAGCGTGGTCTCTTC 600
QY 201 IleValIleProLeuIleValMetIleAlaCyTySerSerValIlePheCysAlaAlaArg 220
DB 601 ATCGTCATTCACCTGATTCATGATGATGCTGCTAGCTCGTGGAGTTCTGTGACGCCGG 660
QY 221 ArgGlnHisAlaLeuLeuTyTyAenValLyArgHisSerLeuGluValArgValIleAsp 240
DB 661 AGGCAGCATGCTCTGTCAATGTCAAAGACACACAGCTTGGAGTGGCAGATCAAGGAC 720
QY 241 CysValGluAenGluAspGluGluGlyAlaGluIleLyLeuGluIlePheGlnAspGluSer 260
DB 721 TGTGTGAGATGATGAGTGAAGAGGAGGACAGAGAAGAGAGAGTTCACGATGTAGAGT 780
QY 261 GluPheArgArgGlnHisGluGlyGluValIleAlaIleGluGlyArgMetGluAlaIle 280
DB 781 GAGTTTCGCCGCCAGCATGAGGTGAGGTCAAGGCCAAGAGGCGCAAGATGGAAGCCAG 840
QY 281 AspGlySerLeuLyAlaIleGluGlySerThGlyThrsGluSerSerValIleGluAla 300
DB 841 GACGGCAGCTCTGAAGCCCAAGAGAGGACACGGCGCCAGTGAAGTGAAGTGAAGGCC 900
QY 301 ArgGlySerGluGluValArgGluSerSerThValAlaSerAspGlySerMetGluGly 320
DB 901 AGGGGCGAGGAGGATGAGAGAGAGGACGATGGCCGACGACGACGACATGAGAGG 960
QY 321 LyseGluGlySerThLyLyValIleGluGluAenSerMetLyAlaAspLyGlyArgTrpGlu 340
DB 961 AAGGAAGGCGACCAAGTTTGAAGAGAACAGCATGAGGCAAGAGGTTCCACAGAG 1020
QY 341 ValAspGlnCysSerIleAspLeuGlyGluAspAspMetGluPheGlyIleuAspAspIle 360
DB 1021 GTCAACCAAGTGCAGCATTCCTGTGGTGAAGATGACATGAGATTGTGTGAAGACGATC 1080
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QY 361 AsnPheSerGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArg 380
DB 1081 AATTTCAGTGAAGATGATCGTCAGGCGAGTGAACATCCCGAAGAGCTCCACCAAGTCGT 1140
QY 381 ArgAsnSerThraSenSerThraProLeuProArgCysTyTyGlnCysAlaAlaIleVal 400
DB 1141 CGTAAACAGAACAGCAACCTCTCTGCGCAGGTGTACAGTGAAGACCTGCTAAAGTG 1200
QY 401 IlePheIleIleIlePheSerTyValIleuSerLeuGlyProTyCysPheLeuAlaVal 420
DB 1201 ATCTTATATCATTTTCTCTATGTCTATGCTATCCCTGGGCCCTTACTGCTTTTAAAGATC 1260
QY 421 LeuAlaValIleValAspValGluThrGlnValProGlnTrpValIleThrIleIleIle 440
DB 1261 CTGGCGGTGTGGGTGATGTCCAAACCCAGTACCCCAATGGGTATCAACATATATC 1320
QY 441 TrpLeuPhePheLeuGlnCysCysIleHisProTyValIleTyGlyTyTyMetHisLyThr 460
DB 1321 TGGCTTTTCTTCTCTGACAGTGTGCATCCACCCCTATGTCTATGTGCTAATGACAAAGACC 1380
QY 461 IleLyLyGluIleGlnAspMetLeuLyLyPhePheCyAspGluLyAspProProLy 480
DB 1381 ATTAAAGAGAAATCCAGACATGTGAAGAGATTCTTCTGCAAGGAAAGCCCGGAAA 1440
QY 481 GluAspSerHisProAspLeuProGlyTyThrGluGlyIleTyGlyIleValIleValIle 500
DB 1441 GAAGATAGCCACCCCAACCTGCCGGAACAGAGGTGGAGCTGAAGGCAAGATTGCTCT 1500
QY 501 SerTyAspSerAlaThrPhePro 508
DB 1501 TCCTACGATTCGTCTACTTTTCTCT 1524
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RESULT 15

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US-10-436-715-13
; Sequence 13, Application US/10436715
; Publication No. US20040018976A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: AND SPLICER VARIANTS THEREOF
; FILE REFERENCE: D0262 NP
; CURRENT APPLICATION NUMBER: US/10/436, 715
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: U.S. 60/380,336
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1524)
US-10-436-715-13
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US-10-712-615-2 (1-508) x US-10-436-715-13 (1-1527)

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 Qy 61 GlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuValThrAspLeuGln 80
 Db 181 CAGGTGTGGAGGATCAACACGGTTTATCTTTAACTTCCTGTCAACCACTGTGTGCG 240
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 Db 241 ATTTCGCTCGTGGCCCCCTGGGGTGGGCACTCTGTCCCTCTCTTCTGGCCCCCTCAAC 300
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 Db 301 AGCCACTTCTGCACGGCCCTGGTTAGCCCTCACCCACTGTTCGCCCTTGCACGCTCAAC 360
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 Db 1501 TCTTACGATTCTGCTACTTTTCT 1524

Search completed: December 10, 2005, 09:27:58
 Job time : 817 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 10, 2005, 07:45:15 ; Search time 150 Seconds
(without alignments)
1266.121 Million cell updates/sec

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Scoring table: BLOSUM62
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Delop 6.0 , Delext 7.0

Searched: 3392430 segs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA_New.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	791	29.9	619	6	US-10-980-388-8
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4	216	8.2	1658	7	US-11-170-153-7
5	216	8.2	2260	7	US-11-090-439-15
6	210	7.9	1658	7	US-11-170-153-1
7	210	7.9	1658	7	US-11-170-153-3
8	204.5	7.7	1059	7	US-11-068-686-19

9	202.5	7.7	1410	6	US-10-992-577-1	Sequence 1, Appl1
10	198	7.5	1334	6	US-10-992-577-43	Sequence 43, Appl1
11	197.5	7.5	1260	7	US-11-067-884-7	Sequence 7, Appl1
12	196	7.4	1594	7	US-11-170-153-9	Sequence 9, Appl1
13	196	7.4	1594	7	US-11-170-153-11	Sequence 11, Appl1
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17	184.5	7.0	1284	6	US-10-502-893-1	Sequence 1, Appl1
18	184	7.0	1224	6	US-10-750-185-40492	Sequence 40492, A
19	181	6.8	1685	6	US-10-750-185-36071	Sequence 36071, A
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24	175	6.6	1834	6	US-10-627-633-1	Sequence 1, Appl1
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26	172	6.5	246960	7	US-11-121-086-8	Sequence 8, Appl1
27	171.5	6.5	1225	6	US-10-955-054A-112	Sequence 112, App
28	171.5	6.5	8747	6	US-10-955-054A-141	Sequence 141, App
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33	164.5	6.2	1058	6	US-10-627-633-5	Sequence 5, Appl1
34	164.5	6.2	1888	7	US-11-080-991-25	Sequence 25, Appl1
35	164	6.2	1965	6	US-10-980-388-57	Sequence 57, Appl1
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45	144	5.4	1776	6	US-10-851-667A-25	Sequence 25, Appl1

ALIGNMENTS

RESULT 1
US-10-980-388-52
; Sequence 52, Application US/10980388
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369


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; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-52

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Pred. No.: 3,886-270 Length: 1527
Score: 2641.00 Matches: 507
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.80% Mismatches: 0
Query Match: 99.89% Indels: 0
DB: 6 Gaps: 0

US-10-712-615-2 (1-508) x US-10-980-388-52 (1-1527)

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; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Rufe, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325, US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
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```

1  APPLICANT: VENEMA, JACOB
2  APPLICANT: BERGER, CLAUDIA
3  APPLICANT: LOKEN, CHRISTIANE
4  TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
5  FILE REFERENCE: 01975-0034
6  CURRENT APPLICATION NUMBER: US/11/170.153
7  CURRENT FILING DATE: 2005-06-30
8  PRIOR APPLICATION NUMBER: US/10/088.744
9  PRIOR FILING DATE: 2002-03-22
10 NUMBER OF SEQ ID NOS: 35
11 SOFTWARE: PatentIn Ver. 3.2
12 SEQ ID NO 7
13 LENGTH: 1658
14 TYPE: DNA
15 ORGANISM: Homo sapiens
16 FEATURE:
17 NAME/KEY: CDS
18 LOCATION: (64)..(1299)
19 OTHER INFORMATION: IGS4B short version
20 US-11-170-153-7

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Alignment Scores:

Pred. No.:	2,54E-12	Length:	1658
Score:	216.00	Matches:	99
Percent Similarity:	33.73%	Conservative:	73
Best Local Similarity:	1.41%	Mismatches:	133
Query Match:	8.17%	Indels:	206
DB:	7	Gaps:	16

US-10-712-615-2 (1-508) x US-11-170-153-7 (1-1658)

QY AmsrTThArglU-----SerAmsrSerHlathCymEc 19
Db 133 AAGAGACCGAGAGATGATGGCTTCCTCCGCGACCTCGGCGACCACTTCTTC 192
QY 20 ProLeuSerLywaeProLieserLeuAlahIsclYlelIearGsetThValLeuAl 39
Db 193 CCGGTG-----TGTGTGTGTATGTG 213
QY 40 IllePheLeuAlaIaserPheValGlYanIleValLeuAlaLeuValLeuGlNArgLyS 59
Db 214 CCAATTTTGTGTGGGGGTCAATGGCAATGCTCGGTGCTCGGTGATTTCTGCAGAC 277
QY 60 ProGlNleuLeuGlNValThraNarPheAlIePheAlLeuLeuValThraPLeuLeu 79
Db 274 CAGGTATGAAAGACGCCCACTACTACCTTCACCTGGGGGTCTGACTCTCG 333
QY 80 GlnIle-SerLeuValAlaProTyr-----ValValAlaThrSerValProLe 95
Db 334 GTCCTCTCTCTGAAATGCCCTGAGGTCTATGATGTGGCCCACTACCTTC-TT 392
QY 95 uPheTyrProLeuAmsrSerHlaPheCyuThAlaLeuValSerLeuThrHlaLeuPheAl 115
Db 393 GTTCGGGCGCGGGGTGTACTTCAAGACGGCCCTTTGAGACCGG-----TG 443
QY 115 aPheAlaIaserValaenThIleValLeuValIserValApharGlyrLeuSerIleleH 135
Db 444 CTTCGGCTCATCTTCAGCATACACACCGCTCAGCGGTGAGGGCTACGCGGCATCCACA 503
QY 135 sProLeuSerLyProSerLyMetThGlnArGArgIlyrLeuLeuTyrGlyTh 155
Db 504 CCGGTTCGGCGGCAACTGCACAGACCCGGGCGCGGCCCTCAGATCTCGGCATCGT 563
QY 155 rTPIleValAlaIleLeuGlNserThPro-----ProLeuTyrGly----- 169
Db 564 CTGGGGCTTCCTCGGTCTCTCTCCCTCCCAACACCGATCATGGCATCAAGTTCCA 623
QY 170 ----TrrpGlyGlnAlaIaIaPheArgGluArgAsnAlaLeuGysSerMetIetrpGlyAl 188
Db 624 CTACTTCCCAATGGGTCCCTGTGCCAGGTGGCCACTGTACGCTATC----- 675
QY 188 aserProSerTyrThr-----IleLeuSerValIaserPheIle-----ValIl 203

QY 290 SerThrGlyThrSerGluSerSerValGluAlaArgGlySerGlu--ValArgGlu 308
Db 1383 -----GCTCTGCCCACTCAGGTGATGAAACAACCTTATGCGAAGA 1421
QY 309 SerSerThrValAlaSerAspGlySerMetGluGlyValGluGlySerThrIysValGlu 328
Db 1422 ACATCCACACAAAT-----GGGAAAAAG----- 1442
QY 329 GluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnGlnCysSerIleAspLeu 348
Db 1442 ----- 1442
QY 349 GlyGluAspAspMetGluPheGlyGluAspAspIleAsnPheSerGluAspAspValGlu 368
Db 1443 -----TCAGTGCAG 1451
QY 369 AlaValAsnIleProGluSerLeuProProSerArgAsnSerAsnSerAsnProPro 388
Db 1452 ACCAATT-----TCCACGACACAG----- 1469
QY 389 LeuProArgCysArgGlnCysLysAlaAlaLysValIlePheIleIleIlePheSerTyr 408
Db 1470 -----AGAGCTCAAAAGCTCCTAGGATGTCGTTTCTCTTT 1508
QY 409 ValLeuSerLeuGlyProTyrCysPheLeuAlaValLeuAlaValIleTyrValAspValGlu 428
Db 1509 TTGCTTATGTGTGTCCTCTTATTACAAATATACTTAGTTTATGTATGATTCCTGT 1568
QY 429 ThrGlnValPro---GlnTyrValIleThrIleIleIleTyrLeuPhePheLeuGlnCys 447
Db 1569 AACCAAACTACTCTCCAAATGCTCCTCGAGATATTGTGTGATAGGCTATGTTCCTCA 1628
QY 448 CysIleIleProTyrValIleTyrValIleTyrValIleTyrValIleTyrValIle 462
Db 1629 GGAGGAAATCCTTGTGTCTACACCCCTCATTAAGACATTTCCG 1673

RESULT 6
US-11-170-153-1
; Sequence 1, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patencin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4A long version
US-11-170-153-1

Alignment Scores:
Pred. No.: 1,1e-11 Length: 1658
Score: 210.00 Matches: 98
Percent Similarity: 33.53% Conservative: 73
Best Local Similarity: 19.22% Mismatches: 134
Query Match: 7.94% Indels: 206
DB: 7 Gaps: 16

QY 7 AsnSerThrArgGlu-----SerAsnSerSerHisThrCysMet 19
Db 133 AACACACCCGAGAGATATCTGACCTTCTCTGCGACCTGCGCAGCACCATTTCTCTC 192
QY 20 ProLeuSerLysMetProIleSerLeuAlaHisGlyIleIleAspSerThrValLeuVal 39
Db 193 CCCGTG-----TCGTGTGTATGTG 213
QY 40 IlePheLeuAlaLaserPheValGlyAsnIleValLeuAlaLeuValLeuGlnArgLys 59
Db 214 CCAATTTTGTGTGTGCGGTGATTCGCAATGTCCTGCTGCTGCTGCTGATTCGACGAC 273
QY 60 ProGlnLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeu 79
Db 274 CAGGCTATGAGAGCCGACCACTACATACCTTACACCTGCGCGCTGCTGACCTCTCG 333
QY 80 GlnIle-SerLeuValAlaProTyr-----ValValAlaThrSerValProLe 95
Db 334 GTCCGTCTCTTGGAAATCCCTCGAGGCTATGAGATGTGCGCGCACTACCTTTTC-TT 392
QY 95 uPheTyrProLeuAsnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
Db 393 GTTCGGGCGCGTGGCTCTACTTCAAGACGCGCTCTTTAGACCGTG-----TG 443
QY 115 aPheAlaSerValAsnThrIleValLeuValSerValAspArgTyrLeuSerIleIleHis 135
Db 444 CTTCGCTCCATCTCCACATACACACCGTCAGCGTGGAGCGCTAGGCGCATCTGACA 503
QY 135 aProLeuSerTyrProSerLysMetThrGlnArgArgGlyTyrLeuLeuLeuTyrGlyTh 155
Db 504 CCCGTTCGCGCCGCAAACTGACAGACACCGCGCGCGCCCTCAGAGATCTTGCGATCGT 563
QY 155 rTyrIleValAlaIleLeuGlnSerThrPro-----ProLeuTyrGly----- 169
Db 564 CTGGGCGCTTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 623
QY 170 ---TyrGlyGlnAlaAlaPheAspGluArgAsnAlaLeuCysSerMetIleTyrGlyAl 188
Db 624 CTACTTCCCAATGAGTCCGTGCTCCAGGTTCCGACCTGTAGCGATC----- 675
QY 188 aSerProSerTyrThr-----IleLeuSerValIleSerPheIle-----ValI 203
Db 676 -AAGCCCAATGAGATCTCAATTCATCATCAGGTGACCTCTCTCTCTCTCTCTCTCT 734
QY 203 aProLeuLeuValMetIleAlaCysTyrSerValIlePheCysAlaAlaArgGlnHis 223
Db 735 CCCATGACTGTCACTACAGTCTCTTAC----- 762
QY 223 aAlaLeuLeuTyrAsnValLysArgHisSerLeuGlnValArgValLysAspCysValG 243
Db 763 -----TACCATGACCTCAGACATAAG----- 786
QY 243 uAsnGluAspGluGluGlyAlaGluLysGluGluPheGlnAspGluSerGluPheArg 263
Db 786 ----- 786
QY 263 gArgGlnHisGluGluGluValLysAlaLysGluGlyArgMetGluAlaLysAspGlySe 283
Db 787 -----AAGACAAATC 797
QY 283 rLeuLysAlaLysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySe 303
Db 798 TCTTAGGCGAGATGAAGGAAT----- 819
QY 303 rGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGlyLysGluG 323
Db 819 ----- 819
QY 323 ySerThrIysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnG 343
Db 819 ----- 819

QY 343 nCySerIleApleuGlyGluAspAspMetGluPheGlyGluAspAspIleAsnPhese 363
DB 819 ----- 819
QY 363 rGluAspAspValGluAlaValAsnIleProGluSerLeuProProSerArgArgAsnse 383
DB 820 -----GCNAATTTTCAAGAA-----CCCTGCAGAAATCAAGT 851
QY 383 rAsnSerAsnProProLeuProArgCysTyrgInCysLysAlaAlaIleValIlePhe11 403
DB 852 CAAC-----AAGATGCTGTTGT 869
QY 403 eIleIlePheSerTyrValleuSerleuGlyProTy-----CysPheleuAl 419
DB 870 CTGTGCTTAGTGTCTATCTGTGTGGCCCGCTGCACATGACCGACTCTTCTTTC 929
QY 419 aValleuAlaValTrrValAspValGluThrGlnValProGlnTrrValIleThrIle11 439
DB 930 CTTTGGAGAGAGTGAAGTGAATCCCTGCTGCTGTTCACCTGCTCATGTGTGTG 989
QY 439 eIleTrrPhePhePheleuGlnCysCysIleHisProTyrrValTyrgIlyrMetHisly 459
DB 990 AGGTGCTTCTTACTAGCTGACCTGACCTGACCACTTATATCTAATCTACTGTCTG 1049
QY 459 eThrIleLysLysGluIleGlnAspMetLeuLysLysPhePheCysLysGluLysProP 479
DB 1050 CCGCTTCCAGCAGCATTCAGATGTGATCTTCTTTC-----CACAAACAGTG 1100
QY 479 oLysGluAspSerHisProAspLeuPro 488
DB 1101 GCACCTCCACGATGACCCACAGTTGCCA 1128
RESULT 7
US-11-170-153-3
; Sequence 3, Application US/11170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4A short version
US-11-170-153-3
Alignment Scores:
Pred. No.: 1,1e-11 Length: 1658
Score: 210.00 Matches: 98
Percent Similarity: 33.53% Conservative: 73
Best Local Similarity: 19.22% Mismatches: 134
Query Match: 7.94% Indels: 206
DB: 7 Gaps: 16
US-10-712-615-2 (1-508) x US-11-170-153-3 (1-1658)
QY 7 AsnSerThrArgGlu-----SerAsnSerSerHisThrCysMet 19
DB 133 AACAGACCGAGAGATATCTGCGCTTCTCTGCGGACCTGCGGACGACCACTTCTTCTTC 192

QY 20 ProLeuSerLysMetProIleSerLeuAlaHisGlyIleIleArgSerThrValleuVal 39
DB 193 CCGGTG-----TCTGTGTGTATGTG 213
QY 40 IlePheLeuAlaAlaSerPheValGlyAsnIleValleuAlaLeuValleuGlnArgLys 59
DB 214 CCAATTTTGTGTGTGGGTGCTATGTCGATGCTGTGTGCTGTGATTTCTGCAGCAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAsnLeuLeuValThrAspLeuLeu 79
DB 274 CAGGCTATGAAGACGCCCACTACTACTCTTCAAGCTGAGCGGTCTGACCTTCCTG 333
QY 80 GlnIle-SerLeuValAlaProTrr-----ValValAlaThrSerValProle 95
DB 334 GTCCGTCTCTTGGATGCGCCCTGAGGCTATGAGATGTGGCGCACTACCTTTC-TT 392
QY 95 uPheTrrProLeuAsnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
DB 393 GTTCCGGCCCGGTGCGCTGCTACTTCAGACGCCCTTGTGAGACCGTG-----TG 443
QY 115 aPheAlaSerValAsnThrIleValleuValSerValAspArgTyrrLeuSerIleIle11 135
DB 444 CTTCGCTCATCTCTCAGCATCAACCGTCAGCGGTGAGCGCTACGTGAGCATCTTACA 503
QY 135 sProLeuSerTyrrProSerLysMetThrGlnArgArgGlyTyrrLeuLeuLeuTyrgIlyth 155
DB 504 CCGGTTCGGCGCAAACTGACAGACCGGGGCGGGCGGCTCAGGATCTGTGGCATCG 563
QY 155 rTrrIleValAlaIleLeuGlnSerThrPro-----ProLeuTyrrGly----- 169
DB 564 CTGGGCGCTTCTCCGCTCTCTCTCCCTGCGCAACACACGATCATGAGTCAAGTTCCA 623
QY 170 -----TrrGlyGlnAlaAlaPheAspGluArgAsnAlaLeuCysSerMetIleTrrGlyAl 188
DB 624 CTACTTCCCAATGGGTCCCTGCTCCAGCTTCGGCACCTGACCTGATC----- 675
QY 188 aSerProSerTyrrThr-----IleLeuSerValIleSerPheIle-----Val11 203
DB 676 -AAGCCCATGTGATTCATCAATTTTCAATTCAGAGTCACCTCTTCTTCTTACCTCCG 734
QY 203 eProLeuIleValMetIleAlaCysTyrrSerValValPheCysAlaAlaArgArgGlnHis 223
DB 735 CCCCATGATGTCATCATGAGTCCCTTAC----- 762
QY 223 sAlaLeuLeuTyrrAsnValLysArgHisSerLeuGlnValArgValLysAspCysValG1 243
DB 763 -----TACCTCATGGCACTTCACACTTAAG----- 786
QY 243 uAsnGluAspGluGluGlyAlaGluLysGluGluPheGlnAspGluSerGluPheAr 263
DB 786 ----- 786
QY 263 gArgGlnHisGluGluGluValLysAlaLysGluGlyArgMetGluAlaLysAspGlyse 283
DB 787 -----AAAGACAAATC 797
QY 283 rLeuLysAlaLysGluGlySerThrCylThrSerGluSerSerValGluAlaArgLysse 303
DB 798 TCTTGAGCAGATGAAGGAAT----- 819
QY 303 rGluGluValArgGluSerSerThrValAlaSerAspGlySerMetGluGlyLysGluG1 323
DB 819 ----- 819
QY 323 ySerThrLysValGluGluAsnSerMetLysAlaAspLysGlyArgThrGluValAsnG1 343
DB 819 ----- 819
QY 343 nCySerIleApleuGlyGluAspAspMetGluPheGlyGluAspAspIleAsnPhese 363
DB 819 ----- 819

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Qy 363 rgluapaspvAlgluAlaValAsnllleProgluSerleuProProSerArgArgAnse 383
Db 820 -----GCAAAATATTCMAAGA-----CCCTCGAGAAATACT 851
Qy 363 rAsnSerAnpProPoleuProArgCysTyrGlnCysylsAlaAlaIleValIlePhe11 403
Db 852 CAAC-----AGATCTGTTTGT 869
Qy 403 eillelPheSerTyValleuSerleuGlyProTyr-----CysPheleuAl 419
Db 870 CTGTGCTTACGTCTTGTCTATCTGTTGGCCCGCTTCACATTGACCGACTCTTCTGAC 929
Qy 419 aValleuAlaValTTPValAspValAlaGluThrGlnValProGlnTTPValIleThrIle11 439
Db 930 CTCTTGAGAGAGTGAATCCCTGCTGCTGTTCAACCTGTCATGATGCTGTC 989
Qy 439 eillelPheleuGlnCysCysIleHisProTyValTyGlyTyMetHisIle 459
Db 990 AGGTCTCTTCTTCTACCTGAGCTCAGCTGTCAACCCATTATCTATACCTTCTGTCG 1049
Qy 459 eThrIleTyGlyGluIleGlnAspMetleuTyblyspPheCysylsGlyLysProBr 479
Db 1050 CCGCTTCAGCAGCATTCACAAATGTATCTCTTCTTC-----CACAAACAGTC 1100
Qy 479 olYsgluAspSerHisProAspLeuPro 488
Db 1101 GCATCTCCAGCATGACCCACAGTTGCCA 1128

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RESULT 8

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US-11-068-686-19
; Sequence 19, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Report, Carol J.
; Schweickart, Vicky L.

```

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; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Marshall, O'Toole, Gerslein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>

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; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448

```

```

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1056
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

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US-11-068-686-19

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Alignment Scores:
Pred. No.: 2,086-11 Length: 1059
Score: 204.50 Matches: 61
Percent Similarity: 47.41% Mismatches: 49
Best Local Similarity: 26.28% Indels: 103
Query Match: 7.73% Gaps: 7
DB: 7

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US-10-712-615-2 (1-508) x US-11-068-686-19 (1-1059)

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Qy 16 HisThrCysMetProleuSerIleMetProleu---SerleuAlaHisGlyIleIleArg 34
Db 43 TATACATCGGAACCTTCCCAAAAATCATGTGAACAATCGCGCCGCTCTGCT 102
Qy 35 SerThrValleuValIlePheleuAlaIleSerPheValIleGlyAsnIleValleuAla 54
Db 103 CCGCTCTACTACTGCTGCTTATC---TTGGTTTGGGCGACATCTGCTGCTC 159
Qy 55 ValIleGlnArgLysProGlnIleuGlnValThrAsnArgPheIlePheAsnIleu 74
Db 160 ATCTGTAAATCTGCAAAAGCTGAAAGCATGACTGACATCTACTCTCACTGAGC 219
Qy 75 ValThrAspLeuGlnIleSerleuValAlaProTTPValAlaIleThrSerValPro 94
Db 220 ACTCTGACCTGCTTCTTCTTACTGCTCCCTTCTG-----GCTCATGCTGCT 273
Qy 95 LeuPheTrpProleuAsnSerHisPheCysThrAlaIleuValSerleuThrIleuPhe 114
Db 274 GCCCAGTGGACTTGGAAATACATGTGTCACTCTGACAGGCTCTATTTTATGAC 333
Qy 115 AlaPheAlaSerValAsnThrIleValleuValSerValAspArgTyIleuSerIle 134
Db 334 TTCTTCTGGAATCTTCTCATCATCTCTCGAACAATGATAGTACTGCTGCTATGTC 393
Qy 135 HisProleuSerTyProSerIleMetThrGlnArgGlyTyIleuLeuLeuTyGly 154
Db 394 CATGCTGCTTGTCTTAAAGCCAGACAGTCACTTGGGCTGTCACAAAGTGTATC 453
Qy 155 ThrTrpIleValAlaIleleuGlnSerThrProProleuTyGlyTTPGlyGlnAla 174
Db 454 ACTGGGTGGTGGCTGTGTGCTGCTCTCTCCAGAAATCATC---TTTACAGATCTCAG 510
Qy 175 PheAspGluArgAsnAlaIleuCysSer-----MetIleTrp 186
Db 511 AGAGAAGGCTTCATACACCTGACCTCATCTTTCATACAGTCAGATCATTTCTG 570
Qy 187 GlyAlaSerProSerTyThrIleleuSerValAlaSerPheIleValIleProleu 206
Db 571 -----AAGAAATTTTCAGACATTAAGAATGTCATCTGGGCTGCTGCTGCT 624
Qy 207 ValMetIleAlaCysTySerValValPheCysAlaAlaIleArgGlnHisAlaIleu 226
Db 625 GTCATGTGATCTGCTACTCTGGGAATCTGAAATCTGCTGCTGCTGCT 672
Qy 227 TyrAsnValLysArgHisSerleuGlnValArgVal 238
Db 673 CGAAACGAGAGAAAGACAGCGCTGTGAGGCTT 708

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RESULT 9

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US-10-992-577-1
; Sequence 1, Application US/10992577
; Publication No. US20050260687A1

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; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.

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; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
; TITLE OF INVENTION: And Uses Thereof
; FILE REFERENCE: 57155-D/UPW
; CURRENT APPLICATION NUMBER: US/10/992,577

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```

; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(942)
; OTHER INFORMATION: IGS4A truncated DNA long version
US-11-170-153-9

Alignment Scores:
Pred. No.: 3,196-10 Length: 1594
Score: 196.00 Matches: 68
Percent Similarity: 47.74% Conservative: 48
Best Local Similarity: 27.98% Mismatches: 84
Query Match: 7.41% Indels: 44
DB: Gaps: 9

US-10-712-615-2 (1-508) x US-11-170-153-9 (1-1594)

QY 7 AenSerThrArgGlu-----SerAnSerSerHisThrCysMet 19
Db 133 AACACACCGAGCATATCTGCGCTTCTGCGGACCTGCGGACGACCTTCTTCC 192
QY 20 ProLeuSerLyMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuVal 39
Db 193 CCCGCG-----TCTGTGTATATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAnIleValIleuAlaLeuValLeuGlnArgLyS 59
Db 214 CCAATTTTGTGTGGGGGTATGTCGCAATGTCCTGTGTGCTGTGATTTCTGCAGCAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAnIleuValThrAspLeuVal 79
Db 274 CAGGCTATGAGACGCCCACTAATCTTCAAGCGCTGCGGTCTGACCTCCG 333
QY 80 GlnIle-SerLeuValAlaProTyr-----ValValAlaThrSerValProLe 95
Db 334 GTCGCTCTCTTGGAAATGCCCTTGAGGTCTATGAGATGTGGCGCAATCACTTTC-TT 392
QY 95 uPheThrProLeuAnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
Db 393 GTTCGGGCCCGGGCTGCTACTTCAAGACGCGCTTTGAGACCGTG-----TG 443
QY 115 aPheAlaSerValaenThrIleValLeuValSerValaIlePArgTyrLeuSerIleIleH 135
Db 444 CTTCCCTTCATCTCCAGCATCACCAACGTCAGCGTGGAGCGCTAGCGCATCTTACA 503
QY 135 aProLeuSerLyTrProSerLyMetThrGlnArgArgGlyYrLeuLeuLeuTyGlyTh 155
Db 504 CCCGTTCCCGCGCAACTGACAGACGCCGCGCGCGCCCTCAGGATCTCGGCATCGT 563
QY 155 rTrpIleValAlaIleLeuGlnSerThrPro-----ProLeuTyGlyY 169
Db 564 CTGGGGCTTCTCCGTCCTTCTCCCTGCCCAACACACATCAGATCAGATCAAGTTCA 623
QY 170 ----TrpGlyGlnAlaIlePheArgPLeuArgAnIleuValCysSerMetIleTrpGlyAl 188
Db 624 CTACTTCGCCCAATGGGTCTGCTGCCAGAGTTCCGCGCACCTGTACCGTATC----- 675
QY 188 aSerProSerLyTrThr-----IleLeuSerValIleSerPheIle-----ValI 203
Db 676 -AAGCCCATGTGATTTACAAATTTCAATCCAGGTCACCTCTTCTATTTCACTCTCT 734
QY 203 eProLeuIleValMetIleAlaIleCysTrpSerValIlePheCysAlaIleArgArgGlnH 223
Db 735 CCCCATGATGTGATCATAGTGTCTCTACTACTCATGAGGACATCAGACTAAAGAAAGACA 794
QY 223 aAlaLeu 225
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Db 795 ATCTCTT 801
RESULT 13
US-11-170-153-11
; Sequence 11, Application US/11170153
; Publication NO. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSMIDDER, WILLY
; APPLICANT: WEBSER, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(942)
; OTHER INFORMATION: IGS4A truncated DNA short version
US-11-170-153-11

Alignment Scores:
Pred. No.: 3,196-10 Length: 1594
Score: 196.00 Matches: 68
Percent Similarity: 47.74% Conservative: 48
Best Local Similarity: 27.98% Mismatches: 84
Query Match: 7.41% Indels: 44
DB: Gaps: 9

US-10-712-615-2 (1-508) x US-11-170-153-11 (1-1594)

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QY 20 ProLeuSerLyMetProIleSerLeuAlaHisGlyIleIleArgSerThrValLeuVal 39
Db 193 CCCGCG-----TCTGTGTATATGTG 213
QY 40 IlePheLeuAlaIleSerPheValGlyAnIleValIleuAlaLeuValLeuGlnArgLyS 59
Db 214 CCAATTTTGTGTGGGGGTATGTCGCAATGTCCTGTGTGCTGTGATTTCTGCAGCAC 273
QY 60 ProGlnLeuLeuGlnValThrAsnArgPheIlePheAnIleuValThrAspLeuVal 79
Db 274 CAGGCTATGAGACGCCCACTAATCTTCAAGCGCTGCGGTCTGACCTCCG 333
QY 80 GlnIle-SerLeuValAlaProTyr-----ValValAlaThrSerValProLe 95
Db 334 GTCGCTCTCTTGGAAATGCCCTTGAGGTCTATGAGATGTGGCGCAATCACTTTC-TT 392
QY 95 uPheThrProLeuAnSerHisPheCysThrAlaLeuValSerLeuThrHisLeuPheAl 115
Db 393 GTTCGGGCCCGGGCTGCTACTTCAAGACGCGCTTTGAGACCGTG-----TG 443
QY 115 aPheAlaSerValaenThrIleValLeuValSerValaIlePArgTyrLeuSerIleIleH 135
Db 444 CTTCCCTTCATCTCCAGCATCACCAACGTCAGCGTGGAGCGCTAGCGCATCTTACA 503
QY 135 aProLeuSerLyTrProSerLyMetThrGlnArgArgGlyYrLeuLeuLeuTyGlyTh 155
Db 504 CCCGTTCCCGCGCAACTGACAGACGCCGCGCGCGCCCTCAGGATCTCGGCATCGT 563
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Qy		155 rTPpIleValAlaIleLeuGlnSerThrPro-----ProLeuTyrglyl-----	169
Dd		564 CTGGGGCTTCTCCGTCTCTTCCTCCTGCCAACACCGCATTCAGGCATCAAGTTCCA	633
Qy		170 ----TPpIGylGlnAlaAlaPheAspGluArgAsnAlaLeuCysSerMetIleTPpIGyl	188
Dd		624 CTACTTCGCCAATGAGTGCTCCGTGGTCCAGAGTTCGGCACCTGTAAAGGTCATC	675
Qy		188 aserProSerTYrThr-----IleLeuSerValValSerPheIle-----ValII	203
Dd		676 -AAGCCCATGTGGATTCATCAATTTCATCATTCAGGTCACTTCCTTCATTTACTCTCT	734
Qy		203 eProLeuIleValMetIleAlaAcetyTHrservalValPheCysAlaIlaArgGlnH	223
Dd		735 CCCATGACTGTCATCATGTCTCTTACTTACTTCAGCATCGACTCAAGTAAGAAGACA	794
Qy		223 saLaLeu 225	
Dd		795 ATCTCTT 801	
 RESULT 14 US-11-068-686-1 ; Sequence 1, Application US/11068686 ; Publication No. US2005026056SAL GENERAL INFORMATION: APPLICANT: Gray, Patrick W. Schweickart, Vicky L. Raport, Carol J. TITLE OF INVENTION: Chemokine Receptor Materials and Methods NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive City: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/11/068,686 APPLICATION NUMBER: US/11/068,686 FILING DATE: 28-Feb-2005 CLASSIFICATION: <Unknown> ATTORNEY/AGENT INFORMATION: NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 27866/33670 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300 TELEFAX: 312-474-0448 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3383 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA FEATURE: NAME/KEY: CDS LOCATION: 55..1110 FEATURE: NAME/KEY: misc feature OTHER INFORMATION: /= "86C polynucleotide and amino acid sequences" SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-11-068-686-1			
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[illegible]

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; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35938
; LENGTH: 1977
; TYPE: DNA
; ORGANISM: Bovine 1986688640615
US-10-750-185-35938
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Query Match: 7.20% Indels: 9
DB: Gaps: 4
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US-10-712-615-2 (1-508) x US-10-750-185-35938 (1-1977)

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QY 53 AlaLeuValIleuGlnArgLysProGlnLeuLeuGlnValThrAsnArgPheIlePheAsn 72
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QY 133 IleIleHisProLeuSerTyrProSerIleMetThrGlnArgArgGlyTyrLeuLeuLeu 152
Db 1679 GTTACTGACCCCTGTGCTATCCACCAAGTTCACGGTGTCTGTGTCAGAGTAGTCATC 1738
QY 153 TyrGlyThrTyrIleValAlaIleLeuGlnSerThrProProLeuTyr---GlyTyrGly 171
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QY 172 GlnAlaAlaPheAspGlnArgAsnAlaLeuCysSerMetIleTyrGlyAla----- 188
Db 1799 GACGATGGAGTGAAGAAATTAGTAAGTCTCTCAACTGTGTAGCGCGTGTCAAAATGTT 1858
QY 189 ---SerProSerTyrThrIleLeuSerValIleSerPheIleValIleProLeuIleVal 207
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Db 1916 ATGGTAATCTTTATGTGAAGATTTTATTGTAGCTAAACAACAA 1960
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Search completed: December 10, 2005, 09:30:21
Job time : 172 sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 04:47:54 ; Search time 3866 Seconds
(without alignments)
6147.915 Million cell updates/sec

Title: US-10-712-615-2

Perfect score: 2644
Sequence: 1 MTSTCTNSTRESNSHTCMP.....GTEGTEKIVPSYDSTAFP 508

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10712615 @CGN 1.1 4015 @runat_02122005_103722_24072 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTER -NEG_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOC
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: gb_hic:*
5: gb_est4:*
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9: gb_gse1:*
10: gb_gse2:*
11: gb_gse3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	544	20.6	646	11	CNS049JM AL280651 Tetradon
4	492	18.6	1064	11	CNS03YI1 AL282450 Tetradon
5	467	17.7	772	8	DR860076 JGI_CABG4
6	435	16.5	641	8	CX254611 CX254611 1307373 N
7	391	14.8	1587	10	AY421262 Mus muscu

8	391	14.8	1590	10	AY421260	AY421260 Homo sapi
9	391	14.8	1590	10	AY421261	AY421261 Pan trogl
10	366	13.8	620	5	BY724046	BY724046 BY724046
11	341	12.9	1401	10	AY399428	AY399428 Mus muscu
12	341	12.9	4124	4	AK085653	AK085653 Mus muscu
13	341	12.9	4135	4	AK079597	AK079597 Mus muscu
14	340.5	12.9	1269	10	AY402237	AY402237 Homo sapi
15	338.5	12.8	1401	10	AY399426	AY399426 Homo sapi
16	331.5	12.5	1269	10	AY402239	AY402239 Mus muscu
17	331.5	12.5	3113	4	AK043668	AK043668 Mus muscu
18	331.5	12.5	3888	4	AK049814	AK049814 Mus muscu
19	331.5	12.5	4356	4	AK049884	AK049884 Mus muscu
20	330.5	12.5	3533	4	AK034017	AK034017 Mus muscu
21	328	12.4	821	8	CX956538	CX956538 JGI_CAO8
22	322	12.2	832	8	CX491699	CX491699 JGI_XZG38
23	319.5	12.1	1213	10	AY402238	AY402238 Pan trogl
24	318	12.0	798	8	CX914631	CX914631 JGI_CAAN4
25	312	11.8	818	8	CX915108	CX915108 JGI_CAAN4
26	311	11.8	797	8	CX419536	CX419536 JGI_XZG14
27	311	11.8	801	8	CX907462	CX907462 JGI_CAN3
28	311	11.8	865	8	CX400009	CX400009 JGI_XZT41
29	308	11.6	802	8	CX843215	CX843215 JGI_CAAK1
30	306	11.6	816	8	CX815278	CX815278 JGI_CAAK1
31	294	11.1	1440	10	AY404934	AY404934 Homo sapi
32	290.5	11.0	722	6	CF147810	CF147810 AGENCOURT
33	290.5	11.0	1397	10	AY399427	AY399427 Pan trogl
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35	287	10.9	1401	11	DO029898	DO029898 Homo sapi
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ALIGNMENTS

RESULT 1
LOCUS BB179791 655 bp mRNA linear EST 19-OCT-2001
DEFINITION BB179791 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230080N06 3', mRNA sequence.

ACCESSION BB179791.2 GI:16269966
VERSION BB179791.2
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komoto,H., Konda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Takeda,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

TITLE

JOURNAL

COMMENT

On Jun 29, 2000 this sequence version replaced gi:8838874.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenro-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216


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Qy 227 TTAAsnValLysArgHisSerLeuGluValArgValLysAspCysValGluasnGluAsp 246
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REFERENCE
1 (bases 1 to 772)
AUTHORS
Richardson,P., Lucas,S., Rokhsar,D., Dettler,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
TITLE
DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL
Unpublished (2004)
COMMENT
Other ESTs: JGI CABG4788.rev
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 226 5600
Fax: 925 226 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
cDNA Library Preparation: Bruce Blumberg Laboratory, University of
California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LINL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
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Stratascript reverse transcriptase. After ligation of
EcoRI adaptors (5'-AATTCGCGACGAGG-3') followed by kinasing
adapters and by XhoI digestion, the cDNA was size selected
by chromatography on Sepharose CL-2B columns and fractions
containing cDNAs larger than 1000 bp were ligated into
EcoRI/XhoI-digested pCS107. Reference for library
construction: Current Genomics 4, 635-644. Library
constructed by Michelle Tabb and Bruce Blumberg (Dept of
Developmental and Cell Biology, University of California,
Irvine)."
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 ACCESSION CX254611
 VERSION CX254611.1 GI:60371143
 KEYWORDS EST.
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 Proacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 641)
 REXROAD,C.E., Goupil,A.-S., Guilguen,Y. and Yao,J.
 02RT IUS, NCCCWA/MVU EST Project, Phase II, in collaboration with
 INRA
 JOURNAL Unpublished (2004)
 COMMENT Contact: REXROAD CE
 USDA, ARS, National Center for Cool and Cold Water Aquaculture
 11876 Leetown Road, Kearneysville, WV 25430, USA
 Tel: 304 724 8340 x2129
 Fax: 304 725 0351
 Email: crexroad@ncccw.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
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 Placer: 115 ROW: J COLUMN: 8
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 A.-S. Goupil and Y. Guilguen who subcloned the NCCCWA 1RT
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 ORIGIN
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 Pred. No.: 4.79e-35 Length: 641
 Score: 435.00 Matches: 90
 Percent Similarity: 59.41% Conservative: 30
 Best Local Similarity: 44.55% Mismatches: 40
 Query Match: 16.45% Indels: 42
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US-10-712-615-2 (1-508) x CX254611 (1-641)
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 DB 35 ACCCGTAGACGTGGGTGGAGAACTGGGAGACCTGTGGAGACTACAGGCACATGCTGT 94
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 QY 26 ----- 26
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 QY 27 SerLeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleSerPhe 46
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 QY 47 ValGlyAenIleValIleuAlaLeuValLeuGlnArgLysProGlnLeuGlnValThr 66
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 QY 67 AenArgPheIlePheAenLeuValThrApleuLeuGlnIleSerLeuValAlaPro 86
 DB 335 AACCGCTTGTGTCTCAACCTCTCTGTGACAGCTGTCCAGACCGTGTGTGTATGACC 394
 QY 87 TrpValValAlaIleThrSerValProleuPheTyrProleuAenSerHisPheCysThrAla 106
 DB 395 TTCGCCATCGCTGCACATGATGCCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 454
 QY 107 LeuValSerLeuThrHisLeuPheAlaPheAlaSerValAenThrIleValLeuValSer 126
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 DB 635 CTCTAC 640
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 LOCUS AY421262
 DEFINITION Mus musculus HCM7498 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY421262
 VERSION AY421262.1 GI:39777219
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 1587)
 CLARK,A.G., GLANOWSKI,S., NIELSON,R., THOMAS,P., KEJARIWAL,A.,
 TODD,M.A., TENENBAUM,D.M., CIVELLO,D.R., LU,F., MURPHY,B.,
 FERRIERA,S., WANG,G., ZHENG,X.H., WHITE,T.J., SNIISKY,J.J.,
 ADAMS,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)
 JOURNAL
 PUBMED 14671302
 2 (bases 1 to 1587)
 REFERENCE
 CLARK,A.G., GLANOWSKI,S., NIELSON,R., THOMAS,P., KEJARIWAL,A.,
 TODD,M.A., TENENBAUM,D.M., CIVELLO,D.R., LU,F., MURPHY,B.,
 FERRIERA,S., WANG,G., ZHENG,X.H., WHITE,T.J., SNIISKY,J.J.,
 FERRIERA,S., WANG,G., ZHENG,X.H., WHITE,T.J., SNIISKY,J.J.,

Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Srinisky, J.J.,
Adams, M.D. and Cargill, M.

TITLE
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers

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/mol_type="genomic DNA"
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ORIGIN

Alignment Scores:

Pred. No.: 1,38e-24 Length: 1401
Score: 341.00 Matches: 115
Percent Similarity: 37.48% Conservative: 75
Best Local Similarity: 22.68% Mismatches: 183
Query Match: 12,90% Indels: 134
DB: 10 Gaps: 13

US-10-712-615-2 (1-508) x AY399428 (1-1401)

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19 AATGCTTTCGAAGGCTCCAACTGACACCAC-----CCGCCAGCAGGGAACATT 69
27 SerLeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaIleSerPhe 46
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47 ValGlyAsnIleValLeuAlaLeuValIleGlnArgLysProGlnLeuGlnValThr 66
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67 AsnArgPheIlePheAsnLeuLeuValThrAspLeuLeuGlnIleSerLeuValAlaPro 86
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364 ATCGACCGGATACCTGTGTGAGTACCGGCTGGCTACCCCACTTGTACCCGAGAG 423
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424 AGGGGGGTGAGGGCTCTGCTGCTGCGCTGGGCGCTTCTCTGCTCATCTCCAGCACC 483
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427 ValGluThrGluValProGlnTrpValIleThrIleIleIleThrPhePheLeuGln 446
895 CCGAATTTTAAACCCAGGAAACAGTTTCAAAATATGATTTTGGCTTGGGATCTTAAT 954
447 CysValIleHisProTyValTyArgIleTyMetHisLysThrIleLysLysGluIleGln 466
955 AGTTCGATCAACCTATCATATACCATGCTCCAGCAGAGGATCAAGAAACCTTTGAG 1014
467 AspMetLeuLysLysPhePheCysLysGluLysProProLysGluAspSer----- 483
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501 SerTyAspSerAlaThrPhe 507
1135 GTGGGCTCAGAGACATTTTC 1155

RESULT 12
AK085653 4124 bp mRNA linear HTC 03-APR-2004
LOCUS AK085653
DEFINITION Mus musculus o day neonate kidney cDNA, RIKEN full-length enriched
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ALPHA 1A-ADRENOCPTOR, full insert sequence.
ACCESSION AK085653.1 GI:26351716
VERSION AK085653.1
KEYWORDS HTC, CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1

AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Mech. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
PUBMED	5
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
PUBMED	6 (bases 1 to 4124)
REFERENCE	Adechi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeuchi, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, FAX: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ location/Qualifiers
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Score:	341.00 Matches: 115
Percent Similarity:	37.48% Conservative: 75
Best Local Similarity:	22.68% Mismatches: 183
Query Match:	12.90% Indels: 134
DB:	4 Gaps: 13
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QY	27 SerLeuAlaHisGlyIleIleIleArgSerThrValLeuValIleIleLeuAlaIleSerPhe 46
DB	1022 TCTAAGGCC-----ATCTCACTTGGGGTGATCTTGGGGGCGCTCATCTTTCCGGGCTC 1075
QY	47 ValGlyAlaIleValLeuAlaLeuValLeuIleArgIleProGlnLeuLeuGlnValThr 66
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DB	1136 CACTACTACATTGTCAACCTGCTGCTGCAACCTCTCTCCACCTCCACCGCTGCTGCC 1195
QY	87 TrpValValAlaIleHisSerValProLeuPheTrpProLeuAsnSerHisPheCysThrAla 106
DB	1196 TTCTGTGCATCTTGAATCCTGGGCTAATGGGCTTTGGCAGGGTGTCTTGCMAACATC 1255
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QY	127 ValAspArgTyTrLeuSerIleIleHisProLeuSerTyTrProSerTyMetThrGlnArg 146
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QY	147 ArgGlyTyTrLeuLeuLeuTyTrGlyThrTrpIleValAlaIleLeuGlnSerThrProPro 166
DB	1376 AGGGCGCGCAGGGCTCTGCTGCGCTCGGGCGCTTCTTGTCATCTCCATCGACGCC 1435
QY	167 LeuTyTrGlyTyTrpGlyGlnAlaIlePheAspGluIleArgAlaIleValCysSerMetIleTrp 186
DB	1436 CTGTTCCGCTGAGGACACAGAGCT---CCGAGAGTGAAGACCATCTGCAATATC----- 1486
QY	187 GlyAlaSerProSerTyThrIleLeuSerValValSerPheIleValIleProLeuIle 206
DB	1487 AATGAGAGCCAGCATACGCTGCTGTTCTCAGCGCTGAGGCTCTTTCTACGTGCACATGACC 1546

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Oy	227	TyrAnValLysArgHisSerLeuGluValArgValLysAspCysValGluAsnGluAsp	246
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Oy	467	AspMetLeuLysLysPhePheCysLysGluLysProProLysGluAspSer-----	483
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Oy	484	-----HisProAspLeuProGlyTyrGlnGlyGlyThrGlnGlyLysIle---ValPro	500
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Oy	501	SerTyrAspSerAlaThrPhe507	
Db	2087	GTGGGCTCAGAGAGACTTTC2107	
RESULT 13			
LOCUS	AK079597	4135 bp	mRNA
DEFINITION	Mus musculus adult male spinal cord cDNA, RIKEN full-length		
FEATURES	enriched library, clone:A330054N1 product:adrenergic receptor, alpha 1a, ALPHA 1A-ADRENOCEPTOR, full insert sequence.		
ACCESSION	AK079597.1	GI:26348091	
KEYWORDS	HTC; CAP trapper.		

SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE TITLE	1 Carninci, P. and Hayashizaki, Y.
REFERENCE JOURNAL	High-efficiency full-length cDNA cloning
REFERENCE PUBLISHED	2 Meth. Enzymol. 303, 19-44 (1999)
REFERENCE AUTHORS	3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
REFERENCE TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
REFERENCE JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE PUBLISHED	11042159
REFERENCE AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, E., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Maruyama, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
REFERENCE TITLE	4 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
REFERENCE JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
REFERENCE PUBLISHED	11076861
REFERENCE AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
REFERENCE TITLE	Functional annotation of a full-length mouse cDNA collection
REFERENCE JOURNAL	Nature 409, 685-690 (2001)
REFERENCE PUBLISHED	5
REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
REFERENCE TITLE	Analysis of the mouse transcriptome based on functional annotation
REFERENCE JOURNAL	of 60,770 full-length cDNAs
REFERENCE PUBLISHED	Nature 420, 563-573 (2002)
REFERENCE AUTHORS	6 (bases 1 to 4135)
REFERENCE TITLE	Aadachi, J., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagatsu, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imcanti, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kuwahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sugahara, Y., Tagami, N., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
REFERENCE TITLE	Direct Submission
REFERENCE JOURNAL	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
REFERENCE COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
REFERENCE FEATURES	Please visit our web site for further details.
REFERENCE SOURCE	URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ location/Qualifiers
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REFERENCE	/mol_type="mRNA"

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ORIGIN

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Best Local Similarity:	22.68%
Query Match:	12.90%
DB:	4
Gaps:	13
Length:	4135
Matches:	115
Conservative:	75
Mismatches:	183
Indels:	134
Gaps:	13

US-10-712-615-2 (1-508) x AK079597 (1-4135)

QY	7	hensrthrrarvgjusefshanserserthshrcyamecProleuSerlysmecProile	26
Db	952	AAATGCTTTTGAAAGGCTCCAACTGACCCAC-----CCGACCAACAGGTAAACTT	1002
QY	27	SerleuAIAhIsglylleleAArgSerThrValleuValIIlePheLeuAlAIASePhe	46
Db	1003	TCTAAGGCC-----ATTCTACTGGGGGTGATCTGGGGGGGGCCATATTTTGGGGGTC	1056
QY	47	ValGlyAenIIleValleuAlaleuValleuGlnArglyshProGlnLeuGlnValThr	66
Db	1057	TTGGGGAATATTATTAGTATCTCTCGGTGGCCCTGTCACTGGCATCTGCATCTGGTACT	1116
QY	67	AenArgPheIIlePheAenLeuValThrAspLeuGlnIIleSerLeuValAlAPro	86
Db	1117	CACACTACTCATTTGTCAACCTGGCTGTGGCAGACCTCTCCACTCCACCGTCTGCC	1176
QY	87	TrpValValAlaIthSerValProleuPheTrpProleuAenSerHisPheCysThrAla	106
Db	1177	TTCTCTGCCATCTTGTAGACTCTGGGCTACATCGGGCTTTGGCAGGCTGTTTGGCAATC	1236
QY	107	LeuValSerleuThrHisleuPheAlaPheAlaSerValAenThrIIleValleuValSer	126
Db	1237	TGGGGGGGGGTGAGCTCTTATGCTGCACACGGCTCCATCATAGGGCTCTGCATATCTCC	1296
QY	127	ValAspArglyrLeuSerIIleHisProleuSerlyrProserLysmecThrGlnArg	146
Db	1297	ATCGACCCATTCATTGTAGGTAGACGACACCGCTGGCTACCCACCATTTGTACCCAGAGG	1356
QY	147	ArgGlyTryleuLeuLeuTrglyThrTrpIIleValAlaIIleGlnSerThrProPro	166
Db	1357	AGGGGCGGTACGGGCTGTCTGTGGCTGTGGGCGCTTCTCTTGTCATCTCATGGAGCC	1416
QY	167	LeuTrglyTrpGlyGlnAlaAlaIaPheAspGlnArgAlaAlaLeuCysSerMetIleTrp	186
Db	1417	CTGTTTGGCTGTGAGGCACAGGCT---CCGAGAGATGACCATCTGCCAATC-----	1467

OY		187	GlyAlaSerProSerTyrThrIleLeuSerValValSerPheIleValIleProLeuIle	206
Db		1468	AATGAGACCGAAGATACGGCTGTTCCTGCACGCGCGGCGCTTTCTACGGCCACTGCACC	1522
OY		207	ValMetCileAlaCysTyrSerValValPheCysValAlaIAsArgGlnIleAlaLeuLeu	226
Db		1528	ATCATCTCGTGTAATGTAAGTCTGCAGCTTAACGGTCAAGGCCAAAGA-----	1577
OY		227	TyrAsnValValArgHisSerLeuGluValArgValValAspCysValGluAsnGluAsp	246
Db		1573	-----GMAAGCCGAGGC	1588
OY		247	GluGluGluValAlaGluLysLeuGluGluPheGluAsnArgGluSerGluPheArgArgGlnHis	266
Db		1585	CTCAAGTCCGGCCTCAAGACCGACAAGTCAGACTCAGACGAAGTAGACGCTCGTATCCAC	1644
OY		267	GluGluGluValValValAlaLysGluGluValArgMetGluValValAspGlySerLeuValAla	286
Db		1645	CCTAAAAATGTCCTGCA-----	1667
OY		287	LysGluGlySerThrGlyThrSerGluSerSerValGluAlaArgGlySerGluGluVal	306
Db		1663	---GAAGGCAGC--CGAGTAAGCAGTCC-----	1688
OY		307	ArgGluSerSerThrValAlaSerAspGlySerMetGluGlyLysGluGlySerThrLys	326
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OY		347	AspLeuGluGluAspAspMetGluPheGlyGluAspIleAsnPheSerGluAspAsp	366
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OY		387	ProProLeuProAspGlyTyrglncysValValAlaLysValIlePheIleIleIlePhe	406
Db		1738	-----AAAGCCGCAAGACGCTGCGCACTGTGGTGGGA	1770
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OY		427	ValGluThrGlnValProGlnTTrpValIleThrIleIleIleTrrLeuPhePheLeuGln	446
Db		1828	CCGAATTTCAGAACCCCGAAAAGATTTTCAAATAATAGATTGTGGCTGGGNACTTAAT	1887
OY		447	CysCysIleIleAspProTyrValTyrGlyLysMetHisLysThrIleLysLysGluIleGln	466
Db		1888	AGTTGCATCAACCCCTATCATATACCCATGCTCCAGCCGAGATTCMAAANAAGCCTTTCAG	1947
OY		467	AspMetLeuLysLysPhePheCysLysGluLysProPolySGLuAspSer-----	483
Db		1948	AATGCTGCGCAATCACTAGTCTTCGCGAAGAGCGATTTCCAGACATGCCCTGGGCTAAC	2007
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OY		501	SerTyrAspSerAlaThrPhe	507
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RESULT 14
AY402237 1269 bp DNA linear GSS 15-DEC-2007

LOCUS Homo sapiens HTR1A gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 1401)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene cios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1401)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tenenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Score: 338.50 Matches: 108
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Query Match: 12.80% Indels: 131
DB: Gaps: 11
US-10-712-615-2 (1-508) x AY399426 (1-1401)
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QY 28 LeuAlaHisGlyIleIleArgSerThrValLeuValIlePheLeuAlaAlaSerPheVal 47
DB 67 ATTTCAGAGGCATCTGCTCGGGGTGATCTTGGGGGGCCCTCATCTTTCCGGGTGCTG 126
QY 48 GlyAlaIleValLeuAlaLeuValLeuGlnArgIlePheProGlnLeuGlnValThrAsn 67
DB 127 GGTACATCTCTAGTATCTCTCCGTAAGCTGTCAACGACCTGCATCTGACGAC 186
QY 68 ArgPheIlePheAsnLeuLeuValThrAsnLeuGlnIleSerLeuValAlaProThr 87
DB 187 TACTACATCTGTAACCTGGCGGTGGCCGACCTCTGCTACTCACTCAACGCTGCTGCCTTC 246
QY 88 ValValAlaIleHisSerValProLeuPheThrProLeuAsnSerHisPheCysThrAlaLeu 107
DB 247 TCCGCATCTTGGAGGTCTCTAGAGTAAGTGGGCTTCGGAGAGGTCTTTCGAACATCTGG 306
QY 108 ValSerLeuThrHisLeuPheAlaPheAlaSerValAlaMetThrIleValLeuValSerVal 127
DB 307 GCGGAGATGGATGTCTGTCTGTCACCGGCTCATCATGAGGCTCTGCATCTTCATC 366
QY 128 AspArgGlyTyrLeuSerIleIleHisProLeuSerTyrProSerIleMetThrGlnArg 147
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QY 148 GlyTyrLeuLeuLeuTyrGlyThrTriPleValAlaIleLeuGlnSerThrProProLeu 167
DB 427 GGTCTCATGTGGCTCTGCTCTGGCTGTGGACATCTCCCTGGTCATATCATTTGACCCCTTG 486
QY 168 TyrGlyTyrPylGlnAlaAlaPheAspGluArgAsnAlaLeuCysSerMetIleTyrGly 187
DB 487 TTGGCTGTGGAGGACCGCGCC-----CCGAGACAGACACCACTCTCCAGATC-----AAC 537
QY 188 AlaSerProSerTyrThrIleLeuSerValValaSerPheIleValIleProLeuIleVal 207
DB 538 GAGAGCGCGGCTCAGTCTGCTCTCTCAAGCCGTGGCTCTTCTCACTGCTCTGCGCATC 597
QY 208 MetIleAlaCysTyrSerValValPheCysAlaAlaArgArgGlnHisAlaLeuLeuTyr 227
DB 598 ATCTGTGATGATCTGCTGCGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 639
QY 228 AsnValIysArgHisSerLeuGlnValArgValIysAspCysValGluAsnGluAspIle 247
DB 640 -----GAGAGCCGGGGCTC 654
QY 248 GluGlyAlaGlyIleValGlyGluGluPheGlnAspGluSerGluPheArgArgGlnHisGlu 267
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QY 288 GluGlySerThrGlyThrSerGluSerSerValGluAlaArgIleGlySerGluGluValArg 307
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QY 308 GluSerSerThrValAlaSerAspGlySerMetGluGlyGlyGluGlySerThrIleVal 327
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QY 468 MetLeuIys---LysPhePheCysIleGlnIleValIleProProIleValIle-----Asp 482
DB 1018 GTCTTGAAATCCAGATGCTCTGCAAGAAAGAGCTTCCAAACATGCCCTGGGCTACACC 1077
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QY 502 TyrAspSerAlaIlePhe 507

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Search completed: December 10, 2005, 07:45:09
Job time : 3884 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 01:51:22 ; Search time 896 Seconds
(without alignments)
14093.014 Million cell updates/sec

Title: US-10-712-615-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications, NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1527	100.0	1527	6	US-10-088-726-26
3	1527	100.0	1527	8	US-10-712-615-1
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5	1527	100.0	1580	6	US-10-712-615-47
6	1527	100.0	4718	8	US-10-293-983-8
7	1525.4	99.9	1527	3	US-08-791-932-52
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9	1525.4	99.9	1527	5	US-10-094-417-5
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14	1525.4	99.9	1527	7	US-10-436-715-13
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18	1525.4	99.9	1527	8	US-10-712-615-45
19	1525.4	99.9	1527	8	US-10-897-815-15
20	1525.4	99.9	1527	9	US-10-930-662-15
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24	1525.4	99.9	1659	8	US-10-712-615-44	Sequence 44, Appl
25	1525.4	99.9	1858	6	US-10-292-798-925	Sequence 925, App
26	1525.4	99.9	1920	6	US-10-276-243-1	Sequence 1, Appl1
27	1525.4	99.9	3024	6	US-10-017-161-1087	Sequence 1087, Ap
28	1525.4	99.9	7524	6	US-10-345-332-3	Sequence 3, Appl1
29	1524	99.8	2241	9	US-10-505-486-233	Sequence 233, App
30	1522.4	99.7	2781	6	US-10-321-807-103	Sequence 103, App
31	1522.4	99.7	2781	7	US-10-321-807-103	Sequence 103, App
32	1522.4	99.7	2781	7	US-10-314-048A-103	Sequence 103, App
33	1522.4	99.7	2781	8	US-10-897-815-103	Sequence 103, App
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38	1520.6	99.6	1527	6	US-10-321-807-91	Sequence 91, Appl
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41	1520.6	99.6	1527	8	US-10-712-615-46	Sequence 46, Appl
42	1520.6	99.6	1527	8	US-10-897-815-91	Sequence 91, Appl
43	1520.6	99.6	1527	9	US-10-930-662-91	Sequence 91, Appl
44	1515.8	99.3	1527	3	US-09-971-269-5	Sequence 5, Appl1
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ALIGNMENTS

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; Publication No. US2003005444A1
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; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992,238
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
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; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-1
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1201 ATCTTCAATCATATTTTCTCTATGTGTATTCCTGTGGGCGCTACTGCTTTTACAGTC 1260
Db 1201 ATCTTCAATCATATTTTCTCTATGTGTATTCCTGTGGGCGCTACTGCTTTTACAGTC 1260
Qy 1261 CTGGCGGTGGGTGATGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 CTGGCGGTGGGTGATGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy 1321 TGGCTTTTCTTCTGAGTGTGCATCCAGCCCTATGTCTATGTGTATGCTACATGACAGAGAC 1380
Db 1321 TGGCTTTTCTTCTGAGTGTGCATCCAGCCCTATGTCTATGTGTATGCTACATGACAGAGAC 1380
Qy 1381 ATTAAGAGAGAGATGAGAGATGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ATTAAGAGAGAGATGAGAGATGCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 GAAGATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAGATGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TCTTACGATTCGTACTTTTCTTGA 1527
Db 1501 TCTTACGATTCGTACTTTTCTTGA 1527

RESULT 2
US-10-088-726-26
; Sequence 26, Application US/10088726
; Publication No. US2003015758A1
; GENERAL INFORMATION:
; APPLICANT: Matsuno et al.
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AND USES THEREOF
; FILE REFERENCE: 62514
; CURRENT APPLICATION NUMBER: US/10/088,726
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: PCT/JP00/09408
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 1999-375152
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: JP 2000-101339
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-088-726-26

Query Match 100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGCTCACCTGACCAAGCAAGCAGCGGAGAGATACAGACAGCAGTGCATGCGC 60
Db 1 ATGAGCTCACCTGACCAAGCAAGCAGCGGAGAGATACAGACAGCAGTGCATGCGC 60
Qy 61 CTCTTCAAAATGCGCATAGCTGTGGCCAGGAGATCACTGCTCAACCGTGTGTTATC 120
Db 61 CTCTTCAAAATGCGCATAGCTGTGGCCAGGAGATCACTGCTCAACCGTGTGTTATC 120
Qy 121 TTCTTGGCGGCTTTTGGTGGCAACATAGTGTGGCGCTAGTGTGGACGCAAGCG 180
Db 121 TTCTTGGCGGCTTTTGGTGGCAACATAGTGTGGCGCTAGTGTGGACGCAAGCG 180
Qy 181 CAGCTGTGAGAGTGAACGCTTTTATCTTAACTCTGTGCAACGCTGCGAG 240
Db 181 CAGCTGTGAGAGTGAACGCTTTTATCTTAACTCTGTGCAACGCTGCGAG 240
Qy 241 ATTTGCGTGTGGCCCTGGTGGTGGCCACTGTGTGCTCTCTTGGCCCTCAAC 300

Db 361 ACCATTGCTTGGTGTCAAGTGAATGCGTCACTTGTCCATCATCAACCTCTCTCCATCCG 420
Qy 421 TCCAAAGATGACCCAGCGCGCGGTTAAGTCTCTCTATGAGCACTGATTTGGCCATC 480
Db 421 TCCAAAGATGACCCAGCGCGCGGTTAAGTCTCTCTATGAGCACTGATTTGGCCATC 480
Qy 481 CTGCAAGACATCTCTCACTTCACTGAGGCTGGGCGCAGGCTGGCTTTGATGAGCGCAATGCT 540
Db 481 CTGCAAGACATCTCTCACTTCACTGAGGCTGGGCGCAGGCTGGCTTTGATGAGCGCAATGCT 540
Qy 541 CTCTGCTCCATGATCTGGGGGGGCGAGCCGACCTTCACTAATCTCAAGCGTGGTTCCTTC 600
Db 541 CTCTGCTCCATGATCTGGGGGGGCGAGCCGACCTTCACTAATCTCAAGCGTGGTTCCTTC 600
Qy 601 ATGCTCATTCACCTGATTTGTCAATGATGCTGCTCACTCCGAGTGTCTGTGCAAGCCG 660
Db 601 ATGCTCATTCACCTGATTTGTCAATGATGCTGCTCACTCCGAGTGTCTGTGCAAGCCG 660
Qy 661 AGGCAAGCATGCTCTGCTGTCAATGATGCTCAAGACACAGCTTGGAAAGTGGAGTCAAGAC 720
Db 661 AGGCAAGCATGCTCTGCTGTCAATGATGCTCAAGACACAGCTTGGAAAGTGGAGTCAAGAC 720
Qy 721 TGTGAGGAATGAGGATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 TGTGAGGAATGAGGATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 GAGTTTCGCGCGCAGCATGAGAGTGAAGTCAAGGCCAAGAGAGAGAGAGAGAGAGAGAG 840
Db 781 GAGTTTCGCGCGCAGCATGAGAGTGAAGTCAAGGCCAAGAGAGAGAGAGAGAGAGAGAG 840
Qy 841 GACGCGAGCTTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GACGCGAGCTTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 AGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 AGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 GTCAACCAAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Db 1021 GTCAACCAAGTGAAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1080
Qy 1081 AATTTTCAGTGAAGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1081 AATTTTCAGTGAAGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy 1141 CGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 CGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy 1201 ATCTTCATCATCATTTTCTCTATGCTATGCTCTGAGGAGCTTCTTTTGAAGAGTC 1260
Db 1201 ATCTTCATCATCATTTTCTCTATGCTATGCTCTGAGGAGCTTCTTTTGAAGAGTC 1260
Qy 1261 CTGGCCGATGAGGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1261 CTGGCCGATGAGGATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy 1321 TGGCTTTTCTCTGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 TGGCTTTTCTCTGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 ATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 ATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Qy 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500

Qy 1501 TCTACAGATTCGCTACTTTTCCTTGA 1527
Db 1501 TCTACAGATTCGCTACTTTTCCTTGA 1527

RESULT 4
US-09-992-238-47
; Sequence 47, Application US/0992238
; Publication No. US200305444A1
; GENERAL INFORMATION:
; APPLICANT: BATTAGLINO, PETER
; APPLICANT: FEDER, JOHN N
; APPLICANT: MINTIER, GABE
; APPLICANT: NELSON, THOMAS C
; APPLICANT: RAMANATHAN, CHANDRA S
; APPLICANT: WESTPHAL, RYAN
; APPLICANT: CACACE, ANGELA
; APPLICANT: BARBER, LAUREN
; APPLICANT: HAWKEN, DONALD R
; APPLICANT: KORNACKER, MICHAEL G
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
; FILE REFERENCE: D0047NP
; CURRENT APPLICATION NUMBER: US/09/992, 238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/317166
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/308285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/268581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/248285
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 1580
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-992-238-47

Query Match 100.0%; Score 1527; DB 3; Length 1580;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGTCCACCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 32 ATGAGGTCCACCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 91
Qy 61 CTCTCAAAATGCCCATGAGCTGGCCCAAGGAGATCATCGCTCAACCGTGGTTATC 120
Db 92 CTCTCAAAATGCCCATGAGCTGGCCCAAGGAGATCATCGCTCAACCGTGGTTATC 151
Qy 121 TTCTCGCGCGCTCTTTGTGAGCAATAGTGTGGCTAGAGTTGACAGCGAAGCG 180
Db 152 TTCTCGCGCGCTCTTTGTGAGCAATAGTGTGGCTAGAGTTGACAGCGAAGCG 211
Qy 181 CAGCTGCGAGAGTGAACCAACCGTTTATCTTTAACCTTCGTCACCGAGCTGTGAG 240
Db 212 CAGCTGCGAGAGTGAACCAACCGTTTATCTTTAACCTTCGTCACCGAGCTGTGAG 271
Qy 241 ATTGCGTGTGGAGCCCTGGGAGTGGAGCACTGTGTGCTCTTCTGAGCCCTCAAC 300
Db 272 ATTGCGTGTGGAGCCCTGGGAGTGGAGCACTGTGTGCTCTTCTGAGCCCTCAAC 331
Qy 301 AGCACTTTCGACGCGCTGGTTAGCTTCAACCAACCTGTTGAGCTTGGCAGGCTCAAC 360
Db 332 AGCACTTTCGACGCGCTGGTTAGCTTCAACCAACCTGTTGAGCTTGGCAGGCTCAAC 391
Qy 361 ACCATTGCTTGGTGTGAGTGAATGCTTGTTCATCATCAACCTCTCTCTCAACCG 420
Db 392 ACCATTGCTTGGTGTGAGTGAATGCTTGTTCATCATCAACCTCTCTCTCAACCG 451

QY	541	TTCTGCTCCATGATCTCTGGGGGGCCAGCCCCAGCTACACTATTTCTCAGGTGCTTC	600
Db	572	CTCTGCTCCATGATCTGGGGGGCCAGCCCCAGCTACACTATTTCTCAGGTGCTTC	631
QY	601	ATCTGATTCACATGATTTGTCAATGATTTCTCCTGCTACTCCGTGTTCTTGTGCAAGCCGG	660
Db	632	ATCTGATTCACATGATTTGTCAATGATTTCTCCTGCTACTCCGTGTTCTTGTGCAAGCCGG	691
QY	661	AGGCAGCATGCTCTCTCTGTACAATGTCAAGAGACACAGCTTGGAAAGTGCAGTCAAGAC	720
Db	692	AGGCAGCATGCTCTCTCTGTACAATGTCAAGAGACACAGCTTGGAAAGTGCAGTCAAGAC	751
QY	721	TGTGTGGAAATGAGATGAGAGGGAGACAGAGAAAGAGAGAGTTCCAGATGAGAGT	780
Db	752	TGTGTGGAAATGAGATGAGAGGGAGACAGAGAAAGAGAGAGTTCCAGATGAGAGT	811
QY	781	GAGTTTCGCGCGCAGCATGAAAGGTGATGAGGTCAAGGCGCAAGGGCGAGATGGAACCCAAAG	840
Db	812	GAGTTTCGCGCGCAGCATGAAAGGTGATGAGGTCAAGGCGCGAAGGGCGAGATGGAACCCAAAG	871
QY	841	GACGGCAGCCTGGAAGGCCAAGGAAGAAAGCACGGGGACCAAGTGAAGTATGTTAGAGGCC	900
Db	872	GACGGCAGCCTGGAAGGCCAAGGAAGAAAGCACGGGGACCAAGTGAAGTATGTTAGAGGCC	931
QY	901	AGGGGCGACGAGGAAGGTGATGAGAGAGCAGCGTGGCGAGGAGCGGACGATGAGAGGT	960
Db	932	AGGGGCGACGAGGAAGGTGATGAGAGAGCAGCGTGGCGAGGAGCGGACGATGAGAGGT	991
QY	961	AAGGAAGCAGCAGCCAAAGTTGAGAGAGAACAGCATGAAAGGCAGACAAAGGTTGCAACAG	1020
Db	992	AAGGAAGCAGCAGCCAAAGTTGAGAGAGAACAGCATGAAAGGCAGACAAAGGTTGCAACAG	1051
QY	1021	GTCACACAGTGCAGCATTGACTTTGGGTGAAGAATGACATGGAATTTGGTGAAGACACATC	1080
Db	1052	GTCACACAGTGCAGCATTGACTTTGGGTGAAGAATGACATGGAATTTGGTGAAGACACATC	1111
QY	1081	AATTTCAGTGAGATGACGTGAGGCAAGTAAATCCGCGAGAGCCTCCACCCAGTGGT	1140
Db	1112	AATTTCAGTGAGATGACGTGAGGCAAGTAAATCCGCGAGAGCCTCCACCCAGTGGT	1171
QY	1141	CGTAACAGCACAGCAACCTCTCTTGCCAGGTCTACACAGTGAAGACTCTAAAGTG	1200
Db	1172	CGTAACAGCACAGCAACCTCTCTTGCCAGGTCTACACAGTGAAGACTCTAAAGTG	1231
QY	1201	ATCTTCATCATCATTTTCTCCCTATGTCATCCCTGGGGCCCTACGCTTTTAAAGTC	1260
Db	1232	ATCTTCATCATCATTTTCTCCCTATGTCATCCCTGGGGCCCTACGCTTTTAAAGTC	1291
QY	1261	CTGGCCGTGTGGGTGATGTCGAAACCAGGTAAACCCAGTGGGTATCAACCAATATCATC	1320
Db	1292	CTGGCCGTGTGGGTGATGTCGAAACCAGGTAAACCCAGTGGGTATCAACCAATATCATC	1351
QY	1321	TGGCTTTTCTTCTGCAAGTGTGCAATCCACCCCTATGTCTATAGGCTACATGCAAGACC	1380
Db	1352	TGGCTTTTCTTCTGCAAGTGTGCAATCCACCCCTATGTCTATAGGCTACATGCAAGACC	1411
QY	1381	ATTAGAAGAAATCCAGGACATGCTGAAAGAGTTCTCTGAAGAAAGAGCCCCGAA	1440
Db	1412	ATTAGAAGAAATCCAGGACATGCTGAAAGAGTTCTCTGAAGAAAGAGCCCCGAA	1471
QY	1441	GAAGATAGCACCCAGACCTGCGCCGGAACAGAGGTTGGACTGAAGGCAGAAATTTGCTT	1500
Db	1472	GAAGATAGCACCCAGACCTGCGCCGGAACAGAGGTTGGACTGAAGGCAGAAATTTGCTT	1531
QY	1501	TTCTTCAATTCGTCTACTTTTCTTTGA	1527
Db	1532	TTCTTCAATTCGTCTACTTTTCTTTGA	1558

```

: Publication No. US2003014998A1
: GENERAL INFORMATION:
: APPLICANT: Wyeth
: APPLICANT: Blatcher, Maria
: APPLICANT: Paulsen, Janet
: APPLICANT: Bates, Brian G
: TITLE OF INVENTION: Genes Encoding G Protein Coupled Receptors and Uses Therefor
: FILE REFERENCE: AM100476
: CURRENT APPLICATION NUMBER: US/10/293,983
: CURRENT FILING DATE: 2002-11-13
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 8
: LENGTH: 4718
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: exon
: LOCATION: (332)..(1858)
: OTHER INFORMATION:
: US-10-293-983-8

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Query Match 100.0%; Score 1527; DB 6; Length 4718;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	ATGACGTCACCTTGACACCAACAGACCGCGGAGAGTAAACAGACCCACAGTCGATGCC	60
Db	332	ATGAGGTCACCTTGACACCAACAGACCGCGGAGAGTAAACAGACCCACAGTCGATGCC	391
QY	61	CTTCGCAAAATGGCCATCAGCTCGCGCCACGGGATCATCCGCTCAACCGTGCTGGTATC	120
Db	392	CTTCGCAAAATGGCCATCAGCTCGCGCCACGGGATCATCCGCTCAACCGTGCTGGTATC	451
QY	121	TTCTCGCGCGCTTTTCGTGCGGACATAGTGTGCGGTAGTGTGACGCGAACCG	180
Db	452	TTCTCGCGCGCTTTTCGTGCGGACATAGTGTGCGGTAGTGTGACGCGAACCG	511
QY	181	CAGCTGCTGCAAGGTGACCAACCGTTTATCTTTAACTCCTCTGCACCGACTGCTGCAG	240
Db	512	CAGCTGCTGCAAGGTGACCAACCGTTTATCTTTAACTCCTCTGCACCGACTGCTGCAG	571
QY	241	ATTTCGCTCGGCGCCCTGGGTGATGGCCACCTGTGAGCTGCTCTGCGCCCTCAAC	300
Db	572	ATTTCGCTCGGCGCCCTGGGTGATGGCCACCTGTGAGCTGCTCTGCGCCCTCAAC	631
QY	301	AGCACCTTCTGCAGCGCCCTGTAGGCTCAACCACTGTGCGCTTCGCGACGGTCAAC	360
Db	632	AGCACCTTCTGCAGCGCCCTGTAGGCTCAACCACTGTGCGCTTCGCGACGGTCAAC	691
QY	361	ACCATTTGCTTGGTGTAGTGGATCGGTACTTGTGCATCATCCACCTCTCTCTCAACCG	420
Db	692	ACCATTTGCTTGGTGTAGTGGATCGGTACTTGTGCATCATCCACCTCTCTCTCAACCG	751
QY	421	TCCAAAGATGACCCAGCGCGCGGTTAACTGCTCCTCTATGGCACCTGGATTGTGGCATC	480
Db	752	TCCAAAGATGACCCAGCGCGCGGTTAACTGCTCCTCTATGGCACCTGGATTGTGGCATC	811
QY	481	CTGAGAGCACTCTCCACTCTAAGGCTGGGGGCGAGGCTGCTTTGATGAGCGCAATGCT	540
Db	812	CTGAGAGCACTCTCCACTCTAAGGCTGGGGGCGAGGCTGCTTTGATGAGCGCAATGCT	871
QY	541	CTTGCTCATGATCTGGGGGGGCGAGCCCAAGTACATAATTCTCAGCGTGTCTCTTC	600
Db	872	CTTGCTCATGATCTGGGGGGGCGAGCCCAAGTACATAATTCTCAGCGTGTGTCTCTTC	931
QY	601	ATGCTCATTCACATGATTTGTATGATATTTGCTCTACTCCGTGATGTCTGTGACGCCGG	660
Db	932	ATGCTCATTCACATGATTTGTATGATATTTGCTCTACTCCGTGATGTCTGTGACGCCGG	991
QY	661	AGGCAGCATGCTCTGCTGTACAAATGTCAAGAGACACAGCTTGGAAATGCCAGTCAAGAC	720
Db	992	AGGCAGCATGCTCTGCTGTACAAATGTCAAGAGACACAGCTTGGAAATGCCAGTCAAGAC	1051

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QY 721 TGTGTGAGAAATGAGATGAAAGAGGAGCAGAGAAAGAGAGTTTCCAGATGAGAGT 780
DB 1052 TGTGTGAGAAATGAGATGAAAGAGGAGCAGAGAAAGAGAGTTTCCAGATGAGAGT 1111
QY 781 GAGTTTCCGCGCCAGATGAAAGTGAAGTCAAGGCCAAGAGGCGCAAGATGGAAGCCAG 840
DB 1112 GAGTTTCCGCGCCAGATGAAAGTGAAGTCAAGGCCAAGAGGCGCAAGATGGAAGCCAG 1171
QY 841 GACGCGAGCTGTAAGGCGCAAGAGAGCAACGAGGAGCCAGTGAAGTGAAGAGGCC 900
DB 1172 GACGCGAGCTGTAAGGCGCAAGAGAGCAACGAGGAGCCAGTGAAGTGAAGAGGCC 1231
QY 901 AGGAGGAGCGAGAGGTGAGAGAGAGCAGACCGGTGAGCCAGCGACCGCAGATGAGAGGT 960
DB 1232 AGGAGGAGCGAGAGGTGAGAGAGAGCAGACCGGTGAGCCAGCGACCGCAGATGAGAGGT 1291
QY 961 AAGGAAGGAGCAGCCAAAGTTGAGAGAAACAGATGAAGGCGACAAAGGTGCGACAGAG 1020
DB 1292 AAGGAAGGAGCAGCCAAAGTTGAGAGAAACAGATGAAGGCGACAAAGGTGCGACAGAG 1351
QY 1021 GTCAACAGTGCAGATGAGTGAAGTGAAGATGATGAGAGTTTGTGAAGAGCAGATC 1080
DB 1352 GTCAACAGTGCAGATGAGTGAAGTGAAGATGATGAGAGTTTGTGAAGAGCAGATC 1411
QY 1081 AATTTGAGTGAAGATGAGTGAAGGAGTGAACATCCCGAGAGCCTCCACCCAGTGGT 1140
DB 1412 AATTTGAGTGAAGATGAGTGAAGGAGTGAACATCCCGAGAGCCTCCACCCAGTGGT 1471
QY 1141 CGTAACAGCAGACAGCAACCTCTCTGCGCCAGGTGCTACCAAGTGCATAAGTG 1200
DB 1472 CGTAACAGCAGACAGCAACCTCTCTGCGCCAGGTGCTACCAAGTGCATAAGTG 1531
QY 1201 AATTCATCATGATTTTCTCTATGATGATCCCTGAGGCGCCATCGCTTTTGAAGATC 1260
DB 1532 AATTCATCATGATTTTCTCTATGATGATCCCTGAGGCGCCATCGCTTTTGAAGATC 1591
QY 1261 CTGGCCGTGTGGGTGATGTCGAAACCCAGTACCCCAAGTGGTATGACCAATATCATC 1320
DB 1592 CTGGCCGTGTGGGTGATGTCGAAACCCAGTACCCCAAGTGGTATGACCAATATCATC 1651
QY 1321 TGGCTTTTCTTCTGTCAGTGTGTCATCCACCCCTATGTCTATGCTACATGACAGACC 1380
DB 1652 TGGCTTTTCTTCTGTCAGTGTGTCATCCACCCCTATGTCTATGCTACATGACAGACC 1711
QY 1381 ATTAAGAAGAAATCCAGAGCAATGCTGAAGAGTTTCTGCAAGAGAAACCCCGGAAA 1440
DB 1712 ATTAAGAAGAAATCCAGAGCAATGCTGAAGAGTTTCTGCAAGAGAAACCCCGGAAA 1771
QY 1441 GAAGATAGCCACCCAGACCTGCGCCGAGACAGAGGTGGAGCTGAAGCAAGATTTGCCCT 1500
DB 1772 GAAGATAGCCACCCAGACCTGCGCCGAGACAGAGGTGGAGCTGAAGCAAGATTTGCCCT 1831
QY 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527
DB 1832 TCTTACGATTTCTGCTACTTTTCTTGA 1858

RESULT 7
US-09-791-932-52
; Sequence 52, Application US/09791932
; Publication No. US20030003451A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030003451A1e1 G Protein-Coupled Receptors Cross-Referen
; FILE REFERENCE: 00325. US1
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; CURRENT APPLICATION NUMBER: US/09/791,932
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/186,810
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/188,064
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: 60/186,457
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 60/213,861
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/194,344
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 60/218,337
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 52
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-932-52

Query Match      99.9%; Score 1525.4; DB 3; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGGTCCACCTGACCCCAAGCAGCAGCGCGAGAGTAACAGAGCCAGCAGTGGAGCCC 60
DB 1 ATGAGGTCCACCTGACCCCAAGCAGCAGCGCGAGAGTAACAGAGCCAGCAGTGGAGCCC 60
QY 61 CTCTCCAAATGCCATCAGCTGAGCCGACGATCATCTCGTCAACCGTGTGTTATC 120
DB 61 CTCTCCAAATGCCATCAGCTGAGCCGACGATCATCTCGTCAACCGTGTGTTATC 120
QY 121 TTCTGCGCGCTCTTTTGTGCGCAACATAGTGTGGCGCTAGTGTGAGGCGCAAGCCG 180
DB 121 TTCTGCGCGCTCTTTTGTGCGCAACATAGTGTGGCGCTAGTGTGAGGCGCAAGCCG 180
QY 181 CAGCTGTGAGGTGACCAACCGTTTAACTTTAACTCTCTGTAACGCAACCTGCGTAG 240
DB 181 CAGCTGTGAGGTGACCAACCGTTTAACTTTAACTCTCTGTAACGCAACCTGCGTAG 240
QY 241 ATTGCGCTGTGAGCCCTGAGTGTGAGCAGCTGTGAGCTCTCTTCTGAGCCCTCAAC 300
DB 241 ATTGCGCTGTGAGCCCTGAGTGTGAGCAGCTGTGAGCTCTCTTCTGAGCCCTCAAC 300
QY 301 AGCCACTTCTGACAGGCGCTGTGAGCTGACCCACCTGTGCTTGGCGCAGCGTCAAC 360
DB 301 AGCCACTTCTGACAGGCGCTGTGAGCTGACCCACCTGTGCTTGGCGCAGCGTCAAC 360
QY 361 ACCATTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 420
DB 361 ACCATTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 420
QY 421 TCCAAGATGACCCAGCGCGCGGTTAACTGTCTCTATGAGCACTGTGATGTGGCCATC 480
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Db	421	TCGAAAGATGACCCAGCGCCGCGGTTACTGCTCTCTATGCGACCTGGATTGTGGCAATC	480
Qy	481	CTGCGAGACACTCTTCCACTTACGCGCTGGGGCCAGGCTGCTTGTATGAGCGCAATGCT	540
Db	481	CTGCGAGACACTCTTCCACTTACGCGCTGGGGCCAGGCTGCTTGTATGAGCGCAATGCT	540
Qy	541	CTTGTCTCCATGATTTGGGGGGGCCAGCCCAAGTCACTATTTCTCAGGGTGGTGTCTTC	600
Db	541	CTTGTCTCCATGATTTGGGGGGGCCAGCCCAAGTCACTATTTCTCAGGGTGGTGTCTTC	600
Qy	601	ATCGCATTTCCACTGATTTGTCAATGTCCTCTACTCCGTGGTGTTCMTGTACAGCCGG	660
Db	601	ATCGCATTTCCACTGATTTGTCAATGTCCTCTACTCCGTGGTGTTCMTGTACAGCCGG	660
Qy	661	AGGCGACATGCTCTGCTGTACAAATGTCAAGACACAGCTTGGAAAGTGCAGTCAAGAC	720
Db	661	AGGCGACATGCTCTGCTGTACAAATGTCAAGACACAGCTTGGAAAGTGCAGTCAAGAC	720
Qy	721	TGTGTGAGAAATGAGATGTAAGAGGAGCAGAAAGAGAGAGATTCCAGATGACGT	780
Db	721	TGTGTGAGAAATGAGATGTAAGAGGAGCAGAAAGAGAGAGATTCCAGATGACGT	780
Qy	781	GAGTTTCGCGGCACATGAAAGTACAGGCGCAAGGGCAAGGAGGAGATGGAATGCCAAG	840
Db	781	GAGTTTCGCGGCACATGAAAGTACAGGCGCAAGGGCAAGGAGGAGATGGAATGCCAAG	840
Qy	841	GACGCGACGCTTGAMGGCCAGAGAAAGAAAGCAGGGGACCAGTGAAGTATGTATAGGCC	900
Db	841	GACGCGACGCTTGAMGGCCAGAGAAAGAAAGCAGGGGACCAGTGAAGTATGTATAGGCC	900
Qy	901	AGGGGACGCGAGAGAGGTCAAGAGAGACAGCAGGTGGCCAGCGACATGAGAGGT	960
Db	901	AGGGGACGCGAGAGAGGTCAAGAGAGACAGCAGGTGGCCAGCGACATGAGAGGT	960
Qy	961	AAGGAAGGACAGCAAAAGTTGAGAGAAACACATGAAGGCAAGAGGTCGCCACAG	1020
Db	961	AAGGAAGGACAGCAAAAGTTGAGAGAAACACATGAAGGCAAGAGGTCGCCACAG	1020
Qy	1021	GTCACACAGTCAGCATTTGACTTTGGGTGAAGATGACATGAGATTTGGTGAACAGACATC	1080
Db	1021	GTCACACAGTCAGCATTTGACTTTGGGTGAAGATGACATGAGATTTGGTGAACAGACATC	1080
Qy	1081	AATTTCAAGAGAGATGACGTGCGAGGCAGTGAACATCCCGAGAGCCTCCACCCAGTGGT	1140
Db	1081	AATTTCAAGAGAGATGACGTGCGAGGCAGTGAACATCCCGAGAGCCTCCACCCAGTGGT	1140
Qy	1141	CGTACACAGCAACGCAACCCTCTCTGCCCCAGGTGCTACAGTGCMAAGCTCTAAAGTG	1200
Db	1141	CGTACACAGCAACGCAACCCTCTCTGCCCCAGGTGCTACAGTGCMAAGCTCTAAAGTG	1200
Qy	1201	ATCTTCATCATATTTTCTCCTATGNGCTATCCGTGGGGCCCTTACMGCTTTTATACAGTC	1260
Db	1201	ATCTTCATCATATTTTCTCCTATGNGCTATCCGTGGGGCCCTTACMGCTTTTATACAGTC	1260
Qy	1261	CTGGCCGTGTGGGTGGATGTGMAAACCCAGGTATCCCAATGGGTATCACTAAATCATC	1320
Db	1261	CTGGCCGTGTGGGTGGATGTGMAAACCCAGGTATCCCAATGGGTATCACTAAATCATC	1320
Qy	1321	TGGCTTTTCTTCTCTGAGTGTCTGACATCCACCCTTATGTCTATGGCTACATGCAAGAC	1380
Db	1321	TGGCTTTTCTTCTCTGAGTGTCTGACATCCACCCTTATGTCTATGGCTACATGCAAGAC	1380
Qy	1381	ATTAGAAGAAATCCAGAGCAATGCGAAGAAAGTTCTTGCAAGAAAGAACGCCCGGAA	1440
Db	1381	ATTAGAAGAAATCCAGAGCAATGCGAAGAAAGTTCTTGCAAGAAAGAACGCCCGGAA	1440
Qy	1441	GAAAGATAGCACCCAGACCTGCCCCGGAACAGAGGGTGGACTGAAGGCAAGATGTCTCT	1500
Db	1441	GAAAGATAGCACCCAGACCTGCCCCGGAACAGAGGGTGGACTGAAGGCAAGATGTCTCT	1500
Qy	1501	TCTACGATTCGTACTTTTCTTTGA	1527

	DB	1501 TCCTACGATTCGTGCATTCTTCCCTGA 1527
		RESULT 8
		US-09-992-238-45
		/ Sequence 45, Application US/09992238
		/ Publication No. US200305444A1
		GENERAL INFORMATION:
		APPLICANT: BATTAGLINO, PETER
		APPLICANT: FEDER, JOHN N
		APPLICANT: MINTIER, GABE
		APPLICANT: NELSON, THOMAS C
		APPLICANT: RAMANATHAN, CHANDRA S
		WESTPHAL, RYAN
		CACCACE, ANGELA
		HAWKEN, DONALD R
		KORNAKGER, MICHAEL G
		TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRPRMBY6,
		TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
		FILE REFERENCE: D0047NP
		CURRENT APPLICATION NUMBER: US/09/992,238
		CURRENT FILING DATE: 2001-11-14
		PRIOR APPLICATION NUMBER: 60/317166
		PRIOR FILING DATE: 2001-09-04
		PRIOR APPLICATION NUMBER: 60/308285
		PRIOR FILING DATE: 2001-07-27
		PRIOR APPLICATION NUMBER: 60/268581
		PRIOR FILING DATE: 2001-02-14
		PRIOR APPLICATION NUMBER: 60/248285
		NUMBER OF SEQ ID NOS: 102
		SOFTWARE: PatentIn Ver. 2.1
		SEQ ID NO 45
		LENGTH: 1527
		TYPE: DNA
		ORGANISM: Homo sapiens
		US-09-992-238-45
		Query Match 99.9% ; Score 1525.4; DB 3; Length 1527;
		Best Local Similarity 99.9%; Pred. No. 0;
		Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy		1 ATGAGCTGCACCTGGCAACAAGCAGCGCGAGAAGTAACAGCAGGCCAGACTGATGCC 60
Dd	1	ATGAGCTGCACCTGGCAACAAGCAGCGCGAGAAGTAACAGCAGGCCAGACTGATGCC 60
Oy	61	CTTGCAAATATGCCCATATAGCTGGCCCAAGGATCATCCGCTCAACCGTGTGGTTATC 120
Dd	61	CTTGCAAATAATGCCCATATAGCTGGCCCAAGGATCATCCGCTCAACCGTGTGGTTATC 120
Oy	121	TTCCTCGCGCGCTCTTTGTCGCGCAATATGTCGTGGGCTTAGTGTGACAGGCAAGCG 180
Dd	121	TTCCTCGCGCGCTCTTTGTCGCGCAATATGTCGTGGGCTTAGTGTGACAGGCAAGCG 180
Oy	181	CAGCTGTCGAGGTGACCAACCGTTTTATCTTTAACTCTTGTCACGACCTGTGTGAG 240
Dd	181	CAGCTGTCGAGGTGACCAACCGTTTTATCTTTAACTCTTGTCACGACCTGTGTGAG 240
Oy	241	ATTTCGCTGTGGCCCCCTGTGGGTGTGGCACCTTGTCCTCTTTCTGAGCCCTCAAC 300
Dd	241	ATTTCGCTGTGGCCCCCTGTGGGTGTGGCACCTTGTCCTCTTTCTGAGCCCTCAAC 300
Oy	301	AGCCACTTCGACGGCCCTGTTAAGCTCAACCAACCGTTTCGCTTGCGCAGGCTCAAC 360
Dd	301	AGCCACTTCGACGGCCCTGTTAAGCTCAACCAACCGTTTCGCTTGCGCAGGCTCAAC 360
Oy	361	ACCATTTCTTGTGTGTCAGTGGATGCTACTTGTGCATCATCAACCTCTCTCTAACCG 420
Dd	361	ACCATTTCTTGTGTGTCAGTGGATGCTACTTGTGCATCATCAACCTCTCTCTAACCG 420
Oy	421	TCCAAGATGACCAAGCGCGCGGTTACTCTCTTATGGCACTGGAATGTGGCATC 480

Db	421	TCCAAGATGACCCAGCGCCGGGTTACTGCTCTCTATGACACCTGGATTGTGGCATC	480
Qy	481	CTGCAGAGCACTCTCCACTCTAGGAGTGGGGCCAGGCTGCCCTTTGATGAGCCGAACTCT	540
Db	481	CTGCAGAGCACTCTCCACTCTAGGAGTGGGGCCAGGCTGCCCTTTGATGAGCCGAACTCT	540
Qy	541	CTGTGCTCATGATCTGGGGGGCCAGGCCCAAGCTACAATATCTCAGGTGAGTGCCTTC	600
Db	541	CTGTGCTCATGATCTGGGGGGCCAGGCCCAAGCTACAATATCTCAGGTGAGTGCCTTC	600
Qy	601	ATCGTCATTCACATGATTTGATGATTTGCCCTGTACTCCGTGTGTTCTGTGCAGCCCGG	660
Db	601	ATCGTCATTCACATGATTTGATGATTTGCCCTGTACTCCGTGTGTTCTGTGCAGCCCGG	660
Qy	661	AGGCAGCATGCTCTGCTGTACATGTCAAGACACACAGCTTGAAGTCCAGTCAAGAC	720
Db	661	AGGCAGCATGCTCTGCTGTACATGTCAAGACACACAGCTTGAAGTCCAGTCAAGAC	720
Qy	721	TGTGTGAGGAATGAGGATGAAAGAGGACACAGAAAGAGAGGATTCACAGATGACAT	780
Db	721	TGTGTGAGGAATGAGGATGAAAGAGGACACAGAAAGAGAGGATTCACAGATGACAT	780
Qy	781	GAGTTTCCGCCCCAGCATGAAAGTGAAGTCAAGGCCAAGAGGGCAGAAATGGAAGCCAA	840
Db	781	GAGTTTCCGCCCCAGCATGAAAGTGAAGTCAAGGCCAAGAGGGCAGAAATGGAAGCCAA	840
Qy	841	GACGCGACCTGAAAGGCCAAGAAAGAAAGCAAGGGACCACTGAGAGTATGTAGAGCC	900
Db	841	GACGCGACCTGAAAGGCCAAGAAAGAAAGCAAGGGACCACTGAGAGTATGTAGAGCC	900
Qy	901	AGGGGACCGAGAGGTCAAGAGACAGCAACGGTGCACGATGAGAGGT	960
Db	901	AGGGGACCGAGAGGTCAAGAGACAGCAACGGTGCACGATGAGAGGT	960
Qy	961	AAGGAAGCAGACACCAAAAGTTGAGAGAAACGATGAAGGAGACAAAGGTGCACAGAG	1020
Db	961	AAGGAAGCAGACACCAAAAGTTGAGAGAAACGATGAAGGAGACAAAGGTGCACAGAG	1020
Qy	1021	GTCAACCAAGTCAGCATTTGACTTGGGTGAAGATGACATGAGTTTGTGAAGACGACATC	1080
Db	1021	GTCAACCAAGTCAGCATTTGACTTGGGTGAAGATGACATGAGTTTGTGAAGACGACATC	1080
Qy	1081	AATTTCAATGAGATGACGTGAGGCAATGTAATCCCGAAGCTTCCACCAAGTCTGT	1140
Db	1081	AATTTCAATGAGATGACGTGAGGCAATGTAATCCCGAAGCTTCCACCAAGTCTGT	1140
Qy	1141	CGTAAACAGCAACAGCAACCTCTCTGCGCCAGGTGCTACAGTGGAAAGCTGTAAAGTG	1200
Db	1141	CGTAAACAGCAACAGCAACCTCTCTGCGCCAGGTGCTACAGTGGAAAGCTGTAAAGTG	1200
Qy	1201	ATCTTCATCATATTTTCTCCTATGTGTATCCCTGGGGGCCCTACTGCTTTTAAAGACTC	1260
Db	1201	ATCTTCATCATATTTTCTCCTATGTGTATCCCTGGGGGCCCTACTGCTTTTAAAGACTC	1260
Qy	1261	CTGGCCGCTGGGTGATGTGAAACCCAGGTAACCCAGTGGGTGATCAACCATATATCTC	1320
Db	1261	CTGGCCGCTGGGTGATGTGAAACCCAGGTAACCCAGTGGGTGATCAACCATATATCTC	1320
Qy	1321	TGGCTTTTCTTCCCTGCAATGCTGATCCACCCCTATGTCTATAGGTAAATGCAAGACC	1380
Db	1321	TGGCTTTTCTTCCCTGCAATGCTGATCCACCCCTATGTCTATAGGTAAATGCAAGACC	1380
Qy	1381	ATTAAAGAGAAATTCAGAGCATGCTGAAGAAGTTCTCTGCAAGAAAGACCCCGGAAA	1440
Db	1381	ATTAAAGAGAAATTCAGAGCATGCTGAAGAAGTTCTCTGCAAGAAAGACCCCGGAAA	1440
Qy	1441	GAAATAGCCACCCAGACTGCGCCGGAAACAGAGGGTGGGACTGAAGCAAGATTGTCCCT	1500
Db	1441	GAAATAGCCACCCAGACTGCGCCGGAAACAGAGGGTGGGACTGAAGCAAGATTGTCCCT	1500
Qy	1501	TCCTACGATTTCTGCTACTTTTCTCTTGA	1527
Db	1501	TCCTACGATTTCTGCTACTTTTCTCTTGA	1527

Query	DB	Score	Length	Matches	Mismatches	Indels	Gaps
Query Match		99.9%	Score 1525.4; DB 5; Length 1527;				
Best Local Similarity		99.9%	Pred. No. 0;				
Matches 1526;		Conservative	0; Mismatches	1; Indels	0; Gaps	0;	
1	ATGACGTCCACCTGCAACAGCAGCCGCGAGAGTAAACAGCAGCCACAGTGCATGCC	60					
1	ATGACGTCCACCTGCAACAGCAGCCGCGAGAGTAAACAGCAGCCACAGTGCATGCC	60					
61	CTCTCCAAATGGCCATCAGCTGCGCCAGGACATCATCCGGTCAACCGTGTGTTATC	120					
61	CTCTCCAAATGGCCATCAGCTGCGCCAGGACATCATCCGGTCAACCGTGTGTTATC	120					
121	TTCTCTGCGCGCTTTTGTGTGCGCAATAGTGTGCGGTAGTGTGCGCGCAACCG	180					
121	TTCTCTGCGCGCTTTTGTGTGCGCAATAGTGTGCGGTAGTGTGCGCGCAACCG	180					
121	TTCTCTGCGCGCTTTTGTGTGCGCAATAGTGTGCGGTAGTGTGCGCGCAACCG	180					
181	CAGCTGCTGCAAGGTGACCAACCGTTTATCTTTAATCTCTCTGTGACCGACTGTGCG	240					
181	CAGCTGCTGCAAGGTGACCAACCGTTTATCTTTAATCTCTCTGTGACCGACTGTGCG	240					
241	ATTTCGCTCGAGGCGCCCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	300					
241	ATTTCGCTCGAGGCGCCCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	300					
301	AGCCACTTTCGCAACGCGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	360					
301	AGCCACTTTCGCAACGCGCGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	360					
361	ACCAATTTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	420					
361	ACCAATTTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	420					
421	TCCAAAGTGAACCGACGCGCGGTTCATCTCTCTATAGCACTTGTGAGTGTGAGTGTGAGT	480					
421	TCCAAAGTGAACCGACGCGCGGTTCATCTCTCTATAGCACTTGTGAGTGTGAGTGTGAGT	480					
421	TCCAAAGTGAACCGACGCGCGGTTCATCTCTCTATAGCACTTGTGAGTGTGAGTGTGAGT	480					
481	CTGAGAGCACTCTCTCACTCTTACGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	540					
481	CTGAGAGCACTCTCTCACTCTTACGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT	540					


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Db 721 TGTGTGGAATGAGATGATGAAGGAGGAGCAAGAAAGAGAGAGATTCCAGATGTGAGCT 780
Qy 781 GAGTTTCGCCGCGACAGTAAAGTGAAGTCAAGGCGCAAGAGGCGCAATGGAAGCCAAG 840
Db 781 GAGTTTCGCCGCGACAGTAAAGTGAAGTCAAGGCGCAAGAGGCGCAATGGAAGCCAAG 840
Qy 841 GACGGCAGCCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GACGGCAGCCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Qy 901 AGGGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 AGGGGCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Qy 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 GTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
Db 1021 GTCAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
Qy 1081 AATTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1140
Db 1081 AATTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1140
Qy 1141 CGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1141 CGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Qy 1201 ATCTTCATCATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ATCTTCATCATATTTTCTCTATGATGATGATGATGATGATGATGATGATGATGATG 1260
Qy 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 TGGCTTTTCTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 TGGCTTTTCTCTCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 ATTAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 ATTAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Qy 1441 GAAAGATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 GAAAGATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Qy 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527
Db 1501 TCTTACGATTTCTGCTACTTTTCTTGA 1527

RESULT 11
US-10-345-332-1
; Sequence 1, Application US/10345332
; Publication No. US20030129705A1
; GENERAL INFORMATION:
; APPLICANT: LI et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000754CON
; CURRENT APPLICATION NUMBER: US/10/345,332
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/769,741
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/205,166
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/638,018
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; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-345-332-1

Query Match
Best Local Similarity 99.9%; Score 1525.4; DB 6; Length 1527;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGCTCCACCTGACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 ATGAGCTCCACCTGACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Qy 61 CTCTCCAAATGCCCATGACCTGCGCCACGCGCATCATCTGCTCAACCGTCTGTTATC 120
Db 61 CTCTCCAAATGCCCATGACCTGCGCCACGCGCATCATCTGCTCAACCGTCTGTTATC 120
Qy 121 TTCTCTGCGCGCTCTTTGCTGCGCAACATAGCTGGGCTGAGTGTGAGAGGCAAGCCG 180
Db 121 TTCTCTGCGCGCTCTTTGCTGCGCAACATAGCTGGGCTGAGTGTGAGAGGCAAGCCG 180
Qy 181 CAGCTGTGACAGTGAACCAACGTTTATCTTTAATCTCTGTCACCGACCTGCTGACG 240
Db 181 CAGCTGTGACAGTGAACCAACGTTTATCTTTAATCTCTGTCACCGACCTGCTGACG 240
Qy 241 ATTTGCTGTGAGCCCTGCTGAGTGTGAGCACTGTGCTCTCTTCTGAGCCCTGAAC 300
Db 241 ATTTGCTGTGAGCCCTGCTGAGTGTGAGCACTGTGCTCTCTTCTGAGCCCTGAAC 300
Qy 301 AGCCACTTGTGAGGCGCTGTGATGCTCAACCACTGTGTGCTTGGCCAGGCTCAAC 360
Db 301 AGCCACTTGTGAGGCGCTGTGATGCTCAACCACTGTGTGCTTGGCCAGGCTCAAC 360
Qy 361 ACCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 ACCATTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 TCCAAAGATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 TCCAAAGATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 CTGCAAGAGACTTCTCACTCTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTGCAAGAGACTTCTCACTCTCAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 CTCTGCTCATGATCTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 CTCTGCTCATGATCTGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy 601 ATGCTCATTTCACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 ATGCTCATTTCACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 AGGCAAGCATGCTCTGCTGATCAATGTCAAGAGACACAGTTTGAAGTGGAGTCAAGAGC 720
Db 661 AGGCAAGCATGCTCTGCTGATCAATGTCAAGAGACACAGTTTGAAGTGGAGTCAAGAGC 720
Qy 721 TGTGTGGAATGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 TGTGTGGAATGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 781 GAGTTTCGCCGCGACAGTAAAGTGAAGTCAAGGCGCAAGAGGCGCAATGGAAGCCAAG 840
Db 781 GAGTTTCGCCGCGACAGTAAAGTGAAGTCAAGGCGCAAGAGGCGCAATGGAAGCCAAG 840
Qy 841 GACGGCAGCCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 GACGGCAGCCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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Oy	841	GA	CGCGCAGCCCTGMAAGGCCCAAGAAAGAAAGCA	CGGGGACCCACTGAGAGTAGTGTAGAGGCC	900
Db	841	GACCGCAGCCCTGMAAGGCCCAAGAAAGAAAGCA	CGGGGACCCACTGAGAGTAGTGTAGAGGCC		900
Oy	901	AGGGGCACGAGAGAGGTGAGAGAGAGCAGCA	CGGGTGGCCACGCA	CGGGAGCATGAGTGTAGAGGCC	960
Db	901	AGGGGCACGAGAGAGGTGAGAGAGAGCAGCA	CGGGTGGCCACGCA	CGGGAGCATGAGTGTAGAGGCC	960
Oy	961	AAGGAAGCGACACCAAAAGTTGAGAGAAACAGCAT	GAAAGGCGACAAGGGTCGACAGAG		1020
Db	961	AAGGAAGCGACACCAAAAGTTGAGAGAAACAGCAT	GAAAGGCGACAAGGGTCGACAGAG		1020
Oy	1021	GTCAACCACTGCACGATTCGACTTGGGTGAGATG	CATGAGATTGGTGGAAAGCAGCATC		1080
Db	1021	GTCAACCACTGCACGATTCGACTTGGGTGAGATG	CATGAGATTGGTGGAAAGCAGCATC		1080
Oy	1081	AAATTCATGAGAGATGAGTGTGAGGCAATGAA	CATCCCGGAGAGCTTCCCA	CCCAAGTCGT	1140
Db	1081	AAATTCATGAGAGATGAGTGTGAGGCAATGAA	CATCCCGGAGAGCTTCCCA	CCCAAGTCGT	1140
Oy	1141	CGTAAACAGCAACAGCAACCTCTCTGTGCCAG	GTGCTACAGTGCMAAGCTGTAAAGTG		1200
Db	1141	CGTAAACAGCAACAGCAACCTCTCTGTGCCAG	GTGCTACAGTGCMAAGCTGTAAAGTG		1200
Oy	1201	ATCTTCATCATCATTTTCTCCTATGTGCTAT	CCCTGGGACCCCTA	CTGCTTTTGAAGCTC	1260
Db	1201	ATCTTCATCATCATTTTCTCCTATGTGCTAT	CCCTGGGACCCCTA	CTGCTTTTGAAGCTC	1260
Oy	1261	CTGGCCGTGTGGGTGTGATGTGAAACCAAGTA	CCCCAGTGGGTGATACCATATATCTC		1320
Db	1261	CTGGCCGTGTGGGTGTGATGTGAAACCAAGTA	CCCCAGTGGGTGATACCATATATCTC		1320
Oy	1321	TGGCTTTTCTTCTGCACTGCGCATGCCAT	TCCACCCCTATGTCTATGGCTATCATGCACAAGACC		1380
Db	1321	TGGCTTTTCTTCTGCACTGCGCATGCCAT	TCCACCCCTATGTCTATGGCTATCATGCACAAGACC		1380
Oy	1381	ATTAAAGAAGAAATCAGAGACATGCTGTGAAGA	AGTTCTTCTGCAAGAAAGAAACCCCCCGAAA		1440
Db	1381	ATTAAAGAAGAAATCAGAGACATGCTGTGAAGA	AGTTCTTCTGCAAGAAAGAAACCCCCCGAAA		1440
Oy	1441	GAAGATAGCCACCCAGACTGTGCCCGGAAA	CAGAGGGTGGGACTGAAAGGCAAGATTGTCCCT		1500
Db	1441	GAAGATAGCCACCCAGACTGTGCCCGGAAA	CAGAGGGTGGGACTGAAAGGCAAGATTGTCCCT		1500
Oy	1501	TCCTACGATTCGTGCTACTTTTCTCTTGA			1527
Db	1501	TCCTACGATTCGTGCTACTTTTCTCTTGA			1527

RESULT 13
US-10-276-243-2

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; Sequence 2 Application US/10276243
; Publication No. US20030187219A1
; GENERAL INFORMATION:
; APPLICANT: Bayer AG
; TITLE OF INVENTION: REGULATION OF HUMAN alpha1 ADRENERGIC RECEPTOR-LIKE G
; TITLE OF INVENTION: PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: L10062 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/276,243
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/204,145
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/250,505
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-243-2

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Query Match	99.9%	Score 1525.4	DB 6	Length 1527
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1526	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	1	ATGACGCTCCACCTGACCAACAGACGCGGAGAGTAAACAGACGACCAACGTCGATGCC	60	
Db	1	ATGAGCTCCACTTGACCAACAGCACCGCGAGAGTAAACAGACGCCACAGCTGCATGCC	60	
QY	61	CTCTCCAAAATGCCCATACAGCTGGCCCAAGGATCATCCGGCTCAACCGTGCTGGTATC	120	
Db	61	CTCTCCAAAATGCCCATACAGCTGGCCCAAGGATCATCCGGCTCAACCGTGCTGGTATC	120	
QY	121	TTCTCTGCGCGCTCTTTTCGTGGCAACATAGTGTGCGCTAGTGTTCAGCGCAACCG	180	
Db	121	TTCTCTGCGCGCTCTTTTCGTGGCAACATAGTGTGCGCTAGTGTTCAGCGCAACCG	180	
QY	181	CAGCTGCTGAGGAGCAACCGTTTATCTTTAACTCCCTCGACACGACTGCTGACG	240	
Db	181	CAGCTGCTGAGGAGCAACCGTTTATCTTTAACTCCCTCGACACGACTGCTGACG	240	
QY	241	ATTTCGCTGCTGGCGCCCTG63TG6TG6GCACACTCTGTGCTCTTCTG6CCCTCAAC	300	
Db	241	ATTTCGCTGCTGGCGCCCTG63TG6TG6GCACACTCTGTGCTCTTCTG6CCCTCAAC	300	
QY	301	AGCCACTTCTGACAGCGCCCTGTGTTAGCTTACCCACCTGTTCCGCTTCGCAAGCTCAAC	360	
Db	301	AGCCACTTCTGACAGCGCCCTGTGTTAGCTTACCCACCTGTTCCGCTTCGCAAGCTCAAC	360	
QY	361	ACCAATTGCTTGGTGTAGTGAACGCTACTGTTCATTCATCAACCCCTCTCTCCACCG	420	
Db	361	ACCAATTGCTTGGTGTAGTGAACGCTACTGTTCATTCATCAACCCCTCTCTCCACCG	420	
QY	421	TCCAAGATGACCCAGCGCCGCGTTTACTCTGCTCTCATG6GCACCTG6ATGTCGCAATC	480	
Db	421	TCCAAGATGACCCAGCGCCGCGTTTACTCTGCTCTCATG6GCACCTG6ATGTCGCAATC	480	
QY'	481	CTGACAGACACTCTCTCACTTACAGGCTG63G6CCAGGCTGCTTGTGATGAGCGCAATGCT	540	
Db	481	CTGACAGACACTCTCTCACTTACAGGCTG63G6CCAGGCTGCTTGTGATGAGCGCAATGCT	540	
QY	541	CTCTGCTCCATGATCTTGGGGGGCCAGGCCAGCTACATTTCTCAAGCTGTGTCCTTC	600	
Db	541	CTCTGCTCCATGATCTTGGGGGGCCAGGCCAGCTACATTTCTCAAGCTGTGTCCTTC	600	
QY	601	ATCGTCATTCACATGATTTGTTCATGATTGCTGCTACTCCGTCGTCTGTCGACCCCG	660	
Db	601	ATCGTCATTCACATGATTTGTTCATGATTGCTGCTACTCCGTCGTCTGTCGACCCCG	660	
QY	661	AGGACGACATGCTCTGCTGTACAAATGTCAAGACACAGCTTGGAAAGTCGAGTCAAGAC	720	
Db	661	AGGACGACATGCTCTGCTGTGTACAAATGTCAAGACACAGCTTGGAAAGTCGAGTCAAGAC	720	
QY	721	TGTGTGGAAATGAGGATGAAAGAGGAGCAGAGAAAGAGAGATTCAGAGATGAGAGT	780	
Db	721	TGTGTGGAAATGAGGATGAAAGAGGAGCAGAGAAAGAGAGATTCAGAGATGAGAGT	780	
QY	781	GAGTTTGGCGCCAGCATGAAAGGTGAGGTCAAGGCCAAGGAGGSCAGAAATGGAAGCCAA	840	
Db	781	GAGTTTGGCGCCAGCATGAAAGGTGAGGTCAAGGCCAAGGAGGSCAGAAATGGAAGCCAA	840	
QY	841	GACGCGACCTTGAAGGCAAGGAAGGAAGCACG6G6GACACTGTGAGTGTGAGAGCC	900	
Db	841	GACGCGACCTTGAAGGCAAGGAAGGAAGCACG6G6GACACTGTGAGTGTGAGAGCC	900	
QY	901	AGGGGACGCGAGAGGTTCAGAGAGACGATCGGTGGCCACGCAACGCAAGATGGAAGGT	960	
Db	901	AGGGGACGCGAGAGGTTCAGAGAGACGATCGGTGGCCACGCAACGCAAGATGGAAGGT	960	
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RESULT 15
US-10-343-650A-89
; Sequence 89, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1527)
US-10-343-650A-89

Query Match 99.9%; Score 1525.4; DB 7; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1 ATGACGTCCACCTGCAACCAAGCAGCGGAGAGTAAACAGACCAACAGTCATGCCCC 60
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Db 121 TTCTCGCGCGCTTTTCTGTCGCAACATAGTCTGGCGCTAGTGTGTCAGCGCAAGCCG 180
Qy 181 CAGCTGCTGAGGTGACCAACGCTTTTATCTTTAACCTCTCTGTCACCGACTGTGACG 240
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Qy 241 ATTTCCTGTCGCGCGCGCGCGGTGGTGGCCACCTGTGCTCTTTTGGCCCCCTCAAC 300
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 Job time : 900 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 03:03:28 / Search time 161 Seconds
(without alignments)
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Title: US-10-712-615-1

Perfect score: 1527

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1525.4	99.9	1527	6	US-10-980-388-52
2	470.2	30.8	619	6	US-10-980-388-8
3	68.2	4.5	1685	6	US-10-750-185-36071
4	63	4.1	3372	6	US-10-750-185-44031
5	57.8	3.8	153376	7	US-11-121-086-5
6	57.6	3.8	246960	7	US-11-121-086-8
7	55.6	3.6	1207	6	US-10-750-185-26665
8	55.4	3.6	1984	6	US-10-502-893-1
9	53.8	3.5	1594	7	US-11-170-153-9
10	53.8	3.5	1594	7	US-11-170-153-11
11	53.8	3.5	1658	7	US-11-170-153-1
12	53.8	3.5	1658	7	US-11-170-153-3
13	53.8	3.5	1658	7	US-11-170-153-5
14	53.8	3.5	1658	7	US-11-170-153-7
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16	51.6	3.4	153376	7	US-11-121-086-5
17	51	3.3	1225	6	US-10-955-054A-112
18	50.2	3.3	126552	7	US-11-121-086-1
19	49.4	3.2	1102	6	US-10-955-054A-121
20	49.4	3.2	8747	6	US-10-955-054A-141
21	49.2	3.2	1410	6	US-10-992-577-1
22	48.4	3.2	173602	7	US-11-121-086-25
23	48.2	3.2	175023	7	US-11-121-086-18

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	26	47.2	3.1	191684	7	US-11-121-086-2	Sequence 2, Appl1
	27	46.8	3.1	1089	7	US-11-110-274-2	Sequence 2, Appl1
	28	46.2	3.0	148920	7	US-11-121-086-90	Sequence 90, Appl1
	29	46.2	3.0	167116	7	US-11-121-086-44	Sequence 44, Appl1
	30	46.2	3.0	172543	7	US-11-121-086-6	Sequence 6, Appl1
	31	46	3.0	137671	7	US-11-121-086-47	Sequence 47, Appl1
	32	45.4	3.0	857	6	US-10-750-185-35457	Sequence 35457, A
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	37	44.2	2.9	176503	7	US-11-121-086-53	Sequence 53, Appl1
	38	43.4	2.8	193084	7	US-11-121-086-82	Sequence 82, Appl1
	39	43	2.8	1977	6	US-10-750-185-35938	Sequence 35938, A
	40	42.6	2.8	215308	7	US-11-121-086-77	Sequence 77, Appl1
	41	42.4	2.8	191684	7	US-11-121-086-2	Sequence 2, Appl1
	42	42.2	2.8	179666	7	US-11-121-086-67	Sequence 67, Appl1
	43	42	2.8	1309	6	US-10-750-185-50916	Sequence 50916, A
	44	41.8	2.7	138821	7	US-11-121-086-80	Sequence 80, Appl1
	45	41.4	2.7	1224	6	US-10-750-185-40492	Sequence 40492, A

ALIGNMENTS

RESULT 1
US-10-980-388-52
Sequence 52, Application US/10980388
Publication No. US20050255490A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiesch, Ronald R.
APPLICANT: Lind, Peter
APPLICANT: Kayes, Paul S.
APPLICANT: Ruff, Valerie
APPLICANT: Huff, Rita M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
FILE REFERENCE: 00325.US1
CURRENT APPLICATION NUMBER: US/10/980,388
CURRENT FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,303
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,397
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,247
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/188,880
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/217,369
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,370
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
PRIOR FILING DATE: 2000-07-20
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 184
SOFTWARE: Patentin version 3.0
SEQ ID NO 52
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-980-388-52

Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
 Beest Local Similarity 99.9%; Pred. No. 0;
 Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 2
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 ; Sequence 8, Application US/10980388
 ; Publication No. US20050255490A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogel, Gabriel
 ; APPLICANT: Parodi, Luis A.
 ; APPLICANT: Hiebsch, Ronald R.
 ; APPLICANT: Lind, Peter
 ; APPLICANT: Kayes, Paul S.
 ; APPLICANT: Rufe, Valerie
 ; APPLICANT: Huff, Rita M.
 ; APPLICANT: Wood, Linda S.
 ; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
 ; FILE REFERENCE: 00325, US1
 ; CURRENT APPLICATION NUMBER: US/10/980,388
 ; PRIORITY FILING DATE: 2004-11-02
 ; PRIORITY FILING DATE: US/09/791,932
 ; PRIORITY FILING DATE: 2001-02-23
 ; PRIORITY FILING DATE: 60/184,305
 ; PRIORITY FILING DATE: 2000-02-23
 ; PRIORITY FILING DATE: 60/184,397
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 ; PRIORITY FILING DATE: 60/188,880
 ; PRIORITY FILING DATE: 2000-03-13
 ; PRIORITY FILING DATE: 60/217,369
 ; PRIORITY FILING DATE: 2000-07-11
 ; PRIORITY FILING DATE: 60/217,370
 ; PRIORITY FILING DATE: 2000-07-11
 ; PRIORITY FILING DATE: 60/218,492
 ; PRIORITY FILING DATE: 2000-07-20

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; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-980-388-8

Query Match 30.8%; Score 470.2; DB 6; Length 619;
Best Local Similarity 99.4%; Pred. No. 1,1e-111;
Matches 472; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 385 ATTTCGCTGTGGCCCGCTGGTGGTGGCCACTCTGTGCTCTCTTGTGGCCCTGCAC 444
QY 301 AGGCATTCTGCAAGCGCGCTGTTAGCTGACCCACTGTTGCGCTTGGCAGGTCAC 360
DB 445 AGGCATTCTGCAAGCGCGCTGTTAGCTGACCCACTGTTGCGCTTGGCAGGTCAC 504
QY 361 ACCATTGTCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
DB 505 ACCATTGTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 564
QY 421 TCCAAATGACCCAGCGCGGCTTACCTGCTCTCTATGAGCACTGGATTGGG 475
DB 565 TCCAAATGACCCAGCGCGGCTTACCTGCTCTCTATGAGCACTGGATTGGG 619

RESULT 3

US-10-750-185-36071/c
; Sequence 36071, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: RANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36071
; LENGTH: 1685
; TYPE: DNA
; ORGANISM: Bovine 19866880675545
US-10-750-185-36071

Query Match 4.5%; Score 68.2; DB 6; Length 1685;

Best Local Similarity 46.9%; Pred. No. 3.8e-08;
Matches 248; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

QY 80 GCGTGCCACGAGCATATCCGCTCAACCGCTGGTATCTTCCGCGGCTCTTTG 139
DB 1352 GCCAGGCGAGCGCTATCTCTATCTCTTTATCTATCTCCGCTGCTGGGCTCT 1293
QY 140 TCGCAACATAGTGTCTGGGCTAGTGTGTCAGCGCAAGCCGCACTGTGAGTGACCA 199
DB 1292 GTGGGAATCTCAATGTCATCTAGTATCTCTGGCTAACCAAGATGAAGACGGCCACCA 1233
QY 200 ACCGTTTATCTTTAACTCTCTCTGTCACCGACTGTGAGATTTGCTGTGGCCCT 259
DB 1232 ACATCTACATCTCTCAACCTGGCCATGCGCAATGAGCTGTCTAT--GCTACGTCCT 1176
QY 260 GGGTGTGACCACTCTGTGCTCTCTTGTGGCCCTCAACAGCACTTGTGACGCGCC 319
DB 1175 TCTGTATCACTCTCAATGCTCTTCCGCACTGAGCCCTTGGCGGCTACTCTGCGCTG 1116
QY 320 TGGTATGCTCAACCACTGTTCGCTTGGCGAGGTCACCAACATTTGTTGTGTCAG 379
DB 1115 TGGTATGCTCAACCACTGTTCGCTTGGCGAGGTCACCAACATTTGTTGTGTCAG 1056
QY 380 TGGATGCTACTTGTCTATCATCATCTCTCTCTCACTCTCTCAAGATGACCAAGCCG 439
DB 1055 TGGATGCTACTTGTCTATCATCATCTCTCTCTCACTCTCTCAAGATGACCAAGCCG 996
QY 440 GGGTATGCTCAACCACTGTTCGCTTGGCGAGGTCACCAACATTTGTTGTGTCAG 499
DB 995 TGGCAAGTGTGTAATGTGGGCTGTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 936
QY 500 TCTACGCTGTGGGCGAGCGCTTGTGATGAGCGCAATCTCTGCTCATGATCTGGG 559
DB 935 TGGTCTTCTGTGGGCGAGCGCTTGTGATGAGCGCAATCTCTGCTCATGATCTGGG 876
QY 560 GGGCGACCCCGAGCTACATATTCTCAGCGTGTCTCTTATGCTGAT 608
DB 875 CCGAGCGCCCGAGCGCTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 827

RESULT 4

US-10-750-185-44031/c
; Sequence 44031, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: RANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44031
; LENGTH: 3372
; TYPE: DNA
; ORGANISM: Bovine 19866881908619
US-10-750-185-44031

Query Match 4.1%; Score 63; DB 6; Length 3372;
Best Local Similarity 45.6%; Pred. No. 1,1e-06;
Matches 222; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

QY 131 CCTCTTTCGTGGCAACATAGTGTGCTGTGGCTGTGCTGTGCTGTGCTGTGCTGTG 190
DB 2232 CCATCTGTGTGGCAACATAGTGTGCTGTGGCTGTGCTGTGCTGTGCTGTGCTGTG 2173

Oy	191	AGTGTGACCAACCGCTTTTATCTTTAACTCTGTGTACCGAGCTGTGTGAGATTTGGCTG	250
Db	2172	CCCCCATGTATCTTCTGTCTCGCAACCTCTCCGCTTGTGACATCTGTCTTCTCCATCA	2113
Oy	251	TGGCCCCCTGGGTGGTGGACCACTCTGTGCTCTCTTCTGTGCCCCCTCAAGCCACATTC	310
Db	2112	CCGCCCCCAAGTCTCTGTGACCTCTCTTTAGAGAGAAAGACCATCTCTTCCATGGCT	2053
Oy	311	GCAAGGCCCTGTGTTAGCTCAACCACTGTTCGCTTGTGCCAGGTGTCAACCATGTCT	370
Db	2052	GCTTCACCGAATGTTTTCTTTCACCTCTCTGGGGGTGCAGACATCTTCTCTCTCG	1993
Oy	371	TGTTGTCAGTGGATGTGCTACTTGTTCATTCACACCTCTCTCTACCCGTCGAAGTGA	430
Db	1992	TCAATGGCTTTTGAACAGTACGTGGCCATCACTAAGCCCTTCACCTAGCGTCCGTATGA	1933
Oy	431	CCAGCGCGCGGGTTACCTGTCTCTATATGACACTGTGATGTGGCCATCTGTGAGACA	490
Db	1932	GTCAGGGGGGTGACATGCTCCTCATGTGGGCTCTGTGGGGGGGGGGTGTGTCCACATCCA	1873
Oy	491	CTCTCCACTTACGGCTGGGCGCCAGGTGCTCTTGAATGAGCGCAATGCTTCTGTCTCA	550
Db	1872	TCTGTGCAATCTCCCTGTACTTCCCCCTCCCTTCTGTGACCGAAGCTCTGTGACCTT	1813
Oy	551	TGATCTGGGGGGCCAGCCCCAGACTATATTCAGCGGTGTGCTCTTACGTGCATATTC	610
Db	1812	TCTACTGGGAGGTCCCCCAGGTCTCAACATTGGCTGTGACGAGACATGTGTCTTGTAGC	1753
Oy	611	CACGTGAT 617	
Db	1752	TCTGTAT 1746	

```

RESULT 5
US-11-121-086-5
; Sequence 5, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567, 570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 153376
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-5

Query Match      3.8%; Score 57.8; DB 7; Length 153376;
Best Local Similarity 46.1%; Pred. No. 9.8e-05;
Matches 194; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

QY       702   GGAAAGTCGAGTCAAGACTGTGTGGAGAATGAGATGAAGAAGGAGCAGAGAAGAAGA    761
Db        15679  GGAGGAGGAGGAAACAGAGAGAGGAGGAGGAGGAACAAGAGAGAGAGAGAGAAACAGAGAGAGGA    15738

QY       762   GGAATTCCAGAGATAGAGCTGAGTTTGCGGCCGCAGCATGAAGGTGAGAGTCAAGGCCCAAAGA    821
Db        15739  GGAGGAAACAGAGAGAGAGAGAGGAACAGAGAGAGGAGAGAGAGGAACAGAGAGAGAGAGA    15798

QY       822   GGGCAGATGGAGACCAGAGCGGCAAGCTGAAAGGCCCAAGGAAGGAAGCAGCGGAGCACAG    881
Db        15799  GGAACAGAGAGAGAGAGAGGAACAAGGTGCTTAGACAACATGTGGGGAAGCTCCCAAGATGCCAG    15858

QY       882   TGAGAGTAGTGTAGAGGCCACAGGGCAGACGAGGAGGTTCAGAGAGACAGCAACGGTGGCCAG    941

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[illegible]

RESULT 6					
US-11-121-086-8					
; Sequence 8, Application US/11121086					
; Publication No. US20050266459A1					
; GENERAL INFORMATION:					
; APPLICANT: POULSEN, TIM S.					
; APPLICANT: NIELSEN, KIRSTEN V.					
; TITLE OF INVENTION: NOCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES					
; FILE REFERENCE: 09138, 6000-00000					
; CURRENT APPLICATION NUMBER: US/11/121, 086					
; PRIOR FILING DATE: 2005-05-04					
; PRIOR APPLICATION NUMBER: 60/567,570					
; PRIOR FILING DATE: 2004-05-04					
; NUMBER OF SEQ ID NOS: 107					
; SOFTWARE: PatentIn version 3.3					
; SEQ ID NO 8					
; LENGTH: 246960					
; TYPE: DNA					
; ORGANISM: Homo sapiens					
US-11-121-086-8					
Query Match: 3 8%; Score 57.6; DB 7; Length 246960;					
Beet Local Similarity 49.5%; Pred. No. 0.00013;					
Matches 181; Conservative 0; Mismatches 179; Indels 6; Gaps 1;					
QY	119	TCTTCCTGCGCGCCCTTTTGGGCAACATAGTGTGAGCTGAGCTGAGTGAGCGCAACC	178		
Db	120678	TCATTTCTCTCTGGGCGGTGATGGCAACGTCCTGTGTGATCCTGGAGCGGCACC	120737		
QY	179	GCGACCTGCTGCAAGGTGACCAACCGTTTTATCTTTAACTCTCTCGTACCGACTGCTGC	238		
Db	120738	GGCAACACGCGAGTTCCAGCGAGACCTTCCTGTTCACCTGGCCGCGGCGCACCTCTGC	120797		
QY	239	AGATTTCCTGTGTGCCCTCCCTGGGTGTGGCCACTCTGTGTCTCTTTTGGCCCCCTCA	298		
Db	120798	TGTCCTCATCTTGGCTTTTGGCCGTGGCCGCGAGGCGCTGTGTGG-----CTGGGTCTCG	120851		
QY	299	ACAGCACTTCGCGACCGGCCCTGTGTAACCTCACCAACCTGTTCGCTTCGGCAGCGTCA	358		
Db	120852	GGACCTTCTCTGCAAAACTGTGATGGCTTGCAAAAAGTCAACTTCTAATGACAGAGCC	120911		
QY	359	ACACCATGTCTTGGGTGCAGNGATGCTACTTGTCCATCATCCACCCTCTCTCTAAC	418		
Db	120912	TGCTCTGAGCTGATCGCCGCTGAGACCGCTTACTGCGCATTTTCCAAGCGCTCATGCTT	120971		
QY	419	CGTCCAGATGACCCGAGCGCGCGGTACCTGCTCCTGTATGGCACTTGATTTGGCCA	478		
Db	120972	ACCGCAACCGCGCGCTCCTCTCATTCACATACCTGTGGGACCAATCTGGCTGTGGGCT	121031		
QY	479	TCCTGC	484		
Db	121032	TCCTGC	121037		

```
RESULT 7
US-10-750-185-26865/c
; Sequence 26865, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26865
; LENGTH: 1207
; TYPE: DNA
; ORGANISM: Bovine 1986881057836
US-10-750-185-26865

Query Match      3.6%; Score 55.6; DB 6; Length 1207;
Best Local Similarity 46.2%; Pred. No. 5.9e-05;
Matches 184; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 93 CATCATCCGCTCAACCGCTGTGTTATCTTCTGCGCGCTCTTTGTCGGCAACATAGT 152
DB 678 CATGTCCTCTTGTCTCTGTCCTGCTATTTACGACCATATGATGGGAATGAC 619
QY 153 GCTGGCGCTAGTGTGACGGCAAGCCGACGCTGTCAGAGTACCAACCGTTTATCTT 212
DB 618 TTATGAGCTGCTCATCTCCCGGACTCCAGGCTCACTCATATGATCTGCTCCG 559
QY 213 TAACCTCTCGTCAACGACCTGTCGAGATTTCGCTGTGCGCCCTGGGTGGTGGCCAC 272
DB 558 TGTCTCTCATGTTATGACATGGGGCTGTCCACAGTATTCGCCAGTTGCTGGCCCA 499
QY 273 CTCTGTCCTCTCTTCTGCGCCCTCAACAGCACTTTCGACGCGCCCTGTGTTACCTTAC 332
DB 498 TCTGTCACCTACGACCGACCATTCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
QY 333 CAACCTGTTCGCTTCCGACGCTCAACACCATTTGTTCTGCTGCTGCTGCTGCTGCT 392
DB 438 TTATGTTTGGGTTACAGACACACTTGTATTCTATCATGAGCTCTGGATGATACAT 379
QY 393 GTTCATCATCCACCCCTCTCTCCATCCGTCAGATGACCCAGCGCGGCTTACCTGCT 452
DB 378 GGCATCTGTGACCTCTGACATTCATTCAGTGAATGCGCAATGCTGTCGCGCTT 319
QY 453 CCTCTATGACACCTGATTTGTGGCCATTCCTGACAGACA 490
DB 318 ACTGCGCTTCTGTTGGGTGTCTGTGTGACACACA 281

RESULT 8
US-10-502-893-1
; Sequence 1, Application US/10502893
; Publication No. US2005025529A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Healthcare AG
; APPLICANT: GOLZ, Stefan
; APPLICANT: Bruggemeier, Ulf
; APPLICANT: Geerts, Andreas
; TITLE OF INVENTION: Diagnostics and Therapeutics for Diseases Associated with a New
; FILE REFERENCE: Lea 35 827
; CURRENT APPLICATION NUMBER: US/10/502,893
; PRIOR FILING DATE: 2004-07-27
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; PRIOR APPLICATION NUMBER: PCT/EP03/000479
; PRIOR FILING DATE: 2003-01-20
; PRIOR APPLICATION NUMBER: EP 02001942.8
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1984
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-502-893-1

Query Match      3.6%; Score 55.4; DB 6; Length 1984;
Best Local Similarity 44.6%; Pred. No. 7.9e-05;
Matches 261; Conservative 0; Mismatches 321; Indels 3; Gaps 1;

QY 107 CCGTCTGCTATCTTCTTCCGCGCTCTTTGTGCGCAATAGTCTGGCGCTAGTGT 166
DB 559 CCGCGCTGCGCGCTGTCATGCGCTGACGCGCGCGCCAACTGCGCTGATGCGCGCTCA 618
QY 167 TGCAGCGCAAGCGGACGCTGACAGTGACCAACGTTTATCTTAACTCTTCGTCA 226
DB 619 TCTGACACTAGCCCGCGCTGCGCAACACTTCTTCTGCTGTGCTCTTACGT 678
QY 227 CCGACCTGCTGAGATTTCGCTGTGCGCCCTGCGGTGCGCACCTGCTGCTCTCT 286
DB 679 CTGACCTGATGAGGGGCTGAGTGTATGCCCGCGCCATGCTGAACGGGCTGACGGG 738
QY 287 TCTGCGCCCTCAACAGCACTTCTGACGCGCCCTGTTAGCTTACCTACCACTGTTGCGCT 346
DB 739 GCTGGGTGCTGGCGCGCGCTCTGCTCTCTGACCGCCCTTCGACGATGATGCTGCA 798
QY 347 TGGCCAGGCTCAACCACTTGTCTTGTGCTGAGTGAATGCTACTTGTCAATCATCACC 406
DB 799 GCGCTCTCACTCTCAACTCTGTCTATAGCTGACCGCTTACCTGCTCATCTCTCG 858
QY 407 CTCTCTCTTACCCGCTTCAAGATGACCCAGCGCGGCTTAACTGCTCTCTATAGGACCT 466
DB 859 CGGTGGCTCAACAGCTGGCGCATGAGCGCCCTGCGTCCCTGAGCCATGATCTGAGGCGCT 918
QY 467 GGA---TTGTGACATCTGACAGACACTCTCTCACTTACGCGCTGGGCGCAGGCTGCT 523
DB 919 GGAGCTTCCCGCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 978
QY 524 TTGATGAGGCAATGCTCTCTCTCATATATGTGGGGGCGAGCCCGACCTACATATTC 583
DB 979 ACGACAGGACACCCGCTCTGCGCAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 584 TCAGCGTGTGCTTCTCATGCTATTCATTCAGATTTGTCAATGCTGCTGCTACTCCGTG 643
DB 1039 TGGCGTGGGCTCACTTCTCTGCTCTGCGGATGCCATATGCTTACCTACTGACAGA 1098
QY 644 TGTCTGTCAGCCCGGAGGACAGATGCTCTGCTGTAATGTCA 688
DB 1099 TCTGTACTAGTCCCGCAAGAGCGCGTGCAGATGAGCTCTCTCA 1143

RESULT 9
US-11-170-153-9
; Sequence 9, Application US/11170153
; Publication No. US2005026629A1
; GENERAL INFORMATION:
; APPLICANT: DELBESNULDER, WILLY
; APPLICANT: WEBER, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
```

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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 9
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(942)
; OTHER INFORMATION: IGS4A truncated DNA long version
US-11-170-153-9

Query Match          3.5%; Score 53.8; DB 7; Length 1594;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

QY 37 AACACGAGCAGCAGCGATGCGCCCTCTCCAAATGCCATGACCTTGCGCCACGCGATC 96
   |||||
DB 133 AACAGACCGAGAGATATGCGCTTCTCTGCGACCTCGGCGCAGCCACTTCTTCTC 192
   |||||

QY 97 ATCCGCTCAACCGTGTGATATCTTCTCGCCGCTCTTTCTGCGCAACATAGTCTG 156
   |||||
DB 193 CCCGTGTGTGTGTATGTGCAATTTTGTGTGGGGTCAATTGGCAATGTCTGTG 252
   |||||

QY 157 GGGCTAGTGTGACAGCGCAAGCCGAGCTGCTGACGTACCAACCGTTTATCTTTAC 216
   |||||
DB 253 TGCCTGTGATTTCTGACAGACAGGCTATGAAGACGCCCAACTACTACTCTTTCAGC 312
   |||||

QY 217 CTCTCTGTCACGACCTGTGCAAGATTTGCTCGTGCCCTTGGGTGTGGCCACCTCT 276
   |||||
DB 313 CTGGGGGTCTTGACCTCTCTGCTCTGCTCTTGGAAATCCCTGAGGTCTATGAGATG 372
   |||||

QY 277 GTGCTCTTCTTGCGCCCTCAACAGCACTT---CTGACAGGCCCTGTGATACCTCACC 333
   |||||
DB 373 TGGCCCACTACCTTTCTTTGTGGGCCCGGTGGCTGTACTTCAAGAGGCCCTCTT 432
   |||||

QY 334 CACCTGTTCCTTGCGCCAGCGTCAACACCATTTGTGTGATGATGCTACTTGG 393
   |||||
DB 433 GAGACCGTGTGCTTGCGCTCAATCTTCAGCATCACCAGCTGAGGTGAGGCTACGTG 492
   |||||

QY 394 TCCATCATCAACCTCTCTCTCTACCCGCTCAAGATGACCCAGCGCGGTTTACCTGCTC 453
   |||||
DB 493 GCCATCTTACACCCGTTCCGCCCAAACTGACAGACCCCGCGGCCCTCAGAGATC 552
   |||||

QY 454 CTCTATGGACCTGTGATTTGTGCCATCCT 482
   |||||
DB 553 CTCGGCATGCTGTGGGGCTTCTCCGTGCT 581
   |||||

RESULT 10
US-11-170-153-11
; Sequence 11, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 11
; LENGTH: 1594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
```

```
; LOCATION: (64)..(942)
; OTHER INFORMATION: IGS4A truncated DNA short version
US-11-170-153-11

Query Match          3.5%; Score 53.8; DB 7; Length 1594;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

QY 37 AACACGAGCAGCAGCGATGCGCCCTCTCCAAATGCCATGACCTTGCGCCACGCGATC 96
   |||||
DB 133 AACAGACCGAGAGATATGCGCTTCTCTGCGACCTCGGCGCAGCCACTTCTTCTC 192
   |||||

QY 97 ATCCGCTCAACCGTGTGATATCTTCTCGCCGCTCTTTCTGCGCAACATAGTCTG 156
   |||||
DB 193 CCCGTGTGTGTGTATGTGCAATTTTGTGTGGGGTCAATTGGCAATGTCTGTG 252
   |||||

QY 157 GGGCTAGTGTGACAGCGCAAGCCGAGCTGCTGACGTACCAACCGTTTATCTTTAC 216
   |||||
DB 253 TGCCTGTGATTTCTGACAGACAGGCTATGAAGACGCCCACTACTACTCTTTCAGC 312
   |||||

QY 217 CTCTCTGTCACGACCTGTGCAAGATTTGCTCGTGCCCTTGGGTGTGGCCACCTCT 276
   |||||
DB 313 CTGGGGGTCTTGACCTCTGCTCTGCTCTTGGAAATGCCCTGAGGTCTATGAGATG 372
   |||||

QY 277 GTGCTCTTCTTGCGCCCTCAACAGCACTT---CTGACAGGCCCTGTGATACCTCACC 333
   |||||
DB 373 TGGCCCACTACCTTTCTTTGTGGGCCCGGTGGCTGTACTTCAAGAGGCCCTCTT 432
   |||||

QY 334 CACCTGTTCCTTGCGCCAGCGTCAACACCATTTGTGTGATGATGCTACTTGG 393
   |||||
DB 433 GAGACCGTGTGCTTGCGCTCAATCTTCAGCATCACCAGCTGAGGTGAGGCTACGTG 492
   |||||

QY 394 TCCATCATCAACCTCTCTCTCTACCCGCTCAAGATGACCCAGCGCGGTTTACCTGCTC 453
   |||||
DB 493 GCCATCTTACACCCGTTCCGCCCAAACTGACAGACCCCGCGGCCCTCAGAGATC 552
   |||||

QY 454 CTCTATGGACCTGTGATTTGTGCCATCCT 482
   |||||
DB 553 CTCGGCATGCTGTGGGGCTTCTCCGTGCT 581
   |||||

RESULT 11
US-11-170-153-1
; Sequence 1, Application US/11170153
; Publication No. US20050266529A1
; GENERAL INFORMATION:
; APPLICANT: DELERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: LOKEN, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; PRIOR FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4A long version
US-11-170-153-1

Query Match          3.5%; Score 53.8; DB 7; Length 1658;
Beet Local Similarity 46.5%; Pred. No. 0.00019;
Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
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```
QY 37 AACAGACGCCACACGTGCATGCCCTCTCCAAATGCCCATCAGCTCGGCCACGGGATC 96
    |||||
DB 133 AACAGACCGAGAGATATCGGCTTCTCTCGGGAACCTCGGCGCAGCCACTTCTTCTC 192
QY 97 ATCCGCTCAACCGTGGGTATCTTCTCGGCGCTCTTTGCTGGCAACATAGTCTG 156
    |||||
DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
QY 157 GCGCTAGTGTGAGCGCAAGCCGACGTGCTGACAGTGAACCAACGTTTATCTTTAAC 216
    |||||
DB 253 TGCCTGTATTTGTGAGACACGAGGTATGAAGACGCCCACTACTACTCTTCAAG 312
QY 217 CTCCTGTCAACGACCTGTGCAAGATTTGCTGTGGCCCTCGGGGTGTGGCACTCT 276
    |||||
DB 313 CTGGCGGTCTGTACCTCTGCTGCTGCTCTTGAATGCCCTGAGAGGTCTATGAGATG 372
QY 277 GTGGCTCTCTTGTGGCCCTCAACAGCCACTT---CTGACAGGCCCTGTAGCTTACCTAC 333
    |||||
DB 373 TGGCGCACTACCTCTTCTTGTGTGGGCCCGGTGGCTACTTCAAGAGCGCTCTTT 432
QY 334 CACCTGTGCGCTTTCGCGACGCTCAACACCATTTGTGTGATGATGCTACTTGG 393
    |||||
DB 433 GAGACCGTGTGCTTCCGCTTCATCTCAGCATCACACCGTCAAGCTGTGAGCGCTACG 492
QY 394 TCCATATCCACCCCTCTCTCTTCCACCGGTCCAGATGACCCAGCGCGCGGTACTGCTC 453
    |||||
DB 493 GCCATCTTACACCGTTCGCGCAACATGACAGACCCGCGCGCGCTCAGAGATC 552
QY 454 CTCATATGCACTGTGATTTGGCCATCT 482
    |||||
DB 553 CTGGCATGTCTTGGGGCTTCTCCGTGCT 581
    |||||
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RESULT 12

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US-11-170-153-3
; Sequence 3, Application US/11/170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: BERGER, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(1299)
; OTHER INFORMATION: IGS4A short version
US-11-170-153-3
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Query Match 3.5%; Score 53.8; DB 7; Length 1658;

Best Local Similarity 46.5%; Pred. No. 0.00019;

Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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QY 97 ATCCGCTCAACCGTGGGTATCTTCTCGGCGCTCTTTGCTGGCAACATAGTCTG 156
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DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
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QY 217 CTCCTGTCAACGACCTGTGCAAGATTTGCTGTGGCCCTCGGGGTGTGGCACTCT 276
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DB 313 CTGGCGGTCTGTACCTCTGCTGCTGCTCTTGAATGCCCTGAGAGGTCTATGAGATG 372
QY 277 GTGGCTCTCTTGTGGCCCTCAACAGCCACTT---CTGACAGGCCCTGTAGCTTACCTAC 333
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QY 394 TCCATATCCACCCCTCTCTCTTCCACCGGTCCAGATGACCCAGCGCGCGGTACTGCTC 453
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QY 454 CTCATATGCACTGTGATTTGGCCATCT 482
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DB 553 CTGGCATGTCTTGGGGCTTCTCCGTGCT 581
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RESULT 13

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; Sequence 5, Application US/11/170153
; Publication No. US2005026529A1
; GENERAL INFORMATION:
; APPLICANT: DELEERSNIJDER, WILLY
; APPLICANT: WEESP, GUY NYS
; APPLICANT: VENEMA, JAKOB
; APPLICANT: BERGER, CLAUDIA
; APPLICANT: BERGER, CHRISTIANE
; TITLE OF INVENTION: HUMAN G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 01975-0034
; CURRENT APPLICATION NUMBER: US/11/170,153
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: US/10/088,744
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 1658
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (55)..(1299)
; OTHER INFORMATION: IGS4B long version
US-11-170-153-5
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Query Match 3.5%; Score 53.8; DB 7; Length 1658;

Best Local Similarity 46.5%; Pred. No. 0.00019;

Matches 209; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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DB 133 AACAGACCGAGAGATATCGGCTTCTCTCGGGAACCTCGGCGCAGCCACTTCTTCTC 192
QY 97 ATCCGCTCAACCGTGGGTATCTTCTCGGCGCTCTTTGCTGGCAACATAGTCTG 156
    |||||
DB 193 CCGGTGTCTGTGTATGTGCAATTTTGTGTGGGGGTCAATGGCAATGTCTGTG 252
QY 157 GCGCTAGTGTGAGCGCAAGCCGACGTGCTGACAGTGAACCAACGTTTATCTTTAAC 216
    |||||
DB 253 TGCCTGTATTTGTGAGACACGAGGTATGAAGACGCCCACTACTACTCTTCAAG 312
QY 217 CTCCTGTCAACGACCTGTGCAAGATTTGCTGTGGCCCTCGGGGTGTGGCACTCT 276
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DB 313 CTGGCGGTCTGTACCTCTGCTGCTGCTCTTGAATGCCCTGAGAGGTCTATGAGATG 372
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 23:55:52 ; Search time 4324 Seconds
(without alignments)
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Sequence: 1 atgacgctccactgcacacaa.....attcgcctactcttccttga 1527

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_esc11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	268.4	17.6	644	BY723772	BY723772 BY723772
3	227.4	14.9	646	CNS0490M	AL280651 Tetradon
4	184.6	12.1	641	CKX24611	CKX24611 1307373 N
5	176.6	11.6	620	BY724046	BY724046 BY724046
6	156.6	10.3	722	DR860076	DR860076 JGI CABG4
7	141.6	9.3	645	CO934586	CO934586 AGENCOURT
8	122.8	8.0	1064	CNS03V11	AL282450 Tetradon
9	107	7.0	1587	AY421262	AY421262 Mus muscu
10	98.6	6.5	1590	AY421261	AY421261 Pan trogl
11	97	6.4	1590	AY421260	AY421260 Homo sapi
12	94.4	6.2	793	DO032256	DO032256 Homo sapi
13	92.2	6.0	721	CP147813	CP147813 AGENCOURT
14	88.8	5.8	768	DO032257	DO032257 Pan trogl
15	88.4	5.8	386	AI457674	AI457674 l348f06.x
16	87.2	5.7	679	CNS075427	CNS075427 EC2BBA10A
17	85.6	5.6	722	CP147810	CP147810 AGENCOURT
18	85	5.6	802	CK843215	CK843215 JGI CAK1
19	84.8	5.6	979	CNS0484L	AL279030 Tetradon
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21	84	5.5	1401	AY399426	AY399426 Homo sapi
22	83.4	5.5	853	AY409236	AY409236 Homo sapi

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C	25	80.4	5.3	803	7	CK146110	CK146110 AGENCOURT
C	26	78.6	5.1	729	8	DR003001	DR003001 TC108456
C	27	78.4	5.1	677	2	BB626313	BB626313 BB626313
C	28	78.4	5.1	1818	4	AK034239	AK034239 Mus muscu
C	29	78	5.1	637	6	CD618076	CD618076 Mus muscu
C	30	77.8	5.1	705	7	CO959341	CO959341 AGENCOURT
C	31	77.4	5.1	640	6	CD618070	CD618070 56030361H
C	32	77.4	5.1	640	6	CD618071	CD618071 56030361H
C	33	77.4	5.1	1052	10	AY407664	AY407664 Homo sapi
C	34	76.2	5.0	682	7	CO959039	CO959039 AGENCOURT
C	35	75.8	5.0	1046	10	AY407666	AY407666 Mus muscu
C	36	75.6	5.0	997	10	CNS005TE	AL060767 Drosophila
C	37	74.8	4.9	1072	10	AY398881	AY398881 Pan trogl
C	38	74.8	4.9	1708	4	AY325170	AY325170 Rattus no
C	39	74.6	4.9	498	3	BM090260	BM090260 505437 MA
C	40	74.2	4.9	608	5	BY724644	BY724644 BY724644
C	41	74.2	4.9	4435	4	AK049671	AK049671 Mus muscu
C	42	73.8	4.8	662	7	CN721896	CN721896 E0831F01
C	43	73.6	4.8	969	10	AY407665	AY407665 Pan trogl
C	44	73.4	4.8	987	10	CNS00418	AL06537 Drosophila
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ALIGNMENTS

RESULT 1
BB179791
LOCUS
DEFINITION
BB179791 RIKEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230080M06 3', mRNA sequence.

ACCESSION
BB179791.2 GI:16269966

VERSION
EST.

KEYWORDS
SOURCE

ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8838874.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagui, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsubara, S., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., and Hayashizaki, Y.

Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, T., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

FEATURES

Source

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/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A230080N06"
/sex="male"
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/clone_lib="RIKEN full-length enriched, adult male
hypothalamus"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGATCCCAAGCTCTTTTCTTTTCTTTTNN 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAATCTCGAGTATTAATTAATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

ORIGIN

Query Match 19.4%; Score 296.4; DB 1; Length 655;
Best Local Similarity 81.3%; Pred. No. 2.8e-60;
Matches 361; Conservative 0; Mismatches 71; Indels 12; Gaps 1;

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1156 AACCTCTCTGCGCAGGTGTAACAGTGAAGTGTAAAGTATTCATCATTT 1215
120 GACCCACCTTTGCTTCATGTATAGTGCAAGCTGAGAGTATCTTCTCATCATTT 179
1216 TTCTCTATGTCATTCCTGGGGGCTTATTTTGTAGCATCTCTGGCCGTGGGG 1275
180 TCCACTTATGTCATTCCTGGGGGCTTATTTTGTAGCATCTCTGGGGGTG 239
1276 GATGTCGAAGACCCAGTACCCAGTGGGTATCAACATATCATCTGGCTTTCTCTG 1335
240 GATATTCGATCCAGGATACCCAGTGGGTATCAACATATCATCTGGCTTTCTCTG 299
1336 CAGTCTGATCCACCCATATGCTATGCTCATGCAACAGCAATTAAGAAGAAATC 1395
300 CAGTGTGATCCACCCATATGCTATGCTCATGCAACAGCAATTAAGAAGAAATC 359
1396 CAGGACATGCTAAGAAAGTTCTTTCGCAAGGAAAAAGCCCCGGAAGAAGATGCCACCA 1455
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Db 360 CAGGAGTCTGAGAGAAATTAATCTGTAAAGAAAGCCCCCTGTGAAGATACCACTT 419
QY 1456 GACCTG-----CCGAAACAGAGGTGGAGCTGAAGGCAAGATTTCCCTTCC 1503
Db 420 GACCTTCATGAAGCAGGAGCTGTACAGAGGAGTATGAAGCGAAGCTGTCCCTCC 479
QY 1504 TAGCATTCGCTACTTTTCTTTGA 1527
Db 480 CATGATTCAGCATCTTCACTTAA 503

RESULT 2

BY723772 644 bp mRNA linear EST 17-DEC-2002
LOCUS BY723772 RIKEN full-length enriched, adult male hypothalamus Mus
DEFINITION musculus cDNA clone A230027F20 5', mRNA sequence.

ACCESSION BY723772
VERSION BY723772.1 GI:27135689
KEYWORDS EST.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 644)
Ozekaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bul, C.,
Hume, D. A., Quackenbush, J., Schirral, L. M., Kanapin, A., Matcude, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brasic, V.,
Chochois, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Glessi, C., Godzik, A., Gough, J., Grimmond, S.,
Guernich, S., Hirokawa, N., Jackson, J., Jarvis, E. D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Namat, K., Okido, T., Pavan, W. J., Petrea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramchandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Sempke, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watande, Y.,
Wells, C., Wilming, L. G., Wymshaw-Boris, A., Yangisawa, M., Yang, T.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arikawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Iehi, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL PUBMED 12466851

COMMENT CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-ree@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P.,
Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
Imocani, K., Iehi, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Kono, H., Koye, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numasaki, R., Ohno, M., Osato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watanabe, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with

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/note="Vector: pCS107; Site 1: EcoRI; Site 2: XhoI; The library was prepared from 5 ug of poly A+ RNA by oligo-dT priming (5'-ACTAGTGGCGGCGCTAGAGCCCTCGAGTTTCTTTTCTTTT-3') and Stratascript reverse transcriptase. After ligation of EcoRI adapters (5'-AATTCGACGAGG-3') followed by kinasing adapters and by XhoI digestion, the cDNA was size selected by chromatography on Sepharose CL-2B columns and fractions containing cDNAs larger than 1000 bp were ligated into EcoRI/XhoI-digested pCS107. Reference for library construction: Current Genomics 4, 635-644. Library constructed by Michelle Tabb and Bruce Blumberg (Dept of Developmental and Cell Biology, University of California, Irvine)."

ORIGIN

Query Match 10.3%; Score 156.6; DB 8; Length 772;
Best Local Similarity 60.3%; Pred. No. 1.5e-26;
Matches 258; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

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Qy 203 GTTTATCTTTAACCTCTGTCACCGACTGCTCAGATTTCGCTGCGGCGCTGGG 262
Db 465 GATTTATTTTCACTCTGCTGAGTGTCTTCTGACAGACTTTGGTTAGCTTTGG 524
Qy 263 TGGTGGCACTCTGTGCTCTCTTCTTGGCCCTCAACAGCCATCTTGCAGGCGCT 322
Db 525 TCATGTTTACCTCCCTCCGTGATCTGCGCCCTTGGATATAGTCTTTGTGAGAGAG 584
Qy 323 TTAGCTTACCCACCTGTTGCTTGGCAGCGTCAACGCAATGTTGTTGTCAGTGG 382
Db 585 TGGTCTATATGATTTATTTGATTTGACGAGATTAACATCAAGTTGTTTGTGG 644
Qy 383 ATCGTACTTGTTCATCTCCACCTCTCTCTTACCGGTCAGAGATGACCGCGCGG 442
Db 645 ACAATATCTGGCCATATTCATCTTTGTCTATATCCCAAGATGACCCCAAGAGAG 704
Qy 443 GTTACCTGCTCTCTTATGAGCAGCTGATTTGGCAGATCTGTGAGACATCTCT 502
Db 705 GAAGCTTCTGATATTTGACCTTGATTTTCAGTGTCTCTCCANAGACACCTCTCT 764
Qy 503 ACGGCTGG 510
Db 765 ATGGCTGG 772

RESULT 7
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LOCUS CO934586
DEFINITION IMAGE:7262003 5', mRNA sequence.
ACCESSION CO934586
VERSION CO934586.1 GI:51289263
KEYWORDS EST.
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
REFERENCE 1 (bases 1 to 645)
NIH-MGC <http://mgc.mci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-remail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
Plate: IRB16 row: a column: 09
High quality sequence stop: 170.
Location/Qualifiers
1. 645

FEATURES

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/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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A Note: this is a NIH_MGC Library."

ORIGIN

Query Match 9.3%; Score 141.6; DB 7; Length 645;
Best Local Similarity 87.0%; Pred. No. 6.1e-23;
Matches 167; Conservative 0; Mismatches 24; Indels 1; Gaps 1;

Qy 1 ATGAGTTCACCTGACCAAGACGAGGAGTAACAGCCAGACGATGATGCC 60
Db 39 ATGAGTTCACCTGACCAAGACGAGGAGTAACAGCCAGACGATGATGCC 98
Qy 61 CTCTCAAAATGCCCATGAGCTGGCCCAAGCATATCCGCTCAACCGTCTGTTATC 120
Db 99 CTCTCAAAATGCCCATGAGCTGGCCCAAGCATATCCGCTCAACCGTCTGTTATC 158
Qy 121 TTCTGCGCGCC-TCCTTGTGCGGACATATGCTGCGCTAGTGTTCAGAGCCAGCC 179
Db 159 TTCTGCGCGCCCTTCTTTCATCAAAATATAGTATGATGAGTAGAGTCTACTCC 218
Qy 180 GCAGCTGCTGCA 191
Db 219 ACATCTCAAGCA 230

RESULT 8
CNS03V11
LOCUS CNS03V11 1064 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetradon nigroviridis genome survey sequence PUC-Orl end of clone 062121 of library G from Tetradon nigroviridis, genomic survey sequence.
ACCESSION AL262450.1 GI:7984076
VERSION AL262450.1
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neopteleostei;
Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1

AUTHORS Roest Croillius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brothier, P., Quetier, F., Saurin, W., and Weissenbach, J.

TITLE Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence

JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

REFERENCE PUBMED 10835645

AUTHORS 2

TITLE Roest Croillius, H., Jaillon, O., Dasilva, C., Ozouf-Coetaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

JOURNAL Characterization and repeat analysis of the compact genome of the freshwater pulmonate Tetradon nigroviridis

REFERENCE PUBMED 10899143

AUTHORS 3 (bases 1 to 1064)

TITLE Genome Res. 10 (7), 939-949 (2000)

JOURNAL Direct Submission

REFERENCE PUBMED Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

AUTHORS This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradon.

COMMENT Location/Qualifiers

FEATURES source 1..1064 /organism="Tetradon nigroviridis" /mol_type="genomic DNA" /db_xref="taxon:99883" /clone="062121" /clone_1lb="cg" /note="Genoscope sequence ID : COBG062A11SP1 end : PUC-Orig"

ORIGIN

Query Match 8.0%; Score 122.8; DB 11; Length 1064; Best Local Similarity 60.9%; Pred. No. 2.3e-18; Matches 196; Conservative 2; Mismatches 124; Indels 0; Gaps 0;

QY 379 GTGGATCGCTACTTGTTCATATCCACCTCTCTCTCAACCCGTCGAAGATGACCCAGCC 438

DB 8 KTGATCGCTACCTGGCTATCATACACCCGCTGCTATCCACCCGTATGACCCCTCAC 67

QY 439 CGGGTTACCTGCTCCATATGAGCAGTGGATTTGGCCATCTCGAGAGACATCCCTCA 498

DB 68 CTGGACACCAATGTATCATCTGACCTGGGTCTAGTCTACTGACAGACAGCCCC 127

QY 499 CTCTACGGCTGGGCGCAGGCTGCTTGTATGAGCGCAATGCTCTGCTTCATGATCTG 558

DB 128 CTCTAAGGCTGGGCGCAGGCTGCTTGTATGAGCGCGGTACAAAGTGTGCTGCTGTTGG 187

QY 559 GGGGCGAGCCCGACGTAATCTTCAGCGGTGTCTCTTCAATCGTCACTGATTT 618

DB 188 TCGTCAGGCTGTCTTCACTTCATCATGTGTGTCCACGTTGCTCTGCTGCTGTTGG 247

QY 619 GTCATGATTTGCTGCTACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 678

DB 248 ATATGTTGGGTGTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 307

QY 679 TACATGTCTAAGAGACAGACT 700

DB 308 CACCCCATACAGACGCAATCTT 329

RESULT 9

AY421262 1587 bp DNA linear GSS 12-DEC-2003

LOCUS Mus musculus HCM7498 gene, VLRUAL, TRANSCRIPT, partial sequence, DEFINITION

ACCESSION AY421262

VERSION AY421262.1 GI:397777219

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE PUBMED 14671302

AUTHORS 2 (bases 1 to 1587)

TITLE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferriere, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.

JOURNAL Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

REFERENCE PUBMED Science 302 (5652), 1960-1963 (2003)

AUTHORS 2 (bases 1 to 1587)

TITLE Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B., Ferriere, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J., Adams, M.D. and Cargill, M.

JOURNAL Direct Submission

COMMENT Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence as made by sequencing genomic exons and ordering them based on alignment.

FEATURES source 1..1587 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>1587 /locus_tag="HCM7498"

ORIGIN

Query Match 7.0%; Score 107; DB 10; Length 1587; Best Local Similarity 48.6%; Pred. No. 1.6e-14; Matches 293; Conservative 0; Mismatches 310; Indels 0; Gaps 0;

QY 106 ACCGTCCTGGTATCTTCTCTCGCCGCTCTTTCGTGCGCAATAGTGGCGCTAGTG 165

DB 91 ATGCGCATCATCATCATCATCTGCTCTTGTCTGCTGGGCACTGGTCAATTGTAGTCAC 150

QY 166 TTGACGCGAAGCCGAGCTGCTGACGAGTACCAACCGTTTATCTTTAACTCTCTGTC 225

DB 151 TTGTACAAAGTCTACCTCTCACCTCTCAGACGACAAAGTGTGCTTACAGCTGACCTTG 210

QY 226 ACCGACTGTGCAATTTGCTGCTGCGGCCCTGGTGGTGTGGCCACTTGTGCTCTC 285

DB 211 TCCAACTTCTGTGTGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 270

QY 286 TTCTGCCCCCAAGCAGCACTTCTGACGAGCCCTGTTAGCCTACCCAGCCTGTGCGC 345

DB 271 GAATGATTTTGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330

QY 346 TTGCGCAGCGTCAACCAATTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 405

DB 331 TCAGCCAGATGTGTACCTTGGGCTCATTTGTCATGATGTGTGTGTGTGTGTGTGTGT 390

QY 406 CCTCTCTCTTACCCGTCGCAAGATGACCCAGCCGCGGTAACTGTCTCTCTATGAGCAC 465

DB 391 CCAATGTGTATCCCCATGAAAGTACACAGGAAACCGAGTGTGTGTGTGTGTGTGTGTGT 450

QY 466 TGGATTGTGGCATCTCTGACAGCACTCTCCACCTACAGGCTGGGCGCAGGCTGCTTT 525

DB 451 TGGCTCCACTCTCTCTATTTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 510

QY 526 GATGAGCGCAATGCTCTCTCTCATGATGTGGGGGCGCAGCCCGACGTAATCTTCT 585

DB 511 GATGAGTTCAAAGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 570

QY 586 AGCGTGTGTCTCTTATCTGTATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 645

DB 571 TGGCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 630

QY 646 TTCTGTGCAAGCCCGGAGGACATGCTCTGTCTACATATGTACAGACACAGCTTGCA 705
|||
Db 631 TTCGGGAGGCGCCAGGAGTCAAGGCCCGGAAAGGTGACCTGTGCGACGGTGTCACTGTGAG 690
706 GTG 708
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Db 691 GAG 693

RESULT 10
AY421261 1590 bp DNA linear GSS 12-DEC-2003
LOCUS Pan troglodytes HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY421261
VERSION AY421261.1 GI:39777218
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pan.
REFERENCE 1 (bases 1 to 1590)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1590)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
location/Qualifiers
source 1..1590
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1590
/locus_tag="HCM7498"

ORIGIN
Query Match 6.5%; Score 98.6; DB 10; Length 1590;
Best Local Similarity 47.4%; Pred. No. 1.7e-12;
Matches 296; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

QY 84 GGGCCACGGCATCATCCGCTCAACCGTGTATCTTCCTCGCCGCTTTTGTCTCG 143
|||
Db 72 GGGCGTCATCATCACCCAGTTCATCGCCATTCATGTCATCACCATTTTGTCTGCTGG 131
144 CAACATAGTCTGGGCTAGTGTGTCAGGCAAGCCGAGCTGCTGAGTATACCAAGC 203
132 AAACCTGTGATCTGAGTCACTTGTACAAAGATCTTACCTCTCAACCTCAGCAACA 191
QY 204 TTTTATCTTTAATCTCTCTGTCACGACCTGTGTCAGATTTGCTGTCGTCGTCGCTGAGGT 263
Db 192 GTTCGCTTCAAGCTGAGACCTGTGCAACTTCTGCTGCTGCTGCTGCTGCTGCTTGT 251
QY 264 GGTGGCAGCTCTGTGCTCTCTCTTCTGCCCCCTCAACAGCCACTTTGCAAGGCGCTGT 323
Db 252 GGTGACGAGCTCATCCGACGAGGAATCTTTGTGTGTGTGTGTGTGCAACTTCTCTGC 311
QY 324 TAGCCATCAACCACTGTGCGCTTGGCAGGCGTCACACCATTTGCTGTGTCAGTGA 383
Db 312 CCTCTTACTGCTGATGATGAGCTGGCGCAGCATGCTTAACCTTGGGGTCAATGGCATGCA 371

QY 384 TGTCTATTTGTTCATCATCAACCTCTCTCTCTACCCGTCAGATGATCAAGCCGCGG 443
|||
Db 372 CCGTACTATGCTGTCTGTACCTGATACCCCATGATGAAGATCAGGGAACCGGAC 431
QY 444 TTAACCTGCTCTCTATGACACCTGTGATGTGGCCATCTCGACAGCACTCTCTCACTCA 503
Db 432 TGTGATGACACTTGTCTATCATCTGCTTCACTGCTCATCGGCTGCGCACCCCTGT 491
QY 504 CGGCTGGGCGCAGCGCTGCTTTGATGAGCGAATGCTCTGCTCCATGATCTGGGGGAC 563
Db 492 TGTGTGTATCCCGTGAGATTGACAGATTTCAAAATGATGTGTGGCTGTGGCACCG 551
QY 564 CAGCCCACTACACTATTTCTACGCGTGTCTTCAATGCTATTCACATGATTTGAT 623
Db 552 GGAGCTGCTACACAGCGCTTCTGGCAGATGCTGTGTGCTCCCTTCCCTTCTGTGAT 611
QY 624 GATTGCTGTATCTCCGCTGTGTGTGTGTGCAAGCCGAGGACGCAATGCTGTCTTACA 683
Db 612 GCTGTGTGTATGAGCTTATCTTCCGCTGGCCAGGCTCAAGGCAAGGTCAGCTG 671
QY 684 TGTCAAGACACACAGCTTGAAGTG 708
Db 672 TGGCAGCTGTTATCTGTGAGAG 696

RESULT 11
AY421260 1590 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM7498 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY421260
VERSION AY421260.1 GI:39777217
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 1590)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
TITLE JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1590)
Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
location/Qualifiers
source 1..1590
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1590
/locus_tag="HCM7498"

ORIGIN
Query Match 6.4%; Score 97; DB 10; Length 1590;
Best Local Similarity 47.2%; Pred. No. 4.2e-12;
Matches 295; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 84 GGGCCACGGCATCATCCGCTCAACCGTGTATCTTCCTCGCCGCTTTTGTCTCG 143
|||

Db 72 GGGCGTCATCATCACCAGTTCATGCCATCATGTTCATCACCATTGTTGTCGCTGGG 131
QY 144 CAACATAGTGTGCGCGCTAGTGTTCAGCGCAAGCCGACGTGTCAGGTGACCAAGC 203
Db 132 AAACCTGTGATGTGTGTACCTTTGACAGAAAGATCTTACCTTCAACCTCAGCAACA 191
QY 204 TTTTATCTTTAACTTCCTGTCACCGACCTGTGACAGATTTTCGCTGTGGCCCCCTGGGT 263
Db 192 GTTCGCTTCAGCTGACCTGTGCAAACTTCGCTGTGCTGCTGTGTGTGCTTCTTGT 251
QY 264 GGTGGCACCTCTGTGCTCTCTTCTGCGCCCTCAACAGCACTTTCGACGCGCCCTGCT 323
Db 252 GGTGACGAGCTTCATCCGACGAGGAATGATCTTTGTGTGTGTGTGTGCAACTTCTCTCG 311
QY 324 TAGCCCTACCCACCTGTGCGCTTCGCGACGCGTCAACCATTTGTGTGTGTGACGTGA 383
Db 312 CCTCTCTTACCTGTGATGAGCTTGTGACAGATGTAACCTTGGGGTCACTTCCATCGA 371
QY 384 TGGCTACTTGTCCATCATCCACCTCTCTCTTCCATCCGTCAGATGACCCAGCGCGCG 443
Db 372 CCGCTACTATGCTGCTCTGTACCCCAATGATGTAACCCATGATCAGAGGGAACCGGGG 431
QY 444 TTAAGTCTCTCTTATGAGCACTGTGATGTGGCCATCTGACAGACATCTCTCACTTA 503
Db 432 TGTGATGAGCACTTGTACATCTGTGCTCATCTGCTCATCTGCTGCACTCCCTGTT 491
QY 504 CGGCTGTGGGCGACGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 563
Db 492 TGGTGTGTGTATCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
QY 564 CAGCCCTACCTACTATCTCTCAGCGTGTGTCTTTCATGTCATTTCACTGATTTGAT 623
Db 552 GGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
QY 624 GATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 683
Db 612 GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
QY 684 TGTCAAGAGACACAGCTTGTGAAGTG 708
Db 672 TGGCACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 696

RESULT 12
LOCUS D0032256 793 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens ADRAID gene, VIRUTAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION D0032256
VERSION D0032256.1 GI:66883465
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 793)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
Chimpanzees
(ex) Plos Biol. 3 (6), E170 (2005)
JOURNAL PUBLISHED 15869325
AUTHORS 2 (bases 1 to 793)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of

FEATURES alignment.
source Location/Qualifiers
1..793
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
<1..>793
/gene="ADRAID"
/locus_tag="HC2398"

ORIGIN
Query Match 6.2%; Score 94.4; DB 11; Length 793;
Best Local Similarity 51.5%; Pred. No. 1.5e-11;
Matches 271; Conservative 0; Mismatches 246; Indels 9; Gaps 2;
gene

QY 137 TGTGCGCAATATGCTGTGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 196
Db 14 TGGAGGTAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 73
QY 197 CCAACCGTTTATCTTAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 256
Db 74 CCACTATTTCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 133
QY 257 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
Db 134 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 193
QY 317 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 376
Db 194 TATGGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 253
QY 377 CAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 436
Db 254 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313
QY 437 GCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 496
Db 314 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
QY 497 CACTTACGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 556
Db 374 CCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 430
QY 557 GGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 616
Db 431 AGGAGG-----CGGCTACGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 484
QY 617 TGTGTATGATTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 662
Db 485 CCGTATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 530

RESULT 13
LOCUS CF147813 721 bp mRNA linear EST 25-JUL-2003
DEFINITION AGENCOURT 14740180 NIH_MGC_145 Homo sapiens cDNA clone
IMAGE:6971910 5', mRNA sequence.
ACCESSION CF147813
VERSION CF147813.1 GI:33244081
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 721)
NIH-MGC http://img.ncbi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsabbs-r@mail.nih.gov
Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: IRB102 row: c column: 05
High quality sequence stop: 684.

FEATURES

source
1..721
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6971910"
/tissue_type="mixed"
/lab_host="DH10B"
/clone_1fb="NH108"
/clone_2fb="NH108"
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2: varies by clone; ORFs were PCR-amplified and cloned into pCDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XbaI/XhoI-3', 5'-EcoRV-XbaI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clone represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/teararrayed_plates/IRB1.presv.dat
a Note: this is a NIH_MGC library."

ORIGIN

Query Match 6.0%; Score 92.2; DB 6; Length 721;
Best Local Similarity 49.5%; Pred. No. 5.1e-11;
Matches 266; Conservative 0; Mismatches 268; Indels 3; Gaps 1;
QY 75 CATCAGCCGCGCCACGCGATCATCGCTCAACCGCTGCTTATCTTCTGCGCGCTC 134
DB 90 CATCGCGCGTGAAGAACTTGTGACGCTGTGTGTGCTGCGCTGATCTTGTGCGCGCT 149
QY 135 TTTCGTGGGCAACATAGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 191
DB 150 GGTGGGCAACACCTGATGATACCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGG 209
QY 192 GGTGACCAACCGTTTATCTTAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 251
DB 210 CACCAACCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 269
QY 252 GCGCCCTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 311
DB 270 CATCCCTTCAAGGCGACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 329
QY 312 CAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 371
DB 330 CAAATTCATCACTACTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 389
QY 372 GGTGTGATGTATCGTACTTGTGTATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
DB 390 GATGTCCGTGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 449
QY 432 CAGGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
DB 450 GTCCGCGCAACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 509
QY 492 TCCCTCACTTCAAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 551
DB 510 GCGCGGTGCTACACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 569
QY 552 GATCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 608
DB 570 GGAGGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 626

RESULT 14

DD032257 768 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes ADRA1D gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION DD032257
VERSION DD032257.1 GI:66893466
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE 1 (bases 1 to 768)
Nielson,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Snieky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
AUTHORS Nielson,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civejlo,D.,
White,T.J., Snieky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

source
1..768
location/Qualifiers
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/gene="ADRA1D"
/locus_tag="HC2398"

ORIGIN

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Best Local Similarity 53.4%; Pred. No. 3.4e-10;
Matches 186; Conservative 0; Mismatches 162; Indels 0; Gaps 0;
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DB 25 GCAAGCCGCGAGCTGTGAGGTGACCAACCGTTTATCTTAACTCTGCTGACGAC 84
QY 233 TGTCTGAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292
DB 85 TGTCTGAGCGCCACCGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
QY 293 CCCTCAAGCGACCTTGTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 352
DB 145 CTTTGGCGGCGCTTGTGCGACGATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 404
QY 353 GCGTCAACACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 412
DB 205 CCATCTGAGCTTGTGACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
QY 413 CTTACCCGCTCAAGATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 472
DB 265 AGTACCCGACCATCTGATGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 520
QY 473 TGGCGATCTGTGAGGACACTCTCTCACTTACGCTGAGGCGCGCGCGCGCGCGCG 520
DB 325 TAGCCCTGTGTGTGTCGTTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 572

RESULT 15

AI457674 386 bp mRNA linear EST 13-APR-1999
LOCUS AI457674/c
DEFINITION tJ48f06.x1 Soares NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone

IMAGE:2144771.3' similar to gb:M76446 ALPHA-1A ADRENERGIC RECEPTOR (HUMAN); mRNA sequence.

ACCESSION AI457674
VERSION AI457674.1 GI:4310543

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 386)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap/

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGS Consortium (info@image.lnl.gov) for further information.

Insert Length: 672 Std Error: 0.00
Seq primer: -40UP from Gibco

High quality sequence stop: 353.

FEATURES
Location/Qualifiers

1..386

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/mol_type="mRNA"

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/clone="IMAGE:2144771"

/lab_host="DH10B"

/clone_11b="Soares_NSP_F8_9W_OT_PA_P_S1"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was

PCR-amplified cDNAs from pools of 5,000 clones made from

the same 5 libraries. The pools consisted of the following

libraries and clones: Soares NBHSP pool 1:

309384-310919, 323208-325895 Soares NB2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares NB2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHSP

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Patima Bonaldo."

ORIGIN

Query Match 5.8%; Score 88.4; DB 1; Length 386;

Best Local Similarity 53.1%; Pred. No. 3.7e-10;

Matches 188; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 85 GCCCAGCGATCATCCGCTCAACCGCTGCTTATCTTCGCGCCCTCTTTCGTGGC 144

DB 365 GCGCAGGGGGTGGGCGCTGGGCGCTTCCTGCGAGCCCTTATCTTATGCGCGCAGGT 306

QY 145 AACATAGTCTGCGCTAGTGTGACGGCAGCGCAGCTGCTGACGGTACCAACCGT 204

DB 305 AACCTGCTGTATCTCTCAAGTGGCTTGAACCGCACCTGACAGCGTCAACCACTAT 246

QY 205 TTATCTTAACCTCTCTGTCACCGACTGCTGCAGATTTCGCTCGTGGCCCTCGGTG 264

DB 245 TTCTATGTAACCTGCGCGGCGGCGACTGCTGTAGGCGCACGTTACTGCGCTTCG 186

QY 265 GTGGCCACTCTGTGCTCTCTTCTGGCCCTCAACAGCACTTCTGACAGCGCTGTG 324

DB 185 GGCACCATGAGGTTCTGGGCTTCTGGGCTTGGCGCGCTTCTGCAACGATGGGCC 126

QY 325 AGCCTACCACTGTTGCGCTTGGCAGGCTCAACCACTTGTGAGTCAAGTAT 384

DB 125 GCGTGAAGTGTGTGCTGCGAGCGCTTCATCTCAAGCTTCTGACCACTTCCTGAGC 66

QY 385 CGCTACTGTTCATCATCAACCTCTCTCTTACCGCTCAAGATGACCGAGCGC 438

DB

65 CGGTAGTGGGCGGTGGCCACTCACTCAAGTACCCAGCCATCATGACCGAGCGC 12

Search completed: December 10, 2005, 03:03:23
Job time : 4328 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 23:55:31 ; Search time 5234 Seconds
(without alignments)
16583.865 Million cell updates/sec

Title: US-10-712-615-1

Perfect score: 1527
Sequence: 1 atgcagctccacctgcaccaa.....attctctactttctctga 1527

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: GenEmbl:*
- 2: gb_ba:*
- 3: gb_in:*
- 4: gb_env:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pr:*
- 9: gb_pro:*
- 10: gb_stc:*
- 11: gb_sy:*
- 12: gb_un:*
- 13: gb_vl:*
- 14: gb_hcg:*
- 15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1527	100.0	1527	6	BD095705	Novel gna
2	1527	100.0	1527	6	AX497863	Sequence
3	1527	100.0	1580	6	AX497909	Sequence
4	1527	100.0	175465	14	ALJ56783	Sequence
5	1525.4	99.9	1527	6	BD144320	Novel sapi
6	1525.4	99.9	1527	6	CQ736967	Sequence
7	1525.4	99.9	1527	6	AR679058	Sequence
8	1525.4	99.9	1527	6	AX148174	Sequence
9	1525.4	99.9	1527	6	AX230165	Sequence
10	1525.4	99.9	1527	6	AX355868	Sequence
11	1525.4	99.9	1527	6	AX497907	Sequence
12	1525.4	99.9	1527	6	AX543321	Sequence
13	1525.4	99.9	1527	6	AX549297	Sequence
14	1525.4	99.9	1527	8	AB083588	Homo sapi
15	1525.4	99.9	1527	8	AF411115	Homo sapi
16	1525.4	99.9	1527	8	BC069439	Homo sapi
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18	1525.4	99.9	1659	6	AX497906	Sequence

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21	1525.4	99.9	1920	6	AX355867	Sequence
22	1525.4	99.9	7524	6	AX543323	Sequence
23	1525.4	99.9	140628	14	AC016468	Sequence
24	1525.4	99.9	172280	8	ALJ90879	Sequence
25	1524	99.8	1524	6	BD173594	Novel G p
26	1522.4	99.7	1524	6	BD173595	Novel G p
27	1522.4	99.7	2781	6	AR679128	Sequence
28	1522.4	99.7	2781	6	AX148262	Sequence
29	1522	99.7	1527	6	AX497910	Sequence
30	1520.6	99.6	1527	6	AR679119	Sequence
31	1520.6	99.6	1527	6	AX148250	Sequence
32	1520.6	99.6	1527	6	AX497908	Sequence
33	1515.8	99.3	1527	6	AX459697	Sequence
34	1515.8	99.3	1704	6	AX459693	Sequence
35	1456.4	95.4	1458	6	AX342674	Sequence
36	1130.2	74.0	212696	14	AC156524	Sequence
37	932.2	61.0	179648	9	AL672122	Mouse DNA
38	912.2	59.7	135462	14	AC123499	Rattus no
39	912.2	59.7	250681	14	AC099159	Rattus no
40	855.4	56.0	1197	6	AX543324	Sequence
41	855.4	56.0	1530	6	AX286523	Sequence
42	722.2	47.3	835	10	BV208535	Sequence
43	649.6	42.5	1697	6	AX647119	Sequence
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ALIGNMENTS

RESULT 1	BD095705	1527 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.				
DEFINITION	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.				
ACCESSION	BD095705				
VERSION	BD095705.1 GI:22641293				
KEYWORDS	WO 0148188-A/17.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 1527)	Saito, Y., Noriyuki, Morikawa, Yoshida, K., Watanabe, S., Oda, T., Suwa, M., Sugiyama, T., Kishimoto, T., Kanzaki, K., Yaeuda, S. and Inoue, Y.			
AUTHORS	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use				
TITLE	Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use				
JOURNAL	Patent: WO 0148188-A 17 05-JUL-2001, HELIX RESEARCH INSTITUTE, SHINICHIRO MATSUMOTO, TANAKI ODA, YOKO SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO YASUDA, YOSHITSUGU INOUE				
COMMENT	OS Homo sapiens (human) PN WO 0148188-A/17 PD 05-JUL-2001 PF 28-DEC-2000 WO 2000JP009408 PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP 00P 101339 PI SHUNICHIRO MATSUMOTO, TANAKI ODA, YOKO SAITO, NORIYUKI PI MORIKAWA, KENJI YOSHIDA, PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, PI SHINICHIRO YASUDA, YOSHITSUGU INOUE PC C12N15/09, C12N1/15, C12N1/19, C12N5/10, C07K14/705, PC C07K16/28, PC C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC GOIN33/15, PC GOIN33/50 CC Novel guanosine triphosphate-bound protein-coupled receptors and genes				

FEATURES
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 1527; DB 6; Length 1527;
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Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1501 TCTTACGATTTCTGCTACTTTTCTTTGA 1527
DB 1501 TCTTACGATTTCTGCTACTTTTCTTTGA 1527

RESULT 2
AX497863 1527 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION
Sequence 1 from Patent WO0240670.
ACCESSION
AX497863
VERSION
AX497863.1 GI:2342970
KEYWORDS

SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE
1 Battaglini P., Feder J., Mintier G., Nelson T., Ramanathan C.,
Westphal R., Caccace A., Barber L., Hawken D. and Kornacker M.
A novel human g-protein coupled receptor, hgrbm7, expressed
highly in brain
Patent: WO 0240670-A 1 23-MAY-2002;
Bristol-Myers Squibb Company (US)

JOURNAL
Bristol-Myers Squibb Company (US)

FEATURES
source
1..1527
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

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Oy	181	CAGCTGTGTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTGTACCGAGCTGTGCAG	240
Db	212	CAGCTGTGTGAGGTGACCAACCGTTTATCTTTTAACTCTCTGTGTACCGAGCTGTGCAG	271
Oy	241	ATTGGCTGTGTGGGCCCCCGGGTGGGGGCGCACTGTGTGGCTCTCTTTCTGGGCCCCCTAAC	300
Db	272	ATTGGCTGTGTGGGCCCCCGGGTGGGGGCGCACTGTGTGGCTCTCTTTCTGGGCCCCCTAAC	331
Oy	301	AGCCACTTCTGACAGGCGCCCTGGTTAGCTTACCCACCACTGTGGCTTTCGACAGCTCAAC	360
Db	332	AGCCACTTCTGACAGGCGCCCTGGTTAGCTTACCCACCACTGTGGCTTTCGACAGCTCAAC	391
Oy	361	ACCATTGTCTTGTGTCAAGTGAATGGCTTCTTGTGCATATATCAACCTCTCTTCAACCG	420
Db	392	ACCATTGTCTTGTGTCAAGTGAATGGCTTCTTGTGCATATATCAACCTCTCTTCAACCG	451
Oy	421	TCCAGATGATACCCAGGCGCGGGTTACTGTCTCTCTATAGGCACTGGATTTGGCCATC	480
Db	452	TCCAGATGATACCCAGGCGCGGGTTACTGTCTCTCTATAGGCACTGGATTTGGCCATC	511
Oy	481	CTGCAAGAGCACTCTTCACCTCTTACCGGCTGGGGCCAGGCTGCTTTGTAGAGCGCAATGCT	540
Db	512	CTGCAAGAGCACTCTTCACCTCTTACCGGCTGGGGCCAGGCTGCTTTGTAGAGCGCAATGCT	571
Oy	541	CTGTGCTCCATATATCTGGGGGGGCGAGGCCAGCTTAACTATCTCAAGCGTGGTGTCTTC	600
Db	572	CTGTGCTCCATATATCTGGGGGGGCGAGGCCAGCTTAACTATCTCAAGCGTGGTGTCTTC	631
Oy	601	ATCGTCATTTCACTGATTTGTCAATGTGCTGTGCTCTCTCTCGTGGTGTCTGTGAGGCCG	660
Db	632	ATCGTCATTTCACTGATTTGTCAATGTGCTGTGCTCTCTCGTGGTGTCTGTGAGGCCG	691
Oy	661	AGGCAGCATGTCTGTCTGTCAAAATGTCAAGAACACAAGCTTGGAAATGGAGTCAAGGAC	720
Db	692	AGGCAGCATGTCTGTCTGTCAAAATGTCAAGAACACAAGCTTGGAAATGGAGTCAAGGAC	751
Oy	721	TGTGTGAGAAATAGAGATTAAGAGGAGCAGAGAAAGAAAGAGAGTTCACAGATGAGAT	780
Db	752	TGTGTGAGAAATAGAGATTAAGAGGAGCAGAGAAAGAAAGAGAGTTCACAGATGAGAT	811
Oy	781	GAGTTTCCCGCCGACGATGAAGGTGAGTTCAGAGCCAGAGAGGCGAAATGGAAGCCAG	840
Db	812	GAGTTTCCCGCCGACGATGAAGGTGAGTTCAGAGCCAGAGAGGCGAAATGGAAGCCAG	871
Oy	841	GACGGCAGCTTAAGGCCAAGGAAGGAAGAACACGGGACCAAGTGAAGTATGTATGAGGAC	900
Db	872	GACGGCAGCTTAAGGCCAAGGAAGGAAGAACCGGGACCAAGTGAAGTATGTATGAGGAC	931
Oy	901	AGGGCAGCGAGAGGCTCAGAGAGACAGCAGGTGGCCAGCGACGGCAGCATGAGGGT	960
Db	932	AGGGCAGCGAGAGGCTCAGAGAGACAGCAGGTGGCCAGCGACGGCAGCATGAGGGT	991
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Db	992	AAGGAAGGACGACCCAAAGTTTGAAGAGAACAGCATGAAGCCAGCAAGGTCGACAGAG	1050
Oy	1021	GTCACACCAAGTGAAGCATTTGAGTGGTGAAGATGACATGAGATGTTTGGTGAAGCAGATC	1080
Db	1052	GTCACACCAAGTGAAGCATTTGAGTGGTGAAGATGACATGAGATGTTTGGTGAAGCAGATC	1110
Oy	1081	AATTTCAGTGAGGATGACGTCGAGGCGATGGAATCTCCGAGAGACCTCCACCCAGTCGT	1140
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QY	1321	TGGCTTTTCTTCTTCGACGTGCTGCATCACCCTATGCTCTATGCTACATGACACAGACC	1380
Db	1352	TGGCTTTTCTTCTTCGACGTGCTGCATCACCCTATGCTCTATGCTACATGACACAGACC	1411
QY	1381	ATTAAAGAAAGAAATCCAGACATCTGTAAGAAAGTTCTTCGCAAGGAAACCCCGGAA	1440
Db	1412	ATTAAAGAAAGAAATCCAGACATCTGTAAGAAAGTTCTTCGCAAGGAAACCCCGGAA	1471
QY	1441	GAAATATAGCCACCCAGACCTGCCGGAACAGAGGTGGAGCTGAAGCAAGATTGTCCT	1500
Db	1472	GAAATATAGCCACCCAGACCTGCCGGAACAGAGGTGGAGCTGAAGCAAGATTGTCCT	1533
QY	1501	TCTACGATTCGTCTACTTTTCCTTGA	1527
Db	1532	TCTACGATTCGTCTACTTTTCCTTGA	1558
RESULT 4	AL356783	175465 bp DNA linear HTG 10-JUL-2001	
LOCUS	AL356783	Homo sapiens chromosome X clone RP13-13u21, 7 unordered pieces.	
DEFINITION	AL356783		
ACCESSION	AL356783.20	GI:144556213	
VERSION	HTG, HTGS_PHASE1, HTGS_CANCELLED.		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1	Heath, P.	
AUTHORS	Direct Submission		
TITLE	Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk		
JOURNAL	On Jun 14, 2001 this sequence version replaced gi:14329943.		
COMMENT	----- Genome Center ----- Center: Sanger Centre Center code: SC Web site: http://www.sanger.ac.uk Contact: humquerry@sanger.ac.uk ----- Project Information ----- Center project name: hb13u21 ----- Summary Statistics ----- Assembly program: XGAP4, version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 35% of reads Dye-terminator Big Dye; 64% of reads Consensus quality: 173062 bases at least Q40 Consensus quality: 174012 bases at least Q30 Consensus quality: 174525 bases at least Q20 Insert size: 174865; sum-of-ctrls Quality coverage: 5.89x in Q20 bases; sum-of-ctrls ----- * NOTE: This is a 'working draft' sequence. It currently * consists of 7 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * 1 102859: contig of 102859 bp in length * 102860 102959: gap of 100 bp * 102960 126878: contig of 23919 bp in length		

* 126879 126978: gap of 100 bp
* 126979 132924: contig of 5946 bp in length
* 132925 133024: gap of 100 bp
* 133025 136361: contig of 3337 bp in length
* 136362 136461: gap of 100 bp
* 136462 142243: contig of 5782 bp in length
* 142244 142343: gap of 100 bp
* 142344 150640: contig of 8297 bp in length
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* 150741 175465: contig of 24725 bp in length.

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Query Match 100.0%; Score 1527; DB 14; Length 175465;
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Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
BD144320

LOCUS BD144320 1527 bp DNA linear PAT 17-JAN-2003

DEFINITION Novel G-protein coupled receptors.

ACCESSION BD144320

VERSION BD144320.1 GI:27850078

KEYWORDS JP 2002112793-A/45.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1527)
Haga, T., Takeda, S. and Miyake, N.
Novel G-protein coupled receptors
Patent: JP 2002112793-A 45 16-APR-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
OS Homo sapiens (human)
PN JP 2002112793-A/45
PD 16-APR-2002
PF 09-FEB-2001 JP 2001034434
PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE

COMMENT

PC C12N15/09, A01K67/027, A61K38/00, A61K39/395, A61K39/395, A61K45/00, PC A61K48/00,
PC A61P43/00, C07K14/705, C07K16/28, C07K19/00, C12N1/15, C12N1/19, PC C12N1/21,
PC C12N5/10, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, PC G01N33/566//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC Novel G-protein coupled receptors
FH Key Location/Qualifiers
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Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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ACCESSION CQ736967
VERSION CQ736967.1 GI:42334039
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ORGANISM Homo sapiens
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Hominoidea; Homo.

REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
AUTHORS Kites, such as nucleic acid arrays, comprising a majority of
TITLE humenexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 22901 06-SEP-2002;
PE Corporation (NY) (US)
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LOCUS Sequence 15 from patent US 6902902.
DEFINITION AR679058
ACCESSION AR679058

VERSION AR679058.1 GI:67620281
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Unetk,D.J., Chen,R., Richman,J.G., Connolly,D.T., Hakak,Y.,
Behan,D.P. and Chalmers,D.T.
TITLE Human G protein-coupled receptors and modulators thereof for the
treatment of metabolic-related disorders
JOURNAL Patent: US 6902902-A 15 07-JUN-2005;
Arena Pharmaceuticals, Inc.; San Diego, CA
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Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX148174
DEFINITION Sequence 15 from Patent WO0136471.
ACCESSION AX148174
VERSION AX148174.1 GI:14347080
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Chen,R., Dang,H.T. and Lowitz,K.P.
TITLE Endogenous and non-endogenous versions of human g protein-coupled
receptors
JOURNAL Patent: WO 0136471-A 15 25-MAY-2001;
Arena Pharmaceuticals, Inc. (US)
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Location/Qualifiers

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ORIGIN

Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX230165
DEFINITION Sequence 52 from Patent WO0162797.
ACCESSION AX230165
VERSION AX230165.1 GI:15592183
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Vogel, G., Wood, L.S., Parodi, L.A. and Lind, P.
AUTHORS Novel g protein-coupled receptors
TITLE Patent: WO 0162797-A 52 30-AUG-2001;
JOURNAL PHARMACIA & UPJOHN COMPANY (US)
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Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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LOCUS AX355868 1527 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent WO0188126.
ACCESSION AX355868
VERSION AX355868.1 GI:18620521
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 Ramakrishnan, S.
TITLE Regulation of human _g(a)1a7adrenergic receptor-like G
protein-coupled receptor
JOURNAL Patent: WO 0188126-A 2 22-NOV-2001;
Bayer Aktiengesellschaft (DE)
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ORIGIN
Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
Best Local Similarity 99.9%; Pred. No. 2e-295;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1		
JOURNAL	Li, Z., Cravchik, A., Milehina, N., Wei, M.H., Ketchum, K.A., di Francesco, V. and Beasley, E.M.		
FEATURES	Isolated human G-protein coupled receptors, nucleic acid molecules encoding human GPCR proteins, and uses thereof		
source	Patent: WO 0205151-A 1 01-AUG-2002; PE Corporation (NY) (US)		
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ORIGIN	1..1527		
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Best Local Similarity	99.9%	Pred. No. 2e-295;	
Matches 1526; Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
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Qy	661	AGCGCAGCATGCTCTGCTGTACATGTCACAAGACACACAGCTTGGAAGTGCAGTCAAGAC	720
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Qy	781	GAGTTTGCSCCGCAGCATGATGAGGTGCAAGGCTCAAGGGCAGAGGGCAGATGGAAGCCAG	840
Db	781	GAGTTTGCSCCGCAGCATGATGAGGTGCAAGGCTCAAGGGCAGAGGGCAGATGGAAGCCAG	840
Qy	841	GACGGCAGCTGAAAGGCCAAGGAAAGAACAGGGGGACCAGTGAGTAGTGTAGAGCC	900
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Qy	901	AGGGGCAGCCGAGAGAGTCAAGAGAGCGACAGGTGTGCTGATGCGCAGCATGGAAGGT	960
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Qy	961	AAGGAAAGCACA CCAAAAGTTGAGGAGAA CAGCATGAAGGCAGACAAGAGGTGCGCAGAG	1020
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Db	1021	GTCAA CCA GTG CAG CATTGACTTGGGTGAAGTGA CATTGAGTTTGTGAAG CCA C ATC	1080
Qy	1081	AATTTCAATGAGATGAGTGTGAGGCACTGAA C ATCCCGGAGGCTCCACCAGTGTG	1140
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Db	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGTGGGCCCTTAC T G C T T T T T A G C A G T C	1260
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Qy	1381	ATTAAAGAGAAATTCAGAGACATGTGTGAAGAGTTCTTCTGCAAGAGAAAGCCCCGAAA	1440
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DEFINITION	Sequence 582 from Patent WO02061087.	linear
ACCESSION	AX549297	PAT 26-NOV-2002

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VERSION      AX549297.1  GI:25813959
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               Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
               Homnidae; Homo.
REFERENCE
AUTHORS      1
               Burner,G.C., Roush,C.L. and Brown,J.P.
TITLE         Antigenic peptides, such as for G protein-coupled receptors
               (GPCRs), antibodies thereto, and systems for identifying such
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               Patent: WO 02061087-A 582 08-AUG-2002;
               Lifespan Biosciences, Inc. (US)
JOURNAL
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SOURCE        1. 1527
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Query Match 99.9%; Score 1525.4; DB 6; Length 1527;

Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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2021-2022

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Db	721	TGTGTGGAGAAATGAGAGTAAGAAAGGACACAGAAAGAAAGAGAACTTCCAGATATAGAT	780
OY	781	GAGTTTCCCGCCAGCATGAAGGTAGGTCAAGGCCAAAGSAGGCGAGATGGAAACCAAG	840
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Db	841	GACGGCAGCCTGGAAGGCCAAGGAAGAAAGCACGGGGACCATGTAAGTAAGTAAAGCC	900
OY	901	AGGGCAGCGAGGAGGTGTCAGAGAGACAGACGATGGCCAGGACGATGGAGGGT	960
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OY	961	AAGGAAGCAGACCAACAAAGTTGAGAGAAACAGCATGAAGGCGACAGCAAGGGTCGACAG	1020
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Db	1021	GTCAACCAAGTCAGCATTTGACTTTGGGTGAAGATGACATGAGATTTGGTGAAGACATC	1080
OY	1081	AATTCAGTGAAGATGACGTGAGGACAGTGAATCTCCGAGAGGCTCCCAACCAAGTGT	1140
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OY	1441	GAAGATAGCCACACAGACCTGCCCGGAAACAGAGGGTGGACTGAAGGCACAAAGTTGTCCCT	1500
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DEFINITION	Homo sapiens GPCR gene for putative G-protein coupled receptor, complete CDS, clone:hgPCR6.				
ACCESSION	AB083588				
VERSION	AB083588.1	GI:20152239			
KEYWORDS	.				
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ORGANISM	Homo sapiens				
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REFERENCE	1				
AUTHORS	Takeda, S., Kadowaki, S., Haga, T., Takesue, H. and Miyaku, S.				
TITLE	Identification of G protein-coupled receptor genes from the human				

JOURNAL REFERENCE AUTHORS TITLE JOURNAL	genome sequence Unpublished 2 (bases 1 to 1527) Takeda,S., Kadowaki,S., Haga,T., Takeaeu,H. and Mitaku,S. Direct Submission Submitted (10-APR-2002) Shigeaki Takeda, Gunma University, Department of Biological and Chemical, Engineering, Faculty of Engineering, 1-5-1, Kiryu, Gunma 376-8515, Japan (E-mail:etakeda@ce.gunma-u.ac.jp, Tel:+81-277-30-1434, Fax:+81-277-30-1434)
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OY	721	TGTGTGAGAAATGAGATGAGAGGAGACACAGAAAGAGAGAGATTCACAGATGAGAGT	780
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OY	1081	AATTTCACTGAGATGAGTGTGAGGCAATGAAATCCCGGAGAGCTTCCCAACCAAGTCTG	1140
Db	1081	AATTTCACTGAGATGAGTGTGAGGCAATGAAATCCCGGAGAGCTTCCCAACCAAGTCTG	1140
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2005, 22:27:06 ; Search time 660 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the local score distribution.

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20	1525.4	99.9	1527	14	Adw44634 Human RUP
21	1525.4	99.9	1527	14	Aea33113 Human GPC
22	1525.4	99.9	1527	14	Aeb20818 Human RUP
23	1525.4	99.9	1527	14	Aaf56818 Human G-P
24	1525.4	99.9	1527	14	Aaf56818 Human G-P
25	1525.4	99.9	1527	14	Aea33112 Human GPC
26	1525.4	99.9	1527	14	Adc86472 Human GPC
27	1525.4	99.9	1527	14	Aas18898 Human G-P
28	1525.4	99.9	1527	14	Aah48673 Human bra
29	1525.4	99.9	1527	14	Abn86855 Human G-P
30	1525.4	99.9	1527	14	Aad62687 Human G-P
31	1525.4	99.9	1527	14	Abv74517 Human G-P
32	1525.4	99.9	1527	14	Aal44179 Human G-P
33	1525.4	99.9	1527	14	Adf70610 Orphan re
34	1525.4	99.9	1527	14	Aal44180 Human G-P
35	1525.4	99.9	1527	14	Aas08274 cDNA enco
36	1525.4	99.9	1527	14	Ad196549 G protein
37	1525.4	99.9	1527	14	Adw44722 Human RUP
38	1525.4	99.9	1527	14	Aeb20906 Human RUP
39	1525.4	99.9	1527	14	Aad41171 Human GGP
40	1525.4	99.9	1527	14	Aea33116 Human GPC
41	1525.4	99.9	1527	14	Aas08265 Human GPC
42	1525.4	99.9	1527	14	Ad196537 Human GPC
43	1525.4	99.9	1527	14	Adw44710 Human RUP
44	1525.4	99.9	1527	14	Aea33114 Human GPC
45	1525.4	99.9	1527	14	Aeb20894 Human RUP

ALIGNMENTS

RESULT 1	AAH73517	standard; DNA; 1527 BP.
ID	AAH73517	
AC	AAH73517	
XX		
DT	25-SEP-2001 (first entry)	
XX		
DE	Human G protein-coupled receptor GPRV72 coding sequence.	
XX		
KW	Human; guanosine triphosphate binding protein-coupled receptor;	
KW	G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;	
KW	GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;	
KW	Alzheimer's disease; cytostatic; hepatotropic; nootropic;	
KW	neuroprotective; gene therapy; peptide therapy; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200148188-A1.	
XX		
PD	05-UTL-2001.	
XX		
PF	28-DEC-2000; 2000WO-JP009408.	
XX		
PR	28-DEC-1999; 99JP-00375152.	
XX		
PR	31-MAR-2000; 2000JP-00103339.	
XX		
PA	(HELI-) HELIX RES INST.	
XX		
PI	Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;	
PI	Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;	
XX		
DR	WPI, 2001-425662/45.	
DR	P-PDB; AAG64126.	
XX		
PT	New DNA encoding guanosine triphosphate binding protein coupled receptors	
PT	and their expression products for screening potential anticancer and	
PT	nootropic drugs and in diagnosis of these diseases.	
XX		
PS	Claim 1, Page 143-144; 170pp; Japanese.	
XX		
CC	The invention relates to nine human guanosine triphosphate binding	

protein (G protein)-coupled receptors designated GPR9, GPR12, GPR16, GPR21, GPR40, GPR47, GPR51, GPR71 and GPR72, and to the genes encoding them. These genes and proteins and antibodies against the protein are useful in the treatment, prevention, diagnosis and investigation of diseases associated with G protein-coupled receptors, including cancer, cirrhosis of the liver and Alzheimer's disease. The present sequence is a G protein-coupled receptor coding sequence of the invention

Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1527;	DB 4;	Length 1527;
-------------	---------	-------------	-------	--------------

Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTGAGGTCCACCTGGACGCAACGACGCGCGAGATGAACAAGACGCCACACTGGCAATGCC	60
Db	1	ATGAGAGTCCACCTGGACGCAACGACGCGCGAGATGAACAAGACGCCACACTGGCAATGCC	60
QY	61	CTCTCCAAAATGCCCATCAGCTCGGCGCCACAGGCATCATCGCTCAACCCGCTGATTATC	120
Db	61	CTCTCCAAAATGCCCATCAGCTCGGCGCCACAGGCATCATCGCTCAACCCGCTGATTATC	120
QY	121	TTCTCGCGCGCTCTTTTGGTGGCAACATATGTCTGGCGCTAGTGTGGACGCCAAGCG	180
Db	121	TTCTCGCGCGCTCTTTTGGTGGCAACATATGTCTGGCGCTAGTGTGGACGCCAAGCG	180
QY	181	CAGCTGCTGCAAGTGAACCAACGGTTTTATCTTTAACTCTCGTCAACCCACTGCTGACG	240
Db	181	CAGCTGCTGCAAGTGAACCAACGGTTTTATCTTTAACTCTCGTCAACCCACTGCTGACG	240
QY	241	ATTGCGCTGTGGCGCCCTCGGAGTGTGGCACCTGTGCGCTCTCTTCTGGCGCCCTCAAC	300
Db	241	ATTGCGCTGTGGCGCCCTCGGAGTGTGGCACCTGTGCGCTCTCTTCTGGCGCCCTCAAC	300
QY	301	AGCCACTTGTGACACGGCGCCTGGTTAGCTTCACCAACTGTGTGGCCTTTCGCAAGCTCAC	360
Db	301	AGCCACTTGTGACACGGCGCCTGGTTAGCTTCACCAACTGTGTGGCCTTTCGCAAGCTCAC	360
QY	361	ACCATTGTTTGGGTGACATGGACATGGCTACTGTTGCATATATCCAACTCTCTCTACCCG	420
Db	361	ACCATTGTTTGGGTGACATGGACATGGCTACTGTTGCATATATCCAACTCTCTCTACCCG	420
QY	421	TCCAAGATGACCCAGCGCGCGGTTACTGTCCTCTCTATGGCACTTGATTTGGCCATC	480
Db	421	TCCAAGATGACCCAGCGCGCGGTTACTGTCCTCTCTATGGCACTTGATTTGGCCATC	480
QY	481	CTGCAAGAGCATCTCTCACTTACCGGCTGGGGCCAGGCTGCTTTGATGAGCCCAATGCT	540
Db	481	CTGCAAGAGCATCTCTCACTTACCGGCTGGGGCCAGGCTGCTTTGATGAGCCCAATGCT	540
QY	541	CTCTGCTCCATATATCTGGGGGGGCAACCCAGCTACATATCTCAAGCGGTGTCTTC	600
Db	541	CTCTGCTCCATATATCTGGGGGGGCAACCCAGCTACATATCTCAAGCGGTGTCTTC	600
QY	601	ATCGTCATTCCA CTGATTGTCAATGATTGGCTGCTCACTCGGTGTTCTGTGACGCCG	660
Db	601	ATCGTCATTCCA CTGATTGTCAATGATTGGCTGCTCACTCGGTGTTCTGTGACGCCG	660
QY	661	AGGCAGCATGCTCTGTGCTTAACAATGTCAAGAGACACAGCTTGGAAATGCGACAGGAC	720
Db	661	AGGCAGCATGCTCTGTGCTTAACAATGTCAAGAGACACAGCTTGGAAATGCGACAGGAC	720
QY	721	TGTGTGGGAATGAGAGATGAAGGGAGACAGAAAGAGAGAGATTCCAGATGTGAGAT	780
Db	721	TGTGTGGGAATGAGAGATGAAGGGAGACAGAAAGAGAGAGATTCCAGATGTGAGAT	780
QY	781	GAGTTTCGCGCGCAGCATGAAGTGAAGTCAAGGCCAAGAGGCGCAGAAATGAAAGCCAA	840
Db	781	GAGTTTCGCGCGCAGCATGAAGTGAAGTCAAGGCCAAGAGGCGCAGAAATGAAAGCCAA	840
QY	841	GACGGCAGCTTGAGGCCAAGGAAGACACGGGGACCATGTAGAGTACTGTAGAGCC	900

Accession	Gene	Species	Protein	Length (aa)	Accession	Gene	Species	Protein	Length (aa)
DB	841	GACGGCAGCCTGMAAGGCCAAGAAAGCAAGCAGCGGGACAGTGAAGTAACTGTAAGAGGCC	900		DB	841	GACGGCAGCCTGMAAGGCCAAGAAAGCAAGCAGCGGGACAGTGAAGTAACTGTAAGAGGCC	900	
QY	901	AGGGGACGCGAGAGGTGTGAGAGAGACAGCAGCGGTGCCACGCGACGGCAGCATGAGAGGGT	960		QY	901	AGGGGACGCGAGAGGTGTGAGAGAGACAGCAGCGGTGCCACGCGACGGCAGCATGAGAGGGT	960	
DB	901	AGGGGACGCGAGAGGTGTGAGAGAGACAGCAGCGGTGCCACGCGACGGCAGCATGAGAGGGT	960		DB	901	AGGGGACGCGAGAGGTGTGAGAGAGACAGCAGCGGTGCCACGCGACGGCAGCATGAGAGGGT	960	
QY	961	AAGGAAGGCACACCAAAAGTTGAGAGAAACAGCATGAAAGGCAGACMAAGGGTCCGACAGAG	1020		QY	961	AAGGAAGGCACACCAAAAGTTGAGAGAAACAGCATGAAAGGCAGACMAAGGGTCCGACAGAG	1020	
DB	961	AAGGAAGGCACACCAAAAGTTGAGAGAAACAGCATGAAAGGCAGACMAAGGGTCCGACAGAG	1020		DB	961	AAGGAAGGCACACCAAAAGTTGAGAGAAACAGCATGAAAGGCAGACMAAGGGTCCGACAGAG	1020	
QY	1021	GTCAACACAGTCAGACATTTGACTTGGGTGAAAGATGACATGAGAGTTTGGTGAAGACGACATC	1080		QY	1021	GTCAACACAGTCAGACATTTGACTTGGGTGAAAGATGACATGAGAGTTTGGTGAAGACGACATC	1080	
DB	1021	GTCAACACAGTCAGACATTTGACTTGGGTGAAAGATGACATGAGAGTTTGGTGAAGACGACATC	1080		DB	1021	GTCAACACAGTCAGACATTTGACTTGGGTGAAAGATGACATGAGAGTTTGGTGAAGACGACATC	1080	
QY	1081	AATTTCAAGTGAAGATGACAGTCGAGGCAAGTGAACATCCCGAGAGACCTTCCACCCAGTCGT	1140		QY	1081	AATTTCAAGTGAAGATGACAGTCGAGGCAAGTGAACATCCCGAGAGACCTTCCACCCAGTCGT	1140	
DB	1081	AATTTCAAGTGAAGATGACAGTCGAGGCAAGTGAACATCCCGAGAGACCTTCCACCCAGTCGT	1140		DB	1081	AATTTCAAGTGAAGATGACAGTCGAGGCAAGTGAACATCCCGAGAGACCTTCCACCCAGTCGT	1140	
QY	1141	CGTAACAGCAACACGCAACCCCTCTCTCCGCCAGGTGCTAACAGTGCACAAAGCTGCTAAAGTG	1200		QY	1141	CGTAACAGCAACACGCAACCCCTCTCTCCGCCAGGTGCTAACAGTGCACAAAGCTGCTAAAGTG	1200	
DB	1141	CGTAACAGCAACACGCAACCCCTCTCTCCGCCAGGTGCTAACAGTGCACAAAGCTGCTAAAGTG	1200		DB	1141	CGTAACAGCAACACGCAACCCCTCTCTCCGCCAGGTGCTAACAGTGCACAAAGCTGCTAAAGTG	1200	
QY	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTATGACAGTC	1260		QY	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTATGACAGTC	1260	
DB	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTATGACAGTC	1260		DB	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTATGACAGTC	1260	
QY	1261	CTGGCCGTGTGGGTGATGTGAAACCAGGTACCCCAAGTGGGTATCACCATATATCATC	1320		QY	1261	CTGGCCGTGTGGGTGATGTGAAACCAGGTACCCCAAGTGGGTATCACCATATATCATC	1320	
DB	1261	CTGGCCGTGTGGGTGATGTGAAACCAGGTACCCCAAGTGGGTATCACCATATATCATC	1320		DB	1261	CTGGCCGTGTGGGTGATGTGAAACCAGGTACCCCAAGTGGGTATCACCATATATCATC	1320	
QY	1321	TGGCTTTTCTTCTCTGCAAGTGTGCATCACCCCTATATGTCTATATGGCTACATGCAACAGACC	1380		QY	1321	TGGCTTTTCTTCTCTGCAAGTGTGCATCACCCCTATATGTCTATATGGCTACATGCAACAGACC	1380	
DB	1321	TGGCTTTTCTTCTCTGCAAGTGTGCATCACCCCTATATGTCTATATGGCTACATGCAACAGACC	1380		DB	1321	TGGCTTTTCTTCTCTGCAAGTGTGCATCACCCCTATATGTCTATATGGCTACATGCAACAGACC	1380	
QY	1381	ATTAAAGAGAAATCCAGGACATGCTGTAAGAAAGTTCTTCTGACAGAAAGAGCCCGGAAA	1440		QY	1381	ATTAAAGAGAAATCCAGGACATGCTGTAAGAAAGTTCTTCTGACAGAAAGAGCCCGGAAA	1440	
DB	1381	ATTAAAGAGAAATCCAGGACATGCTGTAAGAAAGTTCTTCTGACAGAAAGAGCCCGGAAA	1440		DB	1381	ATTAAAGAGAAATCCAGGACATGCTGTAAGAAAGTTCTTCTGACAGAAAGAGCCCGGAAA	1440	
QY	1441	GAAAGTACCCACCCGACACCTGCGCGGAAACAGAGGGTGGACTGAAGGCCAAGATTGTCCT	1500		QY	1441	GAAAGTACCCACCCGACACCTGCGCGGAAACAGAGGGTGGACTGAAGGCCAAGATTGTCCT	1500	
DB	1441	GAAAGTACCCACCCGACACCTGCGCGGAAACAGAGGGTGGACTGAAGGCCAAGATTGTCCT	1500		DB	1441	GAAAGTACCCACCCGACACCTGCGCGGAAACAGAGGGTGGACTGAAGGCCAAGATTGTCCT	1500	
QY	1501	TCTTACGATTCTGCTACTTTTCTTTGA	1527		QY	1501	TCTTACGATTCTGCTACTTTTCTTTGA	1527	
DB	1501	TCTTACGATTCTGCTACTTTTCTTTGA	1527		DB	1501	TCTTACGATTCTGCTACTTTTCTTTGA	1527	
RESULT 2									
ABL53719									
ID	ABL53719	standard; cDNA; 1527 BP.			ID	ABL53719	standard; cDNA; 1527 BP.		
AC	ABL53719;				AC	ABL53719;			
DT	24-JUN-2002	(first entry)			DT	24-JUN-2002	(first entry)		
DE	G-protein coupled receptor AXOR69 cDNA.								
XX									
KW	G-protein coupled receptor; receptor; AXOR69; human; anti-HIV; virucide;								
KW	antimicrobial; analgesic; cyostatic; antidiabetic; anorectic; anabolic;								
KW	antiasthmatic; antiparkinsonian; cardiac; cerebroprotective;								
KW	hypotensive; hypertensive; antidiuretic; antiasthmatic; antiallergic;								

03-APR-2002.
12-JUN-2001; 2001GB-00014287.
16-JUN-2000; 2000US-00596400.
(SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
(SMIK) SMITHKLINE BEECHAM PLC.
Elshourbagy N, Gattu M, Shabon U;
WPI; 2002-294789/34.
P-PSDB; ABB75712.
An isolated human G-protein coupled (7TM) receptor AXOR 69 polypeptide, for treating diseases such as obesity, stroke and anxiety.
Claim 2; Page 27; 34pp; English.
The present sequence is that of cDNA encoding a human G-protein coupled receptor, termed AXOR69 (see ABB75712). AXOR69 shows homology to other members of the G-protein coupled receptor family, such as the human adrenergic alpha-1a receptor. The invention provides AXOR69 polypeptides and polynucleotides, and methods for producing such polypeptides by recombinant techniques. Also provided are methods for using the AXOR69 polypeptides and polynucleotides to screen for compounds that stimulate or inhibit AXOR69 levels or activity. The polypeptides, polynucleotides, agonists and antagonists are used to treat conditions associated with AXOR69 imbalance, including bacterial, fungal, protozoan and viral infections, particularly HIV-1 and HIV-2 infections, pain, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, and dyskinesias such as Huntington's disease and Gilles de la Tourette syndrome. The polynucleotides can also be used for diagnosing mutations, in chromosome localisation studies, in pharmacogenomics, and to construct transgenic animals. The polypeptides and polynucleotides are also useful as vaccines
Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
Query Match 100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 361 ACCATTGCTTGGTGTGTCAGTGTGATGCTACTGTTGTCATCATCCACTCTCTCTCAACCG 420
DB 361 ACCATTGCTTGGTGTGTCAGTGTGATGCTACTGTTGTCATCATCCACTCTCTCTCAACCG 420
QY 421 TCCAAAGTAAACCAACGCGCGGTTAACTGCTCTCTAAGGCACTGGATTGGGCAATC 480
DB 421 TCCAAAGTAAACCAACGCGCGGTTAACTGCTCTCTAAGGCACTGGATTGGGCAATC 480
QY 481 CTGCAAGACATCTCTCACTCTACAGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 540
DB 481 CTGCAAGACATCTCTCACTCTACAGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 540
QY 541 CTGTGCTTCATGATCTGGGGGGCCAGCCCACTACATATTCTGAGCTGTGCTCTTC 600
DB 541 CTGTGCTTCATGATCTGGGGGGCCAGCCCACTACATATTCTGAGCTGTGCTCTTC 600
QY 601 ATGCTCATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATGCTCATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 AGGCAAGATGCTCTGCTGATCAATGTCAGAGACACAGCTTGGAAAGTGCGATCAAGAC 720
DB 661 AGGCAAGATGCTCTGCTGATCAATGTCAGAGACACAGCTTGGAAAGTGCGATCAAGAC 720
QY 721 TGTGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
DB 721 TGTGTGAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 780
QY 781 GAGTTTCCGCGCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 GAGTTTCCGCGCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GACGAGCTTGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
DB 841 GACGAGCTTGAAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
DB 901 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
DB 961 AAGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 1021 GTCAACAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GTCAACAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AATTTCAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 AATTTCAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CGTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
DB 1141 CGTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 ATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 CTGGCGGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 CTGGCGGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 TGGCTTTTCTTCTGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 TGGCTTTTCTTCTGAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 ATTAAGAAGGAATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
DB 1381 ATTAAGAAGGAATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1441 GAAGATAGCAACCAAGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500

Db	1441	GAAGATGACGCCAGACCTGCGCCGAGACAGGGGTGGGACTGAAGGCAAGATTGTCCCT	1500
Qy	1501	TCCTACGATTCTGCTACTCTTTTCCTTGA	1527
Db	1501	TCCTACGATTCTGCTACTCTTTTCCTTGA	1527
RESULT 3			
ID	AAD41159	standard; cDNA; 1527 BP.	
AC	AAD41159;		
DT	30-OCT-2002	(first entry)	
DE	Human HGPRBMY8 cDNA.		
KW	Human; G-protein coupled receptor; GPCR; HGPRBMY8; drug screening; neurological disorder; brain; immunological; cell growth; cytostatic; neoplastic disease; cAMP; signalling pathway; immune disorder; cancer; gene therapy; tumour; gene; ss.		
OS	Homo sapiens.		
PH	Key	Location/Qualifiers	
FT	CDS	1..1527	
FT		/*tag= a	
FT		/product= "Human HGPRBMY8 protein"	
FT		replace(370, G)	
FT		/*tag= b	
FT		/standard_name= "Single nucleotide polymorphism"	
FT		replace(1055, G)	
FT		/*tag= c	
FT		/standard_name= "Single nucleotide polymorphism"	
FT		replace(1192, A)	
FT		/*tag= d	
FT		/standard_name= "Single nucleotide polymorphism"	
FT		replace(1193, A)	
FT		/*tag= e	
FT		/standard_name= "Single nucleotide polymorphism"	
FT		replace(1194, G)	
FT		/*tag= f	
FT		/standard_name= "Single nucleotide polymorphism"	
XX	WO200240670-A2.		
XX	PN		
XX	23-MAY-2002.		
XX	PD		
XX	PF	14-NOV-2001; 2001WO-US043909.	
XX	PR	14-NOV-2000; 2000US-0248285P.	
XX	PR	14-FEB-2001; 2001US-0246581P.	
XX	PR	27-JUL-2001; 2001US-0308285P.	
XX	PR	04-SEP-2001; 2001US-0317166P.	
XX	PA	(BRIM) BRISTOL-MYERS SQUIBB CO.	
XX	PI	Batrangino P, Feder J, Mintlier G, Nelson T, Ramanathan C;	
XX	PI	Weepthal R, Cacace A, Barber L, Hawken D, Kornacker M;	
XX	DR	WPI; 2002-519383/55.	
XX	DR	P-PSDB; AAE25236.	
XX	PT	A substantially purified human G-protein coupled receptor polypeptide, termed HGPRBMY8, useful for treating a neurological disorder or brain disorder in a mammal.	
XX	PS	Claim 1; Page 160-161; 223pp; English.	
CC	The invention relates to human G-protein coupled receptor (GPCR), termed HGPRBMY8 and its corresponding nucleic acid. HGPRBMY8 DNA is useful for screening for candidate compounds which are small molecules, biological		

CC	agents,therapeutics or drugs. HGPBWM8 or its homologue is useful for
CC	treating a neurological disorder or a disease, a disorder or condition
CC	related to the brain in a mammal. It is used for treating or preventing
CC	neurological disorders, conditions or diseases and for inducing an
CC	immunological response in a mammal. HGPBWM8 DNA, protein and its
CC	antibody are useful in the diagnosis, treatment or prevention of
CC	disorders associated with aberrant or uncontrolled cellular growth and/
CC	or function, such as neoplastic diseases e.g., cancers and tumours and
CC	diseases or disorders related to the brain, e.g., neurological disorders.
CC	HGPBWM8 DNA and protein are useful for modulating intracellular cAMP
CC	associated signalling pathways. An expression vector containing HGPBWM8
CC	DNA is useful to treat or prevent neoplastic disorders such as cancer or
CC	tumours, immune disorders or neurological disorders. HGPBWM8 DNA is used
CC	in gene therapy. The present sequence is human HGPBWM8 CDNA
XX	
XX	
Sequence 1527 BP; 347 A; 439 G; 419 G; 322 T; 0 U; 0 Other;	
Query Match	100.0%; Score 1527; DB 6; Length 1527;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1527; Conservative	100.0%; Mismatches 0; Indels 0; Gaps 0
1	ATGAGCTCCACCTGCAACCAAGCAGCGCGAGATTAACAGCAGCCACACGTGATGCC 60
1	ATGAGCTCCACCTGCAACCAAGCAGCGCGAGATTAACAGCAGCCACACGTGATGCC 60
61	CTCTCCAAAATGCCATCAGCCTGGCCCAACGGCATATCCGCTCAACGCTGCTGTTATC 120
61	CTCTCCAAAATGCCATCAGCCTGGCCCAACGGCATATCCGCTCAACGCTGCTGTTATC 120
121	TTCCCTGCGCGGCTCTTTGCTGGGCAAAATAGTGCCTGGGGCTAAGTTCAGAGCGAAAGCG 180
121	TTCCCTGCGCGGCTCTTTGCTGGGCAAAATAGTGCCTGGGGCTAAGTTCAGAGCGAAAGCG 180
181	CAGCTGCTGAGAGTAGCAACCAACGGTTTATCTTTAACTCTCTGACACGACCTGCTGAG 240
181	CAGCTGCTGAGAGTAGCAACCAACGGTTTATCTTTAACTCTCTGACACGACCTGCTGAG 240
241	ATTGGCTCTGAGCCGCCCTGGGTGGGCCACACTCTGTGCTCTCTTCTGAGCCCTCAAC 300
241	ATTGGCTCTGAGCCGCCCTGGGTGGGCCACACTCTGTGCTCTCTTCTGAGCCCTCAAC 300
301	AGCCACTTCTGACGGGCCCTGGTTAGCTCAACCCACCTGTTGCTTGGCCAGGCTCAAC 360
301	AGCCACTTCTGACGGGCCCTGGTTAGCTCAACCCACCTGTTGCTTGGCCAGGCTCAAC 360
361	ACCATTTGCTTGGTGTGACGTGGATGCGTACTTGTGCATCATCAACCTCTCTCTCAACCG 420
361	ACCATTTGCTTGGTGTGACGTGGATGCGTACTTGTGCATCATCAACCTCTCTCTCAACCG 420
421	TCCAAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGCGACCTGGAATTGTGGCCATC 480
421	TCCAAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGCGACCTGGAATTGTGGCCATC 480
481	CTGCGAGAGCACTCTCTCACTCTACGGCTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT 540
481	CTGCGAGAGCACTCTCTCACTCTACGGCTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT 540
541	CTGCGAGAGCACTCTCTCACTCTACGGCTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT 540
541	CTGCGAGAGCACTCTCTCACTCTACGGCTGGGGCCAGGCTGCTTGTGATGAGCGCAATGCT 540
601	ATTCGTCATTCACATGATTGTCAATGATGCTGCTCACTCCGTGCTGTTCTGTGCAACCGCG 660
601	ATTCGTCATTCACATGATTGTCAATGATGCTGCTCACTCCGTGCTGTTCTGTGCAACCGCG 660
661	AGGCGAGCATGCTCTGCTGTACATGTCAAAGACAACAGCTTGGAGTGGAGTCAAAGAC 720
661	AGGCGAGCATGCTCTGCTGTACATGTCAAAGACAACAGCTTGGAGTGGAGTCAAAGAC 720
721	TGTGTGAGGAATGAGAGTGAAGAGGACACAGAGAAGAGAGAGATTCAGATGAGAGT 780
721	TGTGTGAGGAATGAGAGTGAAGAGGACACAGAGAAGAGAGAGATTCAGATGAGAGT 780

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QY 781 GAGTTTCCGCCGACGATGAAGGTGAGTTCAGAGCCAGAGGCGCAAGATGAGAGCCAAAG 840
DB 781 GAGTTTCCGCCGACGATGAAGGTGAGTTCAGAGCCAGAGGCGCAAGATGAGAGCCAAAG 840
QY 841 GACGGAGGCTGAGAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GACGGAGGCTGAGAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 AGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 AGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GTCACACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GTCACACAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 AATTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1140
DB 1081 AATTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1140
QY 1141 CGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 CGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 ATCTTATCATATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
DB 1201 ATCTTATCATATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1260
QY 1261 CTGGCCGTGGGTGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 CTGGCCGTGGGTGAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 TGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
DB 1321 TGGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1380
QY 1381 ATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB 1381 ATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB 1441 GAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY 1501 TCTACGATTTGCTACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1527
DB 1501 TCTACGATTTGCTACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1527

RESULT 4
ID AEA33069 standard; DNA; 1527 BP.
AC AEA33069;
XX
XX 11-AUG-2005 (first entry)
DB Human G-protein coupled receptor HGRPMY8 gene Seg1.
XX
XX protein purification; cytosolic; neuroprotective; antiparkinsonian;
XX tranquilizer; hypotension; anti-HIV; virucide; osteopathic cancer;
XX asthma; allergy; HIV infection; osteoporosis; Parkinson's disease;
XX anxiety disorder; hypertension; neurological disease; gene; ds; HGRPMY8;
XX G protein coupled receptor.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1527
```

```
FT FT /*tag= a
FT FT /product= "Human G-protein coupled receptor HGRPMY8
FT FT protein"
XX
XX MO2005048951-A2.
XX
XX 02-JUN-2005.
XX
XX 12-NOV-2004; 2004WO-US038387.
XX
XX 13-NOV-2003; 2003US-00712615.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Battaglini P, Feder JN, Mintier G, Nelson TC, Ramanathan CS;
XX Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX WPI; 2005-395945/40.
XX
XX P-PSDB; AEA33070.
XX
XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
XX polynucleotide, useful for diagnosing or treating cancer, asthma,
XX allergies, HIV, osteoporosis, anxiety, hypertension and neurological
XX diseases.
XX
XX Claim 1; SEQ ID NO 1; 261pp; English.
XX
XX This invention relates to a novel isolated human G-protein and the DNA
XX sequence which encodes it. The invention may be useful for the
XX development of compounds with a cytosolic, neuroprotective,
XX antiparkinsonian, tranquilizer, hypotension, anti-HIV, virucide or
XX osteopathic activity acting as G-protein antagonists. The methods and
XX compositions of the present invention are useful for the diagnosis,
XX prevention and/or treatment of diseases or conditions associated with
XX aberrant expression or activity of the human G-protein coupled receptor,
XX HGRPMY8, such as cancer, asthma, allergies, HIV infections,
XX osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
XX diseases. The present sequence is that of the human HGRPMY8 gene of the
XX invention.
XX
XX Sequence 1527 BP; 347 A; 439 C; 419 G; 322 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1527; DB 14; Length 1527;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ATGAGCTCCAGCTGACCAACAGCAGCGCGAGAGTACAGAGCCACAGTGCATGCC 60
DB 1 ATGAGCTCCAGCTGACCAACAGCAGCGCGAGAGTACAGAGCCACAGTGCATGCC 60
QY 61 CTCTCCAAATGCCATGAGCTGGCGGCGGAGATCATCCGCTCAACCGTGGCTATTC 120
DB 61 CTCTCCAAATGCCATGAGCTGGCGGCGGAGATCATCCGCTCAACCGTGGCTATTC 120
QY 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCGG 180
DB 121 TTCCTGCGCGCTCTTTCGTCGCAACATAGTGTGCGCTAGTGTGAGCGCAAGCGG 180
QY 181 CAGCTGCTGAGAGTGAACCAACCGTTTATCTTTAACTTCTTGTCACGAGCTGTCAG 240
DB 181 CAGCTGCTGAGAGTGAACCAACCGTTTATCTTTAACTTCTTGTCACGAGCTGTCAG 240
QY 241 ATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 ATTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 AGCACTTGTGACAGCGCGCTGTGAGAGCTTCAACCACTGTTGCGCTTGCAGAGCTCAAC 360
DB 301 AGCACTTGTGACAGCGCGCTGTGAGAGCTTCAACCACTGTTGCGCTTGCAGAGCTCAAC 360
QY 361 ACCATTGCTTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
DB 361 ACCATTGCTTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 420
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QY 61 CTCCTCAAAATGCCCATTGACCTGCGCCAGGCGATCATCCGCTCAACCGGTGCTGATTATC 120
Db 92 CTCCTCAAAATGCCCATTGACCTGCGCCAGGCGATCATCCGCTCAACCGGTGCTGATTATC 151
QY 121 TTCCTGCGGCGCTCTTTCGTGGGCAACATATGCTGGCGGTATGTTTGACGCCAAGCCG 180
Db 152 TTCCTGCGGCGCTCTTTCGTGGGCAACATATGCTGGCGGTATGTTTGACGCCAAGCCG 211
QY 181 CAGCTCTGAGGTGACCAACCGTTTATCTTAACTCTGCTGTCACCGGACCTGTGACG 240
Db 212 CAGCTCTGAGGTGACCAACCGTTTATCTTAACTCTGCTGTCACCGGACCTGTGACG 271
QY 241 ATTTGCTGCTGCGGCGCCCTGCTGGGTGATGGCCACCTGTGCTCTCTTCTGGCCCTCAAC 300
Db 272 ATTTGCTGCTGCGGCGCCCTGCTGGGTGATGGCCACCTGTGCTCTCTTCTGGCCCTCAAC 331
QY 301 AGGCACCTTGTGCAAGGCGCCCTGGTTAGCTCAACCACTGTGCGCTTGGCCAGCGTCAAC 360
Db 332 AGGCACCTTGTGCAAGGCGCCCTGGTTAGCTCAACCACTGTGCGCTTGGCCAGCGTCAAC 391
QY 361 ACCATTGCTTGGTGTCAAGTATGCTAGTCTTGTGCTATGTCACCACTCTCTCTCAACCG 420
Db 392 ACCATTGCTTGGTGTCAAGTATGCTAGTCTTGTGCTATGTCACCACTCTCTCTCAACCG 451
QY 421 TCCAAAGATGACCCAGGCGCGCGGTTACCTGCTCTATGGACCTGGATTGTGGCCATC 480
Db 452 TCCAAAGATGACCCAGGCGCGCGGTTACCTGCTCTATGGACCTGGATTGTGGCCATC 511
QY 481 CTGCGAGAGCACTCTTCACTCTACCGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 540
Db 512 CTGCGAGAGCACTCTTCACTCTACCGGCTGGGGCCAGGCTGCTTTGATGAGCGCAATGCT 571
QY 541 CTCTGCTCATGATCTCTGGGGGGGCGGACCCCAAGTACATATTTCTCAGCGTGTGCTCTTC 600
Db 572 CTCTGCTCATGATCTCTGGGGGGGCGGACCCCAAGTACATATTTCTCAGCGTGTGCTCTTC 631
QY 601 ATCGTCAATTCACATGATGTTGTCATGATGCTGCTGCTACCTCGGTGTTCTGTGACGCCG 660
Db 632 ATCGTCAATTCACATGATGTTGTCATGATGCTGCTGCTACCTCGGTGTTCTGTGACGCCG 691
QY 661 AGGCACCATGCTCTGCTGTGTCATGATGTCATGAGACACACAGCTTGGAGTGCAGTCAAGAC 720
Db 692 AGGCACCATGCTCTGCTGTGTCATGATGTCATGAGACACACAGCTTGGAGTGCAGTCAAGAC 751
QY 721 TGTGTGGAAGATGAGATGAAAGGAGGACGAGAAGAGAGAGATTCACGATGAGAGT 780
Db 752 TGTGTGGAAGATGAGATGAAAGGAGGACGAGAAGAGAGAGATTCACGATGAGAGT 811
QY 781 GAGTTTCGCGCGCAGCATGAGGTGAGGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAAAG 840
Db 812 GAGTTTCGCGCGCAGCATGAGGTGAGGTCAAGGCCAAGAGGCGCAAGATGAAAGCCAAAG 871
QY 841 GACGGGAGCTTGAAAGGCCAAAGAAAGAAAGCAAGGAGGACCAAGTGAAGTGAAGGCC 900
Db 872 GACGGGAGCTTGAAAGGCCAAAGAAAGAAAGCAAGGAGGACCAAGTGAAGTGAAGGCC 931
QY 901 AGGGGAGAGGAGAGGTGACAGAGAGAGACGCTGTGGCCAGCGACCGCATGAGAGGGT 960
Db 932 AGGGGAGAGGAGAGGTGACAGAGAGAGACGCTGTGGCCAGCGACCGCATGAGAGGGT 991
QY 961 AAGGAAGGAGAGCAACAAAGTTGAGAGAAAGACAGCATGAAGGACAGCAAGGGTGCACAGAG 1020
Db 992 AAGGAAGGAGAGCAACAAAGTTGAGAGAAAGACAGCATGAAGGACAGCAAGGGTGCACAGAG 1051
QY 1021 GTCAACCAAGTGAAGATGCACTTGGGTGAAGATGACATGAGAGTTTGGTGAAGACGATC 1080
Db 1052 GTCAACCAAGTGAAGATGCACTTGGGTGAAGATGAGATGAGAGTTTGGTGAAGACGATC 1111
QY 1081 AATTTCAAGTGAAGATGACGTCGAGGAGAGTGAACAATCCCGAGAGCTTCCACCAAGTCCGT 1140
Db 1112 AATTTCAAGTGAAGATGACGTCGAGGAGAGTGAACAATCCCGAGAGCTTCCACCAAGTCCGT 1171
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QY 1141 CGTAACAGACAGCAACCTCTCTGCTGCCAGGTGCTTACCAAGTCTGTAAGTG 1200
Db 1172 CGTAACAGACAGCAACCTCTCTGCTGCCAGGTGCTTACCAAGTCTGTAAGTG 1231
QY 1201 ATCTTATCATATTTTCTCTATGTCATATCCCTGGGGCCCTACTGCTTTTAAAGATC 1260
Db 1232 ATCTTATCATATTTTCTCTATGTCATATCCCTGGGGCCCTACTGCTTTTAAAGATC 1291
QY 1261 CTGGCCGTGGGTGATGTCAGAAACCAAGGTACCCAGTGGGTATCAACATATCATC 1320
Db 1292 CTGGCCGTGGGTGATGTCAGAAACCAAGGTACCCAGTGGGTATCAACATATCATC 1351
QY 1321 TGGCTTTTCTCTGTCAGTGTGTCATCAACCCCTATGTATATGCTATGCAAGAC 1380
Db 1352 TGGCTTTTCTCTGTCAGTGTGTCATCAACCCCTATGTATATGCTATGCAAGAC 1411
QY 1381 ATTAAAGAAAGAAATCCAGACATGCTGAAGAAAGTTTCTTGCAGAGAAAGCCCCGAAA 1440
Db 1412 ATTAAAGAAAGAAATCCAGACATGCTGAAGAAAGTTTCTTGCAGAGAAAGCCCCGAAA 1471
QY 1441 GAAAGATGACCAACCAAGCTGCGCCGGAACAGAGGGGTGGAAGGCAAGATTCCT 1500
Db 1472 GAAAGATGACCAACCAAGCTGCGCCGGAACAGAGGGGTGGAAGGCAAGATTCCT 1531
QY 1501 TCCTACGATTCGCTACTTTCTCTTGA 1527
Db 1532 TCCTACGATTCGCTACTTTCTCTTGA 1558
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RESULT 6
ID AEA33115 standard; DNA; 1580 BP.
AC AEA33115;
XX
XX
XX 11-AUG-2005 (first entry)
XX
XX
XX Human GPCR HGRPMY8 gene region SegId47.
DE
XX
XX protein purification; cyrostatic; neuroprotective; antiparkinsonian;
XX tranquillizer; hypotension; anti-HIV; virucide; osteoporosis; cancer;
XX asthma; allergy; HIV infection; osteoporosis; Parkinsons disease;
XX anxiety disorder; hypertension; neurological disease; gene; ds; HGRPMY8;
XX G protein coupled receptor.
XX
XX Homo sapiens.
OS
XX
XX WO2005048951-A2.
XX
XX 02-JUN-2005.
XX
XX 12-NOV-2004; 2004WO-US038387.
XX
XX 13-NOV-2003; 2003US-00712615.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Bategialino P, Feder JN, Mintier G, Nelson TC, Ramanathan CS,
XX Westphal R, Cacace AM, Barber LE, Hawken DR, Kornacker MG;
XX WPI; 2005-395945/40.
XX
XX New isolated human G-protein coupled receptor, HGRPMY8, and encoding
XX polynucleotide, useful for diagnosing or treating cancer, asthma,
XX allergies, HIV, osteoporosis, anxiety, hypertension and neurological
XX diseases.
XX
XX Disclosure; SEQ ID NO 47; 261bp; English.
XX
XX This invention relates to a novel isolated human G-protein and the DNA
XX sequence which encodes it. The invention may be useful for the
XX development of compounds with a cyrostatic, neuroprotective,
XX antiparkinsonian, tranquillizer, hypotension, anti-HIV, virucide or
```


CC osteopathic activity acting as G-protein antagonists. The methods and
 CC compositions of the present invention are useful for the diagnosis,
 CC prevention and/or treatment of diseases or conditions associated with
 CC aberrant expression or activity of the human G-protein coupled receptor,
 CC HGPBM8, such as cancer, asthma, allergies, HIV infections,
 CC osteoporosis, Parkinson's disease, anxiety, hypertension and neurological
 CC diseases. The present sequence is that of a region of the human HGPBM8
 CC gene of the invention.
 CC XX
 SQ Sequence 1580 BP; 357 A; 456 C; 430 G; 337 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1527; DB 14; Length 1580;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGTCACCTGACCAACAGACGCGAGAGTAACAGAGCCACAGTCGATGCC 60
 DB 32 ATGAGTCACCTGACCAACAGACGCGAGAGTAACAGAGCCACAGTCGATGCC 91
 QY 61 CTCTCCAAATGCCATCAGCCTGGCCAGGCATCATCCGCTCAACCGCTGTTATC 120
 DB 92 CTCTCCAAATGCCATCAGCCTGGCCAGGCATCATCCGCTCAACCGCTGTTATC 151
 QY 121 TTCTCGCGCGCTTTTGTGGCAACATAGTCGGCGCTAGTGTGGAGGCAAGCCG 180
 DB 152 TTCTCGCGCGCTTTTGTGGCAACATAGTCGGCGCTAGTGTGGAGGCAAGCCG 211
 QY 181 CAGCTGCTGACAGTGCACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTCAG 240
 DB 212 CAGCTGCTGACAGTGCACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTCAG 271
 QY 241 ATTTGGCTGTGGCCCGCTGGGTGGTGGCCACTCTGTGCTCTCTTCTGGCCCTCAAC 300
 DB 272 ATTTGGCTGTGGCCCGCTGGGTGGTGGCCACTCTGTGCTCTCTTCTGGCCCTCAAC 331
 QY 301 ACCCACTTGTGACGGCGCTGGTTAGCTCACCACCTGTGGCGCTGGCCAGCGTCAAC 360
 DB 332 ACCCACTTGTGACGGCGCTGGTTAGCTCACCACCTGTGGCGCTGGCCAGCGTCAAC 391
 QY 361 ACCATTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 DB 392 ACCATTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 451
 QY 421 TCCAAAGTATCCAGCGCGCGGTTAAGCTGCTCTCTATGGAACCTGATTTGGCCATC 480
 DB 452 TCCAAAGTATCCAGCGCGCGGTTAAGCTGCTCTCTATGGAACCTGATTTGGCCATC 511
 QY 481 CTGCGAGACATCTCCACTCTAAGCGCTGGGCGAGGCTGCTTTGATGAGGCAATGCT 540
 DB 512 CTGCGAGACATCTCTCACTCTAAGCGCTGGGCGAGGCTGCTTTGATGAGGCAATGCT 571
 QY 541 CTCTGCTCATGATCTGGGGGGCCAGGCCAGCTACATATTCTCAGCTGATCTCTTC 600
 DB 572 CTCTGCTCATGATCTGGGGGGCCAGGCCAGCTACATATTCTCAGCTGATCTCTTC 631
 QY 601 ATGCTCATTTCCACTGATTTGATGATGCTGCTGCTACTCCGTGGTGTCTGTGACCGCG 660
 DB 632 ATGCTCATTTCCACTGATTTGATGATGCTGCTGCTACTCCGTGGTGTCTGTGACCGCG 691
 QY 661 AAGGAGCATGCTCTGTGTAACAATGTCAGAGACACAGCTGGAATGGAGTCAAGAC 720
 DB 692 AAGGAGCATGCTCTGTGTAACAATGTCAGAGACACAGCTGGAATGGAGTCAAGAC 751
 QY 721 TGTGTGAGAAATGAGATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 752 TGTGTGAGAAATGAGATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 811
 QY 781 GAGTTTCCGCGCCAGCATGAAGGTGAGTCAAGGCCAAGAGGCGCAATGAAAGCCAG 840
 DB 812 GAGTTTCCGCGCCAGCATGAAGGTGAGTCAAGGCCAAGAGGCGCAATGAAAGCCAG 871
 QY 841 GACGGAGGCTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 900

DB 872 GACGGAGGCTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGCC 931
 QY 901 AAGGGACAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 960
 DB 922 AAGGGACAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGT 991
 QY 961 AAGGAGGACAGACCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 992 AAGGAGGACAGACCAAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1051
 QY 1021 GTCAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1052 GTCAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1111
 QY 1081 AATTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1140
 DB 1112 AATTTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1171
 QY 1141 GGTAAACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1172 GGTAAACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1231
 QY 1201 ATCTTCATCATATTTTCTCTCATATGCTATCCCTGGGGCCCTACTGCTTTTATGACAG 1260
 DB 1232 ATCTTCATCATATTTTCTCTCATATGCTATCCCTGGGGCCCTACTGCTTTTATGACAG 1291
 QY 1261 CTGGCGGTGTGGTGAATGTGAAACCCAGATACCCAGAGTGGTGAATCAATTAATATC 1320
 DB 1292 CTGGCGGTGTGGTGAATGTGAAACCCAGATACCCAGAGTGGTGAATCAATTAATATC 1351
 QY 1321 TGGCTTTTCTTCTGCAATGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1380
 DB 1352 TGGCTTTTCTTCTGCAATGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1411
 QY 1381 ATTAAGAAGAAATCCAGAGATGCTGAAGAGTCTCTGCAAGAAAGCCCGGAAA 1440
 DB 1412 ATTAAGAAGAAATCCAGAGATGCTGAAGAGTCTCTGCAAGAAAGCCCGGAAA 1471
 QY 1441 GAAAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
 DB 1472 GAAAGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
 QY 1501 TCCTAAGATTCGCTACTTTTCTTTGA 1527
 DB 1532 TCCTAAGATTCGCTACTTTTCTTTGA 1558
 RESULT 7
 ACF03567
 ID ACF03567 standard; cDNA, 1584 BP.
 XX
 AC ACF03567;
 XX
 DT 15-SEP-2003 (first entry)
 XX
 DE Human NOV14a protein encoding cDNA SEQ ID NO:41.
 XX
 XX Human; NOV1; cytosolic; cardiac; antiinflammatory; immunosuppressive;
 KW antiallergic; haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic;
 KW anorectic; antiaesthetic; nephroretropic; antiarrhythmic; hepatotropic;
 KW neuroprotective; nootropic; antibacterial; vinorel; antiparasitic;
 KW relaxant; anticonvulsant; hypotensive; vasodilator; antiparkinsonian;
 KW vulnery; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
 KW cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KW autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KW acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KW Alzheimer's disease; Parkinson's disease; scit; infection; stroke;
 KW muscular dystrophy; epilepsy; wasting disorder; chromosome X; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200294870-A2.
 XX

PD 28-NOV-2002.
XX
XX 02-NOV-2001; 2001WO-US051580.
XX
XX 02-NOV-2000; 2000US-0245291P.
PR 02-NOV-2000; 2000US-0245317P.
PR 07-NOV-2000; 2000US-0246562P.
PR 08-NOV-2000; 2000US-0246871P.
PR 26-JAN-2001; 2001US-0264389P.
PR 26-JAN-2001; 2001US-0264423P.
PR 29-JAN-2001; 2001US-0264799P.
XX
XX (CURA-) CUBAGEN CORP.
XX
XX Groese WM, MacDougall JR, Smithson G, Millet I, Stone DJ,
PI Gunther E, Ellerman K, Alsbrook JP, Leplay DM, Bugues CE,
PI Spytek KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L,
PI Guo X, Fernandes ER, Varner CM, Tchernev VT, Casman SO, Shenoy S,
PI Mishra V, Furtak K, Baumgartner JC, Colman SD,
XX
XX MPI; 2003-140359/13.
DR P-PSDB; ABR57432.
XX
XX New NOVX polypeptide useful for preventing or treating NOVX-associated
PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
PT in chromosome mapping, tissue typing or pharmacogenomics.
XX
XX
XX Claim 8; Page 129; 346pp; English.
XX
XX ACF03547 to ACF03570 encode the human NOVX proteins (I) given in ABR57412
CC to ABR57435. (I) have cytostatic, cardiant, antiinflammatory, nootropic,
CC immunosuppressive, antifibrotic, haemostatic, anti-HIV, antidiabetic,
CC antiatherosclerotic, anorectic, antiaesthetic, nephroprotective, virucide,
CC antiaflibrotic, hepatotropic, neuroprotective, antibacterial, relaxant,
CC antiparasitic, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
CC vulnerary, angiogenic, and angiogenic activities, and can be used in
CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
CC be used to determine the presence or absence of (I) in a sample. The NOVX
CC polypeptides, polynucleotides encoding them, and antibodies against them,
CC are useful in manufacturing a medicament for treating or preventing a
CC syndrome associated with a NOVX-associated disorder such as hypertension,
CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,
CC autoimmune disorders, allergies, blood disorders, obesity, acquired
CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) A nephropathy,
CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
CC dystrophy, epilepsy, and other wasting disorders associated with chronic
CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX
CC sequence, which are used in an example from the present invention
XX
XX
SQ Sequence 1584 BP; 359 A; 457 C; 430 G; 338 T; 0 U; 0 Other;
Query Match 100.0%; Score 1527; DB 8; Length 1584;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTGCACCTGCACCAACAGACGCGGAGAGTAACAGACGCCACAGTCATGCC 60
DB 31 ATGAGCTGCACCTGCACCAACAGACGCGGAGAGTAACAGACGCCACAGTCATGCC 90
QY 61 CTCTCCAAATGCGCATCAGCCTGGCCACAGGCGATCATCGCTCAACCGTGTGTTATC 120
DB 91 CTCTCCAAATGCGCATCAGCCTGGCCACAGGCGATCATCGCTCAACCGTGTGTTATC 150
QY 121 TTCTCTGGCGGCTCTTTTCTGTCGCAACATATGTCCTGCGCTATGTTGACGCCAAGCCG 180
DB 151 TTCTCTGGCGGCTCTTTTCTGTCGCAACATATGTCCTGCGCTATGTTGACGCCAAGCCG 210
QY 181 CAGCTCTGAGGTGACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTGTCAG 240
DB 211 CAGCTCTGAGGTGACCAACCGTTTATCTTTAACTCTGTCACCGACCTGTGTCAG 270
QY 241 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTCTGTGCTCTCTTGTGGCCCCCTCAAC 300

DB 271 ATTTCGCTGTGGCCCCCTGGGTGTGGCCACCTCTGTGCTCTCTTGTGGCCCCCTCAAC 330
QY 301 AGCAGCTTTCGACGGCCCTGGTTAGCTCACCAACCTGTGCGCTTCCGACAGCTCAAC 360
DB 331 AGCAGCTTTCGACGGCCCTGGTTAGCTCACCAACCTGTGCGCTTCCGACAGCTCAAC 390
QY 361 ACCATTGTCTTGATGTGTCAGTGAATGCTTATGTCATCATCAACCTCTCTCAACCG 420
DB 391 ACCATTGTCTTGATGTGTCAGTGAATGCTTATGTCATCATCAACCTCTCTCAACCG 450
QY 421 TCCAGATGACCCAGGCGCGGTTTACTGCTCTCTTATGSGACCTGGAATTTGGGCATC 480
DB 451 TCCAGATGACCCAGGCGCGGTTTACTGCTCTCTTATGSGACCTGGAATTTGGGCATC 510
QY 481 CTGACAGACCTCTCAGCTTCAACGCTGCGGCGAGGCGTGCCTTTGATGAGCGCAATGCT 540
DB 511 CTGACAGACCTCTCAGCTTCAACGCTGCGGCGAGGCGTGCCTTTGATGAGCGCAATGCT 570
QY 541 CTCTGCTCATGATCTGGGGGGCCAGCCAGCTACATATTCTCAGCGTGTGTCCTTC 600
DB 571 CTCTGCTCATGATCTGGGGGGCCAGCCAGCTACATATTCTCAGCGTGTGTCCTTC 630
QY 601 ATTCGTATTCACCTGATTTGTATGATTCCTGCTACTCCGTGTGTTCTGTGACGCCG 660
DB 631 ATTCGTATTCACCTGATTTGTATGATTCCTGCTACTCCGTGTGTTCTGTGACGCCG 690
QY 661 AGGAGCATGCTCTGCTGTCATATGTCATGATTCAGAGACACAGCTTGGAGTGGAGCAAGAC 720
DB 691 AGGAGCATGCTCTGCTGTCATATGTCATGATTCAGAGACACAGCTTGGAGTGGAGCAAGAC 750
QY 721 TGTGTGAGAAATGAGATGAAGAGGAGAGAGAGAGAGAGAGTTCAGATGAGAGT 780
DB 751 TGTGTGAGAAATGAGATGAAGAGGAGAGAGAGAGAGAGAGTTCAGATGAGAGT 810
QY 781 GAGTTTCCGCGCAGCATTAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 811 GAGTTTCCGCGCAGCATTAAGGTGATGATGATGATGATGATGATGATGATGATGATGAT 870
QY 841 GACGGAGGCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 871 GACGGAGGCTGAAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 901 AGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 931 AGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
QY 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 991 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
QY 1021 GTCAACCAATGACAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1051 GTCAACCAATGACAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1110
QY 1081 AATTTCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1111 AATTTCAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1170
QY 1141 CGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1171 CGTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1230
QY 1201 ATCTTCATATCATATTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1231 ATCTTCATATCATATTTCTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 1290
QY 1261 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1291 CTGGCCGTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1350
QY 1321 TGGCTTTTCTTCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380

DB 1351 TGGCTTTCTTCCTGACGTGCTGATCCACCCCTTGTCTATGCTATGCAACAAGACC 1410
QY 1351 ATTAAGAAGAAATCCAGACATGCTGAAGAATTCTTCTGCAAGAAAAGCCCGAAA 1440
DB 1411 ATTAAGAAGAAATCCAGACATGCTGAAGAATTCTTCTGCAAGAAAAGCCCGAAA 1470
QY 1441 GAAATAGCCACCCGACCTGCGGAAACAGAGGCTGGAGCTGAAGGCAAGTTGTCCCT 1500
DB 1471 GAAATAGCCACCCGACCTGCGGAAACAGAGGCTGGAGCTGAAGGCAAGTTGTCCCT 1530
QY 1501 TCCCTAGATTCTGCTACTTTCTTCTGA 1527
DB 1531 TCTTAGCATTCCTACTACTTTCTTCTGA 1557

RESULT 8
ACCS8886
ID ACCS8886 standard; cDNA, 4718 BP.
ACCS8886;
ACCS8886;
22-SEP-2003 (first entry)
XX Human G-protein coupled receptor OM_10 cDNA.
DE
XX G-protein coupled receptor; OM_10; human; receptor; cardiac;
KW hypertensive; hypotensive; antianginal; cyostatic; antipariatic;
KW analgesic; gynaecological; antidepressant; antispasmodic;
KW neurologic; tranquilizer; nephrotoxic; antitumor; antiallergic;
KW nocotropic; anticonvulsant; neuroprotective; antiparkinsonian;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 332.1858
FT CDS /tag=a
FT /product="OM_10"
XX
XX MO200304162-A2.
XX
XX 30-MAY-2003.
XX
XX 12-NOV-2002; 2002MO-US036204.
XX
XX 16-NOV-2001; 2001US-0332110P.
XX
XX (AMHP) WYETH.
XX
XX Blacher M, Paulsen JE, Bates BG;
XX
XX MPI; 2003-449811/42.
DR P-PDB; ABR42865.
XX
XX New polynucleotides encoding G-protein coupled receptor, i.e. OM-10 and
PT UP-11 polypeptides, useful for diagnosing, preventing and treating, e.g.
PT Parkinson's disease, acute heart failure, hypertension, cancer or
PT osteoporosis.
XX
XX Claim 49; Page 174-178; 190pp; English.
XX
XX The present sequence is that of cDNA encoding a novel human G-protein
CC coupled receptor (GPCR) termed OM_10. This orphan GPCR was identified
CC from a genome database search using the human 5-HT6 receptor sequence.
CC Identified regions of genomic DNA were used to predict full-length genes,
CC and these gene predictions were used to isolate the present sequence from
CC a cDNA library. OM_10 is predominantly expressed in the putamen and
CC caudate nucleus. OM_10 and UP_11 polypeptides, polynucleotides, agonists
CC and antagonists of the invention are useful in drug screening assays,
CC pharmacogenomics, monitoring of effects during clinical trial, or for
CC diagnosing, preventing and treating diseases associated with enhanced or
CC inhibited GPCR activity, e.g. acute heart failure, hypertension,
CC hypertension, angina pectoris, myocardial infarction, hyperproliferative

CC diseases such as cancers and psoriasis, apoptotic diseases, pain,
CC endometriosis, anorexia, bulimia, asthma, osteoporosis, schizophrenia,
CC delirium, depression, anxiety, urinary retention, ulcer, allergies,
CC dyskinesias such as Huntington's disorder or Gilles de la Tourette's
CC syndrome, Alzheimer's disease, or Parkinson's disease
XX
SQ Sequence 4718 BP; 1359 A; 1078 C; 1060 G; 1221 T; 0 U; 0 Other;
Query Match 100.0%; Score 1527; DB 9; Length 4718;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1527; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGTCACTCTGACCAACAGACAGCGGCAAGTAAACAGACACCACTGATGCCC 60
DB 332 ATGAGTCACTCTGACCAACAGACAGCGGCAAGTAAACAGACACCACTGATGCCC 391
QY 61 CTCTCAAAATGCCATCAGCTGAGCCGCAAGCAATCATCGCTCAACCGCTGGATTATC 120
DB 392 CTCTCAAAATGCCATCAGCTGAGCCGCAAGCAATCATCGCTCAACCGCTGGATTATC 451
QY 121 TTCTCGCGGCTCTTTTGTGCGCAACATAGTGTGCGCTAGTGTTCAGCGCAAGCCG 180
DB 452 TTCTCGCGGCTCTTTTGTGCGCAACATAGTGTGCGCTAGTGTTCAGCGCAAGCCG 511
QY 181 CAGCTGCTGCAAGTACCAACCGTTTATCTTTAACCCTCTGCTCAACGACCTGCTGAG 240
DB 512 CAGCTGCTGCAAGTACCAACCGTTTATCTTTAACCCTCTGCTCAACGACCTGCTGAG 571
QY 241 ATTTGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
DB 572 ATTTGCGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 631
QY 301 AGCCATTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 632 AGCCATTCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 691
QY 361 ACCATTGCTTGGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCT 420
DB 692 ACCATTGCTTGGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCTAGTGTGCT 751
QY 421 TCCAGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 752 TCCAGATGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 811
QY 481 CTGAGAGCACTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 540
DB 812 CTGAGAGCACTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 871
QY 541 CTCTGCTCAATGATCTGGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
DB 872 CTCTGCTCAATGATCTGGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 931
QY 601 ATCGCATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 932 ATCGCATTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991
QY 661 AGGAGCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 992 AGGAGCACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
QY 721 TGTGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 780
DB 1052 TGTGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1111
QY 781 GAGTTTCCCGCGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 840
DB 1112 GAGTTTCCCGCGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1171
QY 841 GAGCGACCTGTAAGGCGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 900
DB 1172 GAGCGACCTGTAAGGCGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 1231
QY 901 AGGGGACGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 960

Dd	1232	AGGGGACACGAGAGGTCAAGAGAAGCAGCACGGTGGCCACCGACGAACGGACGATGGAAGGT	1291
Oy	961	AAGGAAAGCAGCAACCAANGTTGAGAGAAACAGCATGAAGGCACAAGGGTGCGACAGAG	1020
Dd	1292	AAGGAAAGCAGCACCAAAAGTTGAGAGAAACAGCATGAAGGCAGACAAAGGGTGCGACAGAG	1351
Oy	1021	GTCAACCACTGCACGATTGACTTGGGTGAATAATGACATGAGATTGGTAAGAAGACGACATC	1080
Dd	1352	GTC AACCACTGCACGATTGACTTGGGTGAATAATGACATGAGATTGGTAAGAAGACGACATC	1411
Oy	1081	AATTTCACTGAGSATTGACGTGCGAGSAGTGAACATCCCGAGAGAGCTCCACCAGTGGT	1140
Dd	1412	AATTTCACTGAGSATTGACGTGCGAGSAGTGAACATCCCGAGAGAGCTCCACCAGTGGT	1471
Oy	1141	CGTAAACAGCAAACAGCAACCTCTCTGCCCCAGGTCTACCAATGCCAAGCTCTAAAGTG	1200
Dd	1472	CGTAAACAGCAAACAGCAACCTCTCTGCCCCAGGTCTACCAATGCCAAGCTCTAAAGTG	1531
Oy	1201	ATCTTCATCATCATTTTCTCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTTAGCACTC	1266
Dd	1532	ATCTTCATCATCATTTTCTCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTTAGCACTC	1591
Oy	1261	CTGGCCGCTGGGGGTGAGATGTGAAAACCAAGGATCCCAGTGGGTGATGACCATATATATC	1320
Dd	1592	CTGGCCGCTGGGGGTGAGATGTGAAAACCAAGGATCCCAGTGGGTGATGACCATATATATC	1651
Oy	1321	TGGCTTTTCTTCTCTGCACTGCTGATCCACCCCTATGTCTATAGCTACATGACAAAGCC	1380
Dd	1652	TGGCTTTTCTTCTCTGCACTGCTGATCCACCCCTATGTCTATAGCTACATGACAAAGCC	1711
Oy	1381	ATTAAAGANGAATATCCAGACATGCTGAAAGATTCTTCTCGAAGAAAGACCCCGGAA	1440
Dd	1712	ATTAAAGANGAATATCCAGACATGCTGAAAGATTCTTCTCGAAGAAAGACCCCGGAA	1771
Oy	1441	GAAAGTAGCCACCCAGACCTGCCCCGGGAAACAAAGGTTGGGACCTGAAGAGCAATGTCCCT	1500
Dd	1772	GAAAGTAGCCACCCAGACCTGCCCCGGGAAACAAAGGTTGGGACCTGAAGAGCAATGTCCCT	1831
Oy	1501	TCCTACGATTCGTGCTACTTTTCTCTTGA	1527
Dd	1832	TCCTACGATTCGTGCTACTTTTCTCTTGA	1858
RESULT 9			
AAS42857			
ID	AAS42857	standard; cDNA; 1527 BP.	
XX	AAS42857;		
DT	18-DEC-2001	(first entry)	
DE	Human G Protein-Coupled Receptor (GPCR) cDNA #52.		
XX	Human, G-protein coupled receptor; GPCR; mental disorder; schizophrenia;		
KM	attention deficit disorder; anxiety; depression; bipolar disorder; ss;		
KW	neurological disorder; Huntington's disease; dementia; obesity; anorexia;		
KM	metabolic disorder; Parkinson's disease; Tourette's syndrome; chondro-		
KW	type 2 diabetes; cardiovascular disorder; myocardial infarction; cancer;		
KM	cardiomyopathy; atherosclerosis; human immunodeficiency virus; HIV;		
KW	viral infection; immunostimulant; neuroleptic; nootropic; tranquilizer;		
KM	antidepressant; anorectic; PCR primer; gene therapy.		
OS	Homo sapiens.		
PN	WO200162797-A2.		
PD	30-AUG-2001.		
PF	23-FEB-2001; 2001WO-US005676.		
PR	23-FEB-2000; 2000US-0184247P.		
PR	23-FEB-2000; 2000US-0184303P.		

XX	23-FEB-2000;	2000US-0184304P.	
PR	23-FEB-2000;	2000US-0184305P.	
PR	23-FEB-2000;	2000US-0184357P.	
PR	02-MAR-2000;	2000US-0186457P.	
PR	03-MAR-2000;	2000US-0186810P.	
PR	09-MAR-2000;	2000US-0188064P.	
PR	13-MAR-2000;	2000US-0188880P.	
PR	03-APR-2000;	2000US-0194344P.	
PR	23-JUN-2000;	2000US-0213861P.	
PR	11-JUL-2000;	2000US-0217369P.	
PR	11-JUL-2000;	2000US-0217370P.	
PR	14-JUL-2000;	2000US-0218337P.	
PR	20-JUL-2000;	2000US-0218492P.	
XX	(PHAA)	PHARMACIA & UPJOHN CO.	
FA			
XX			
PI	Vogel G, Wood LS, Parodi LA, Lind P;		
XX			
DR	WPI: 2001-570628/64.		
DR	P-PSDB; AAU25605.		
XX			
XX	New isolated nucleic acid encoding a new G-protein coupled receptor		
PT	polypeptide for detecting receptor modulators that can treat mental		
PT	disorders, such as schizophrenia, anxiety, depression, or obesity.		
XX			
XX	Claim 4; Page 89-90; 279pp; English.		
CC	Sequences AAS42806-AA42926 represent cDNA molecules and PCR primers for		
CC	cDNA molecules encoding human G-protein coupled receptor (GPCR)		
CC	polypeptides. The protein and DNA sequences of the invention can be used		
CC	to identify compounds which bind to GPCR polypeptides and in screening		
CC	for compounds that modulate GPCR activity. By screening a human subject		
CC	for the presence of mutations in GPCR DNA, a GPCR-related disorder or a		
CC	genetic predisposition can be diagnosed. The sequences can also be used		
CC	for treatment and prevention of mental disorders such as schizophrenia,		
CC	attention deficit disorder, anxiety, depression, dementia and bipolar		
CC	disorder, neurological disorders such as Huntington's disease,		
CC	Parkinson's disease and Tourette's syndrome, metabolic disorders such as		
CC	obesity, anorexia and type 2 diabetes, cardiovascular disorders such as		
CC	thrombosis, myocardial infarction, cardiomyopathy and atherosclerosis,		
CC	viral infections caused by HIV and cancers		
XX			
XX			
SQ	Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;		
Query Match	99.9%; Score 1525.4; DB 4; Length 1527;		
Best Local Similarity	99.9%; Pred. No. 0;		
Matches 1526; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
OY	1 ATGAGCTGCACCTTGCACCAACAGACGCGGAGAGTAAACAGACGACACAGTGCATGCC	60	
DB	1 ATGAGCTGCACCTTGCACCAACAGACGCGGAGAGTAAACAGACGACACAGTGCATGCC	60	
OY	61 CTCCTCCAAAATGCCATCAGCGTGGCCGACGAGCATATCCGCTCAACCGTGTGTTATC	120	
DB	61 CTCCTCCAAAATGCCATCAGCGTGGCCGACGAGCATATCCGCTCAACCGTGTGTTATC	120	
OY	121 TTCTCTCCGCGCTTTTGTGTGCGCAATATGTCGCTAGTGTGACGCGAAGCCG	180	
DB	121 TTCTCTCCGCGCTTTTGTGTGCGCAATATGTCGCTAGTGTGACGCGAAGCCG	180	
OY	181 CAGCTGTGTCAGAGTACCAACCGTTTATCTTTAACTCTCTGTACCGACTGTCTGCAG	240	
DB	181 CAGCTGTGTCAGAGTACCAACCGTTTATCTTTAACTCTCTGTACCGACTGTCTGCAG	240	
OY	241 ATTTCGCTGTGGGCGCCCTGGGTGTGGCCACTCTGTGCTCTTCTGGCCGCTCAAC	300	
DB	241 ATTTCGCTGTGGGCGCCCTGGGTGTGGCCACTCTGTGCTCTTCTGGCCGCTCAAC	300	
OY	301 AGCCACTTTCGACAGGCGCTGTAGGCTCAACCACTGTTCGCTTCGCGACAGGTCAAC	360	
DB	301 AGCCACTTTCGACAGGCGCTGTAGGCTCAACCACTGTTCGCTTCGCGACAGGTCAAC	360	
OY	361 ACGATGTGCTTGGTGTAGTGGATCGTACTTGTGCATCATCAACCTCTCTCTACCG	420	

Db	361	ACCATTGTCGTGATGTCAGATGGATGCTACTTGTCCATATCCACCCTCTCTCAACCG	420
Qy	421	TCCAAGATACCCAGCGCCGCGGTTACCTGCTCTCTATAGGCACTGGATTGGCCATC	480
Db	421	TCCAAAGATACCCAGCGCGCGGTTACCTGCTCTCTATAGGCACTGGATTGGCCATC	480
Qy	481	CTGCAGAGCATCTCTCACTTACCGGCTGGGGCCAGGCTGCCCTTTGATAGCGCAATGCT	540
Db	481	CTGCAGAGCATCTCTCACTTACCGGCTGGGGCCAGGCTGCCCTTTGATAGCGCAATGCT	540
Qy	541	CTCTGTCATATGATCTGGGGGGCCAGGCCAGCTACATATTCTACGCTGGTGTCTTC	600
Db	541	CTCTGTCATATGATCTGGGGGGCCAGGCCAGCTACATATTCTACGCTGGTGTCTTC	600
Qy	601	ATCGTCATTCACATGATTGTCAATGATTGCTCTACTCCGTGGTGTCTGTGCAAGCCGG	660
Db	601	ATCGTCATTCACATGATTGTCAATGATTGCTCTACTCCGTGGTGTCTGTGCAAGCCGG	660
Qy	661	AGGCAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAAAGTGGAGTCAAGAC	720
Db	661	AGGCAGCATGCTCTGCTGTACATGTCAAGAGACACAGCTTGGAAAGTGGAGTCAAGAC	720
Qy	721	TGTGTGAGAAATGAGGAATGAAGGGAGAGAGAAAGAGAGATTCAGAGATGAGAT	780
Db	721	TGTGTGAGAAATGAGGAATGAAGGGAGAGAGAAAGAGAGATTCAGAGATGAGAT	780
Qy	781	GAGTTTCGCGCCAGCATGAAAGTGAGTCAAGGCCAAGGAGGCGAATGGAAGCCAG	840
Db	781	GAGTTTCGCGCCAGCATGAAAGTGAGTCAAGGCCAAGGAGGCGAATGGAAGCCAG	840
Qy	841	GACGGCAGCTCTGAAGGCCAAGGAAGAGACCGGGACCAAGTGAAGTATGTAAGGCC	900
Db	841	GACGGCAGCTCTGAAGGCCAAGGAAGAGACCGGGACCAAGTGAAGTATGTAAGGCC	900
Qy	901	AGGGCAGCAGAGAGGTCTAGAGAGACACAGCTGGCCAGGACCGGCATGAGAGGT	960
Db	901	AGGGCAGCAGAGAGGTCTAGAGAGACACAGCTGGCCAGGACCGGCATGAGAGGT	960
Qy	961	AAGGAAGCAGACCCAAAGTTAGAGAGACAGCATGAAGGCAAGCAAGGATGCGACAG	1020
Db	961	AAGGAAGCAGACCCAAAGTTAGAGAGACAGCATGAAGGCAAGCAAGGATGCGACAG	1020
Qy	1021	GTCAAACAGTGCAGCATTTGACTTGGGTGAAGTGAATGACATGAGATTTGGTGAAGCAGATC	1080
Db	1021	GTCAAACAGTGCAGCATTTGACTTGGGTGAAGTGAATGACATGAGATTTGGTGAAGCAGATC	1080
Qy	1081	AATTTCACTGAGAGATGACGTCCAGGGCAGTGAACATCCCGGAAGGCTCCACCCAGTCT	1140
Db	1081	AATTTCACTGAGAGATGACGTCCAGGGCAGTGAACATCCCGGAAGGCTCCACCCAGTCT	1140
Qy	1141	CGTAAACAGCAACAGCAACCTCTCTCTGCCCAGGTGCTTACAGTGCAGAACTCTTAAAGTG	1200
Db	1141	CGTAAACAGCAACAGCAACCTCTCTCTGCCCAGGTGCTTACAGTGCAGAACTCTTAAAGTG	1200
Qy	1201	ATCTTCATCATATTTTCTCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGAGCTC	1260
Db	1201	ATCTTCATCATATTTTCTCTATGTGCTATCCCTGGGGCCCTACTGCTTTTATAGAGCTC	1260
Qy	1261	CTGGCCGTGTGGGTGATGTCCAAACCCAGGTACCCCAATGGGTATCAACAATATCATC	1320
Db	1261	CTGGCCGTGTGGGTGATGTCCAAACCCAGGTACCCCAATGGGTATCAACAATATCATC	1320
Qy	1321	TGGCTTTTCTCTCTGAGTGTGACACCAACCTTATGTCTTAAGGCTTACATGCAAGAC	1380
Db	1321	TGGCTTTTCTCTCTGAGTGTGACACCAACCTTATGTCTTAAGGCTTACATGCAAGAC	1380
Qy	1381	ATTAAAGAGAAATCCAGGACATGCTGAAGAAATTCTTCTGCAAGGAAAAGCCCCGAAA	1440
Db	1381	ATTAAAGAGAAATCCAGGACATGCTGAAGAAATTCTTCTGCAAGGAAAAGCCCCGAAA	1440
Qy	1441	GAAATAGCCACCCAGACTTGGCCCGGACAGAGGGTGGGACTGAAAGCAAGATTGTCTT	1500
Db	1441	GAAATAGCCACCCAGACTTGGCCCGGACAGAGGGTGGGACTGAAAGCAAGATTGTCTT	1500

Db	1441	GAAATATGCCACCCAGACCTGCCCCGAGACAGAGGGTGGGACTGAAGCAAGATTGTCCT	1500
Qy	1501	TCCTACGATTCTGCTACTTTTCTTGA	1527
Db	1501	TCCTACGATTCTGCTACTTTTCTTGA	1527
RESULT 10			
AA507942			
ID	AA507942	standard; cDNA; 1527 BP.	
XX			
AC	AA507942;		
XX			
DT	23-OCT-2001	(first entry)	
XX			
DE	Human cDNA encoding G-protein coupled receptor, hrup15.		
XX			
KM	Human; G-protein coupled receptor; GPCR; hrup15; agonist;		
XX	inverse agonist; lung cancer; ss.		
OS	Homo sapiens.		
XX			
FM	Key	Location/Qualifiers	
FT	CDS	1..1527	
FT		/*tag= a	
XX		/product= "hrup15"	
PN	MO200136471-A2.		
XX			
PD	25-MAY-2001.		
XX			
PF	16-NOV-2000; 2000WO-US031509.		
XX			
PR	17-NOV-1999; 99US-0166088P.		
PR	17-NOV-1999; 99US-0166099P.		
PR	17-NOV-1999; 99US-0166369P.		
PR	23-DEC-1999; 99US-0171900P.		
PR	23-DEC-1999; 99US-0171901P.		
PR	23-DEC-1999; 99US-0171902P.		
PR	11-FEB-2000; 2000US-0181749P.		
PR	14-MAR-2000; 2000US-0189258P.		
PR	14-MAR-2000; 2000US-0189259P.		
PR	10-APR-2000; 2000US-0195898P.		
PR	10-APR-2000; 2000US-0195899P.		
PR	10-APR-2000; 2000US-0196078P.		
PR	28-APR-2000; 2000US-0200419P.		
PR	12-MAY-2000; 2000US-0203630P.		
PR	12-JUN-2000; 2000US-0210741P.		
PR	12-JUN-2000; 2000US-0210982P.		
PR	21-AUG-2000; 2000US-0226760P.		
PR	26-SEP-2000; 2000US-0235418P.		
PR	26-SEP-2000; 2000US-0235779P.		
PR	20-OCT-2000; 2000US-0242332P.		
PR	20-OCT-2000; 2000US-0242343P.		
PR	24-OCT-2000; 2000US-0243019P.		
XX			
PA	(AREN-) ARENA PHARM INC.		
XX			
PI	Chen R, Dang HT, Lowitz KP;		
XX			
DR	WP1; 2001-355616/37.		
XX			
DR	P-PSDB; AAU04369.		
XX			
PT	Endogenous and non-endogenous versions of human G-protein coupled		
PT	receptors for direct identification of candidate compounds as agonists,		
XX	inverse agonists or partial agonists for use as therapeutic agents.		
PS	Claim 31; Page 102; 160pp; English.		
XX			
CC	The sequence encodes a human G-protein coupled receptor (GPCR), hrup15.		
CC	The endogenous and non-endogenous, constitutively activated versions of		
CC	human G-protein coupled receptors (GPCR), are useful for direct		
CC	identification of candidate compounds as receptor agonists, inverse		

CC agonists or partial agonists having applicability as therapeutic agents
CC for treating diseases related to GPCR, e.g. lung cancer. Non-endogenous
CC version of human GPCRs are also utilized in research settings and in
CC vitro and in vivo system, incorporating GPCRs can be utilized to
CC elucidate and understand the roles these receptors play in the human
CC condition, both normal and diseased

XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

Query Match 99.9%; Score 1525.4; DB 5; Length 1527;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCTGCACTGCAACCAACAGACGCGGAGAGTAACAGACCAACGTCATGCCC 60
DB 1 ATGAGCTGCACTGCAACCAACAGACGCGGAGAGTAACAGACCAACGTCATGCCC 60
QY 61 CTCTCCAAAATGCCATCAAGCCCTGCGCCAGGATCATCGCTCAACCGTGTGTTATC 120
DB 61 CTCTCCAAAATGCCATCAAGCCCTGCGCCAGGATCATCGCTCAACCGTGTGTTATC 120
QY 121 TTCTCTGCGGCGCTCTTTCGTGCGCAACATGATGCTGCGCTAGTGTGAGCGCAAGCCG 180
DB 121 TTCTCTGCGGCGCTCTTTCGTGCGCAACATGATGCTGCGCTAGTGTGAGCGCAAGCCG 180
QY 181 CAGCTGCTGCAAGTGAACCAACCGTTTATCTTTAACCTCTCTGTCACGACCTGTGACG 240
DB 181 CAGCTGCTGCAAGTGAACCAACCGTTTATCTTTAACCTCTCTGTCACGACCTGTGACG 240
QY 241 ATTTGGCTGTGGCCCCCTGGTGGTGGCACTCTGTGCTCTTCTTGGCCCCCTGAC 300
DB 241 ATTTGGCTGTGGCCCCCTGGTGGTGGCACTCTGTGCTCTTCTTGGCCCCCTGAC 300
QY 301 AGGCAATTTGACGCGCGCGTGTAGCTCAACCACTGTGCGCTTCCGCAAGCTCAAC 360
DB 301 AGGCAATTTGACGCGCGCGTGTAGCTCAACCACTGTGCGCTTCCGCAAGCTCAAC 360
QY 361 ACCATTGTCTGTGTGTCAGTGTATCCCTACTTGTCCATCATCCACCTCTCTCTACCG 420
DB 361 ACCATTGTCTGTGTGTCAGTGTATCCCTACTTGTCCATCATCCACCTCTCTCTACCG 420
QY 421 TCCAAAGATACCAAGCGCGGTTACTGTCTCTATGAGCACTGTGATGTGGCCATC 480
DB 421 TCCAAAGATACCAAGCGCGGTTACTGTCTCTATGAGCACTGTGATGTGGCCATC 480
QY 481 CTGAGAGCACTCTCTCACTCTACGAGCTGGGCGCAGGCTGCTTATGAGCGCATGCT 540
DB 481 CTGAGAGCACTCTCTCACTCTACGAGCTGGGCGCAGGCTGCTTATGAGCGCATGCT 540
QY 541 CTCTGCTCATGATCTGTGGGGGCGACAGCCAGCTACATATTCTCAGCGTGTCTTC 600
DB 541 CTCTGCTCATGATCTGTGGGGGCGACAGCCAGCTACATATTCTCAGCGTGTCTTC 600
QY 601 ATCGTCATTCACACTGATTTGATGATGCTGCTACTCCGTGGTGTCTGTGACGCCG 660
DB 601 ATCGTCATTCACACTGATTTGATGATGCTGCTACTCCGTGGTGTCTGTGACGCCG 660
QY 661 AGGAGCATGCTCTGTGTACATGTCAGAGACACAGCTGTGAATGTGCAAGTCAAGAC 720
DB 661 AGGAGCATGCTCTGTGTACATGTCAGAGACACAGCTGTGAATGTGCAAGTCAAGAC 720
QY 721 TGTGTGAGAAATGAGATGAAAGAGGAGAGAGAAAGAGAGAGTTCAGAGTGAAGT 780
DB 721 TGTGTGAGAAATGAGATGAAAGAGGAGAGAGAAAGAGAGAGTTCAGAGTGAAGT 780
QY 781 GAGTTTCCGCGCCAGCATGAGGTGAGTCAAGGCGCAAGAGGCGAGATGGAAGCAAG 840
DB 781 GAGTTTCCGCGCCAGCATGAGGTGAGTCAAGGCGCAAGAGGCGAGATGGAAGCAAG 840
QY 841 GACGGAGGCTGAGAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GACGGAGGCTGAGAGGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900

QY 901 AGGAGGAGGAGAGAGTCAAGAGAGACAGACCGTGGCCAGCGGAGCATGAGGGT 960
DB 901 AGGAGGAGGAGAGAGTCAAGAGAGACAGACCGTGGCCAGCGGAGCATGAGGGT 960
QY 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 AAGGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GTCAACAGTGCAGCATTTGAGTGGTGAAGATGACATGAGTGTGGTGAAGAGCATC 1080
DB 1021 GTCAACAGTGCAGCATTTGAGTGGTGAAGATGACATGAGTGTGGTGAAGAGCATC 1080
QY 1081 AATTTCAGTGAAGATGAGTGCAGAGGAGTGAACATCCGAGAGACCTCCACCACTGCT 1140
DB 1081 AATTTCAGTGAAGATGAGTGCAGAGGAGTGAACATCCGAGAGACCTCCACCACTGCT 1140
QY 1141 CGTAAAGCAACAGCAACCTCTCTGCGCCAGGTGTACAGTGCAGAAAGTGTAAAGT 1200
DB 1141 CGTAAAGCAACAGCAACCTCTCTGCGCCAGGTGTACAGTGCAGAAAGTGTAAAGT 1200
QY 1201 ATCTTCATCATATTTTCTCTATGAGTATCCCTGGGCGCTACTGCTTTTATGAGATC 1260
DB 1201 ATCTTCATCATATTTTCTCTATGAGTATCCCTGGGCGCTACTGCTTTTATGAGATC 1260
QY 1261 CTGGCCGTTGGGTGAGATGAGAAACCAAGTACCCCACTGGGTATCAATATATC 1320
DB 1261 CTGGCCGTTGGGTGAGATGAGAAACCAAGTACCCCACTGGGTATCAATATATC 1320
QY 1321 TGGCTTTTCTCTGAGTGTGATCCACCCCTATGTCTATGAGTCAATGCAAGAGC 1380
DB 1321 TGGCTTTTCTCTGAGTGTGATCCACCCCTATGTCTATGAGTCAATGCAAGAGC 1380
QY 1381 ATTTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTTGAAGAAAGCCCGGAA 1440
DB 1381 ATTTAAGAAAGAAATCCAGGACATGCTGAAGAAAGTTCTTGAAGAAAGCCCGGAA 1440
QY 1441 GAAGATAGCACCCAGACCTGCGCGGAGAGAGGTGAGATGAAAGCAAGATTGTCCCT 1500
DB 1441 GAAGATAGCACCCAGACCTGCGCGGAGAGAGGTGAGATGAAAGCAAGATTGTCCCT 1500
QY 1501 TCTACGATTCGTGCTACTTTTCTTTGA 1527
DB 1501 TCTACGATTCGTGCTACTTTTCTTTGA 1527

RESULT 11
AA18899
ID AA18899 standard; cDNA; 1527 BP.
XX
XX AA18899;
AC
XX
DT 26-MAR-2002 (first entry)
XX
XX Human cDNA encoding alpha1a adrenergic receptor-1-like GPCR.
DE Human; ss; alpha1a adrenergic receptor; G protein-coupled receptor; GPCR;
XX
XX Human; ss; peripheral nervous system disease; central nervous system disease;
KW urinary incontinence; benign prostatic hypertrophy; infection;
KW HIV infection; human immunodeficiency virus; pain; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; obesity; acute heart failure;
KW hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergy; psychosis;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Tourette's syndrome.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT 1..1527
FT /'tag= a
FT /product= "Alpha1a adrenergic receptor"

Db 1321 TGGCTTTTCTTCTGCAAGTCGATCCACCCCTATGTCTATGCTATGCAACAAGACC 1380
 QY 1381 ATTAAGAAGAAATCCAGACATGCTGAAGAAGTTCTTCTGCAAGAAAAAGCCCGAAA 1440
 Db 1381 ATTAAGAAGAAATCCAGACATGCTGAAGAAGTTCTTCTGCAAGAAAAAGCCCGAAA 1440
 QY 1441 GAAGATAGCCACCCAGACCTGCCCCGAAACAGAGGTGGGACTGAAGGCAAGATTGTCCCT 1500
 Db 1441 GAAGATAGCCACCCAGACCTGCCCCGAAACAGAGGTGGGACTGAAGGCAAGATTGTCCCT 1500
 QY 1501 TCTACGATTCGCTACTTTTCTTGA 1527
 Db 1501 TCTACGATTCGCTACTTTTCTTGA 1527

RESULT 12

ABN86854
 ID ABN86854 standard; cDNA, 1527 BP.

AC ABN86854;

DT 10-OCT-2002 (first entry)

DE Human G-protein coupled receptor form 1 transcript cDNA.

Human; GPCR; G-protein coupled receptor; form 1; cytosolic;
 antiParkinsonian; neuroleptic; antidiabetic; antidepressant; anorectic;
 ophthalmological; gene therapy; Parkinson's disease; schizophrenia;
 retinitis pigmentosa; diabetes; depression; cancer; obesity; gene; ss;
 X chromosome.
 Homo sapiens.

Key Location/Qualifiers
 FT CDS 1..1527
 FT /tag= a
 FT /product= "GPCR form 1"

PN MO200259151-A2.

PD 01-AUG-2002.

PF 06-NOV-2001; 2001WO-US042978.

PR 26-JAN-2001; 2001US-00769741.

PA (PEKE) PE CORP NY.

PI Li Z, Cravchik A, Mlishina N, Wei M, Ketchum KA, Di Francesco V,
 Beasley EM;

XX WPI, 2002-583725/62.

DR P-PSDB; ABB81923.

PT New human G-protein coupled receptor (GPCR) peptides and nucleic acids,
 useful for treating disorders associated with abnormal expression of GPCR
 PT proteins, e.g. schizophrenia or cancer, and in screening assays or
 PT pharmacogenomics.

XX Claim 5; Fig 1; 77pp; English.

CC The invention relates to novel human G-protein coupled receptor (GPCR)
 CC polypeptides. The proteins of the invention have cytosolic, anorectic,
 CC antiParkinsonian, neuroleptic, antidiabetic, antidepressant, anorectic,
 CC and ophthalmological activity. The polynucleotides of the invention may
 CC have a use in gene therapy. The polypeptides are useful in treating
 CC disorders associated with the absence of, inappropriate, or unwanted
 CC expression of the GPCR protein, e.g. Parkinson's disease, schizophrenia,
 CC retinitis pigmentosa, diabetes, depression, cancer, or obesity. The
 CC sequence encodes the form 1 GPCR of the invention. The sequence is
 CC located on the X chromosome

XX Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;

Query Match 99.9%; Score 1525.4; DB 6; Length 1527;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCTCAACCTGCAACCAAGCAGCGCGAGAGTAAACAGACCAACGTCATGCCCC 60
 Db 1 ATGAGCTCAACCTGCAACCAAGCAGCGCGAGAGTAAACAGACCAACGTCATGCCCC 60
 QY 61 CTCTCAAAATGCGCATCAAGCCGCGCAGGATATCGCTCAACCGTGGTTATC 120
 Db 61 CTCTCAAAATGCGCATCAAGCCGCGCAGGATATCGCTCAACCGTGGTTATC 120
 QY 121 TTCCTGCGCGCTCTTTCGTCGCAACATATGTCGCGCTAGTGTGAGCGCAAGCCG 180
 Db 121 TTCCTGCGCGCTCTTTCGTCGCAACATATGTCGCGCTAGTGTGAGCGCAAGCCG 180
 QY 181 CAGCTGCTGAGGTGACCAACCGTTTATCTTTAACCTCGTCAACCGACTGTGCAG 240
 Db 181 CAGCTGCTGAGGTGACCAACCGTTTATCTTTAACCTCGTCAACCGACTGTGCAG 240
 QY 241 ATTTGCTGTGGCCCCCTGGGTGGTGGCCACTCTGTGCTCTTCTGGCCCCCTCAAC 300
 Db 241 ATTTGCTGTGGCCCCCTGGGTGGTGGCCACTCTGTGCTCTTCTGGCCCCCTCAAC 300
 QY 301 AGCACTTCTGACGCGCCCTGTTAGCTCAACCACTGTCGCTTGGCGACGTCAC 360
 Db 301 AGCACTTCTGACGCGCCCTGTTAGCTCAACCACTGTCGCTTGGCGACGTCAC 360
 QY 361 ACCATTGTCTGTGTGTCAGTGTGATGCTTGTTCATCATCAACCTCTCTCAACCG 420
 Db 361 ACCATTGTCTGTGTGTCAGTGTGATGCTTGTTCATCATCAACCTCTCTCAACCG 420
 QY 421 TCCAAATGATCCAGCGCGCGGTTACCTGCTCTTATGAGCACTTGATTTGGGCATC 480
 Db 421 TCCAAATGATCCAGCGCGCGGTTACCTGCTCTTATGAGCACTTGATTTGGGCATC 480
 QY 481 CTGCAAGACATCTCTCACTCTACGCTGAGGCGAGCTGCTTTGATAGCGCAATGCT 540
 Db 481 CTGCAAGACATCTCTCACTCTACGCTGAGGCGAGCTGCTTTGATAGCGCAATGCT 540
 QY 541 CTCTGCTCATGATCTGGGGGGGCGACGCCAGCTACATATTCTACGCTGTGCTCTTC 600
 Db 541 CTCTGCTCATGATCTGGGGGGGCGACGCCAGCTACATATTCTACGCTGTGCTCTTC 600
 QY 601 ATCGTATTCACATGATTTGTCATGATGCTGCTCTACCTGCTGCTGCTGCTGCTG 660
 Db 601 ATCGTATTCACATGATTTGTCATGATGCTGCTCTACCTGCTGCTGCTGCTGCTG 660
 QY 661 AGGCAAGCATGCTCTGCTGATCAATGTCAGAGACACAGCTTGGAGTGGAGTCAAGGAC 720
 Db 661 AGGCAAGCATGCTCTGCTGATCAATGTCAGAGACACAGCTTGGAGTGGAGTCAAGGAC 720
 QY 721 TGTGTGAAGATGAGGATGAAGAGGAGAGAGAGAGAGAGTTCAGAGTGAAGT 780
 Db 721 TGTGTGAAGATGAGGATGAAGAGGAGAGAGAGAGAGAGTTCAGAGTGAAGT 780
 QY 781 GAGTTTCGCGCGCAGCATGAAGGTGAGTCAAGGCGCAAGAGGAGTGAAGTGAAG 840
 Db 781 GAGTTTCGCGCGCAGCATGAAGGTGAGTCAAGGCGCAAGAGGAGTGAAGTGAAG 840
 QY 841 GACGCGAGCTGAAGGCGCAAGAGAGAGAGAGAGAGAGTGAAGTGAAGGCGC 900
 Db 841 GACGCGAGCTGAAGGCGCAAGAGAGAGAGAGAGAGTGAAGTGAAGGCGC 900
 QY 901 AGGCGAGCGAGAGAGTTCAGAGAGAGAGAGAGAGAGTTCAGAGTGAAGGCT 960
 Db 901 AGGCGAGCGAGAGAGTTCAGAGAGAGAGAGAGAGAGTTCAGAGTGAAGGCT 960
 QY 961 AAGGAAGGAGAGAGAGTTCAGAGAGAGAGAGAGAGAGTTCAGAGTGAAGGCT 1020
 Db 961 AAGGAAGGAGAGAGAGTTCAGAGAGAGAGAGAGAGAGTTCAGAGTGAAGGCT 1020

QY	1021	FTCAACCACTGCACGATTGACTTGGGTGGAATGACATGAGATTGTGGGAAGACGATC	1080
Db	1021	GTCAACCACTGCACGATTGACTTGGGTGGAATGACATGAGATTGTGGGAAGACGATC	1080
QY	1081	AATTTCACTGAGATGACGTGGAAGCAGTGAACATCCCGAGAGCCTTCCACCCAGTCGT	1140
Db	1081	AATTTCACTGAGATGACGTGGAAGCAGTGAACATCCCGAGAGCCTTCCACCCAGTCGT	1140
QY	1141	CGTAAACAGCAACGAAACCTCTCTGCGCCAGGTGCTACGATGCAAAAGCTGTAAGTG	1200
Db	1141	CGTAAACAGCAACGAAACCTCTCTGCGCCAGGTGCTACGATGCAAAAGCTGTAAGTG	1200
QY	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGCCCTACTGCTTTTATGACATC	1260
Db	1201	ATCTTCATCATCATTTTCTCCTATGTGCTATCCCTGGGCCCTACTGCTTTTATGACATC	1260
QY	1261	CTGGCCGCTGTGGGTGATGTGGAAACCCAGGTACCCAGTGGGTGATACCATATATCATC	1320
Db	1261	CTGGCCGCTGTGGGTGATGTGGAAACCCAGGTACCCAGTGGGTGATACCATATATCATC	1320
QY	1321	TGGCTTTTCTTCTCTGACGTGCTGATCACCCTTATGTCTATGTGCTACATGACAAAGCC	1380
Db	1321	TGGCTTTTCTTCTCTGACGTGCTGATCACCCTTATGTCTATGTGCTACATGACAAAGCC	1380
QY	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTCTTCTGCAAGAAAGCCCCCGAAA	1440
Db	1381	ATTAAAGAGAAATCCAGACATGCTGAAGAAATTCTTCTGCAAGAAAGCCCCCGAAA	1440
QY	1441	GAAAGATACCAACCCAGACCTGCCCGGAAACAGAGGTTGGAGCTGAAGCAAGATTGTCCCT	1500
Db	1441	GAAAGATACCAACCCAGACCTGCCCGGAAACAGAGGTTGGAGCTGAAGCAAGATTGTCCCT	1500
QY	1501	TCTTAGATCTGCTACTTTTCTTTGA	1527
Db	1501	TCTTAGATCTGCTACTTTTCTTTGA	1527

XX	Query Match	99.9%	Score 1525.4	DB 6	Length 1527
XX	Best Local Similarity	99.9%	Pred. No. 0		
XX	Matches 1526	Conservative 0	Mismatches 1	Indels 0	Gaps 0
CC	The invention relates to a method for screening G protein-coupled				
CC	receptor (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-				
CC	ABP95942) by extracting open-reading frames containing 6-8 transmembrane				
CC	domains with 250-1000 amino acid residues to give a gene homologous with				
CC	a known GPCR gene. The receptor proteins and encoded genes are useful for				
CC	studying in vivo signal transduction mechanism and identifying targets				
CC	for drug development e.g. based on olfactory and gustatory receptors in				
CC	form of agonists and antagonists by screening intrinsic and extrinsic				
CC	ligands as bitter taste inhibitors, taste enhancers and fragrance				
CC	improvers. Note: The sequence data for this patent did not form part of				
CC	the printed specification, but was obtained in electronic format directly				
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences				
XX	Sequence 1527 BP, 347 A, 439 C, 420 G, 321 T, 0 U, 0 Other;				
QY	1 ATGAGCTGCACCTGACCAACAGACGCGGAGAGTAAACAGACCAACGTCATGCC 60				
DB	1 ATGAGCTGCACCTGACCAACAGACGCGGAGAGTAAACAGACCAACGTCATGCC 60				
QY	61 CTCTCCAAAATGCCATCAGCTGGGCCAAGGCATCATCCGTCMAACGTCGTGATTAC 120				
DB	61 CTCTCCAAAATGCCATCAGCTGGGCCAAGGCATCATCCGTCMAACGTCGTGATTAC 120				
QY	121 TTCCTCGCGCCTCTTTCGTGCGCAACATGAGCTGGGCTAGTGTTCAGCGCAAGCGG 180				
DB	121 TTCCTCGCGCCTCTTTCGTGCGCAACATGAGCTGGGCTAGTGTTCAGCGCAAGCGG 180				
QY	181 CAGCTGCTGACAGTACCAACCCGTTTATCTTTAACTCTCTGTCACCGACTGCTGCAG 240				
DB	181 CAGCTGCTGACAGTACCAACCCGTTTATCTTTAACTCTCTGTCACCGACTGCTGCAG 240				
QY	241 ATTTCGCTGTCGCGCCCTCGGTGTGTGGCCACTGTGCGCTCTTTCGCGCCCTCAAC 300				
DB	241 ATTTCGCTGTCGCGCCCTCGGTGTGTGGCCACTGTGCGCTCTTTCGCGCCCTCAAC 300				
QY	301 AGCCACTTCTGACGCGCCCTGGTTAGCTCAACCCACTGTTGCGCTTCGCGCAGCGTCAAC 360				
DB	301 AGCCACTTCTGACGCGCCCTGGTTAGCTCAACCCACTGTTGCGCTTCGCGCAGCGTCAAC 360				
QY	361 ACCATTGTCCTGGTGTCAGTGATGCTACTTGTCCATATCACAACCTCTCTCTTCAACCG 420				
DB	361 ACCATTGTCCTGGTGTCAGTGATGCTACTTGTCCATATCACAACCTCTCTCTTCAACCG 420				
QY	421 TCCAAGATGACCCAGCGCGCGCTTACCTGCTCTCTATGACCACTCGATTGTGGCCATC 480				
DB	421 TCCAAGATGACCCAGCGCGCGCTTACCTGCTCTCTATGACCACTCGATTGTGGCCATC 480				
QY	481 CTGCAGAGCACTTCCTCACTACGAGCTGGGGCCAGGCGCTTGTGATGAGGCAATGCT 540				
DB	481 CTGCAGAGCACTTCCTCACTACGAGCTGGGGCCAGGCGCTTGTGATGAGGCAATGCT 540				
QY	541 CTCTGCTCCATGATCTGGGGGCGCAGCCCACTACACTATTCTCAGCGTGTGTCTTTC 600				
DB	541 CTCTGCTCCATGATCTGGGGGCGCAGCCCACTACACTATTCTCAGCGTGTGTCTTTC 600				
QY	601 ATGCTCATTCACAATGATGTCAATGATGCTCTCTACTCCGTGTGTTCTGTCCAGCCCG 660				
DB	601 ATGCTCATTCACAATGATGTCAATGATGCTCTCTACTCCGTGTGTTCTGTCCAGCCCG 660				
QY	661 AGGAGAGCATGCTCTGCTGTACAAATGTCMAAGACACACAGTTTGAAAGTGAAGTCAAGAC 720				
DB	661 AGGAGAGCATGCTCTGCTGTACAAATGTCMAAGACACACAGTTTGAAAGTGAAGTCAAGAC 720				
QY	721 TGTGTGAGAAATGAGAGATTAAGAGGAGCAGAGAAAGAGAGATTCCAGATGAGAGT 780				
DB	721 TGTGTGAGAAATGAGAGATTAAGAGGAGCAGAGAAAGAGAGATTCCAGATGAGAGT 780				
QY	781 GAGTTTCGCCGACAGATGAGTGAAGTCAAGGCGCAAGAGGCGCAATGGAACCAAG 840				

Accession	Position	Sequence	Feature
Dp	781	GAGTTTCGCCCCGACGATGAAGGTGAGTCAAGCCAGAGGACAGATGGAAGCCAA	
Qy	841	GACGGCAGCCCTGAAGGCCAAGAAAGAAAGCAAGCGGGACCAAGTGAAGTGTGAGAGCC	
Dp	841	GACGGCAGCCCTGAAGGCCAAGAAAGAAAGCAAGCGGGACCAAGTGAAGTGTGAGAGCC	
Qy	901	AGGGGCAAGCCAGAGGCTCAAGAGAAGCAGCAGCGTGGCCAGCCAGCATGAGAGGT	
Dp	901	AGGGGCAAGCCAGAGGCTCAAGAGAAGCAGCAGCGTGGCCAGCCAGCATGAGAGGT	
Qy	961	AAGGAAGCAGACCAAAAGTTGAGAGAGAAGCAGTGAAGGACAGCAAGGGGTCCGACAGAG	
Dp	961	AAGGAAGCAGACCAAAAGTTGAGAGAGAAGCAGTGAAGGACAGCAAGGGGTCCGACAGAG	
Qy	1021	GTCAACCAAGTCAGACATTTGACTTGGGTGAAGATGACATGAGATTGGTGAAGACGACATC	
Dp	1021	GTCAACCAAGTCAGACATTTGACTTGGGTGAAGATGACATGAGATTGGTGAAGACGACATC	
Qy	1081	AATTTCAAGTGAAGATGACATGAGCAGTGAACATCCCGAGAGCTTCCACCAAGTCGT	
Dp	1081	AATTTCAAGTGAAGATGACATGAGCAGTGAACATCCCGAGAGCTTCCACCAAGTCGT	
Qy	1141	CGTAACAGCAACAGCAACCCCTCTCTGCGCCAGGTGCTACCAAGTCAAAAGCTGCTAAAGTG	
Dp	1141	CGTAACAGCAACAGCAACCCCTCTCTGCGCCAGGTGCTACCAAGTCAAAAGCTGCTAAAGTG	
Qy	1201	ATCTTTCATCATCATTTTCTCCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTGTAGCAGTC	
Dp	1201	ATCTTTCATCATCATTTTCTCCCTATGTGCTATCCCTGGGGGCCCTACTGCTTTTGTAGCAGTC	
Qy	1261	CTGGCCCGGTGGGTGAGATGTGGAACCCAGGTACCCAGTGGGTGATCACCATAATCATC	
Dp	1261	CTGGCCCGGTGGGTGAGATGTGGAACCCAGGTACCCAGTGGGTGATCACCATAATCATC	
Qy	1321	TGGCTTTTCTTCTCTGCAATGCTGCATCCACCCCTATGTCTATGGCTACATGCAAAAGCC	
Dp	1321	TGGCTTTTCTTCTCTGCAATGCTGCATCCACCCCTATGTCTATGGCTACATGCAAAAGCC	
Qy	1381	ATTAAAGAAAGAAATTCAGAGACATGCTGAAGAAAGTTCTTCTGCAAGAAAGAGCCCGGAAA	
Dp	1381	ATTAAAGAAAGAAATTCAGAGACATGCTGAAGAAAGTTCTTCTGCAAGAAAGAGCCCGGAAA	
Qy	1441	GAAAGTACGCAACCCAGACCTTCCCGGAAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT	
Dp	1441	GAAAGTACGCAACCCAGACCTTCCCGGAAACAGAGGGTGGGACTGAAGGCAAGATTGTCCCT	
Qy	1501	TCCTACGATTTCTGCTACTTTTTCCTTGA	
Dp	1501	TCCTACGATTTCTGCTACTTTTTCCTTGA	

XX	Homo sapiens.
XX	
XX	MO200261087-A2.
XX	
XX	08-AUG-2002.
XX	
PF	19-DEC-2001; 2001MO-US050107.
XX	
XX	19-DEC-2000; 2000US-0257144P.
XX	
PA	(LIFE-) LIFESPAN BIOSCIENCES INC.
PI	Butner GC, Roush CL, Brown JP;
XX	
XX	WPI; 2003-046718/04.
DR	P-PSDB; ABP81704.
PT	New isolated antigenic peptides e.g., for G protein-coupled receptors
PT	(GPCR), useful for diagnosing and designing drugs for treating conditions
PT	in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT	autoimmune diseases.
XX	
PS	
XX	Disclosure; Fig 1; 523pp; English.
XX	
CC	The present invention describes antigenic peptides (I) comprising: (a)
CC	any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC	acids. Also described: (1) an assay for the detection of a particular G
CC	protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC	and (2) an isolated antibody having high specificity and high affinity or
CC	avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC	gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC	antibody against a particular GPCR, and in the production of specific
CC	antibodies. The peptides and antibodies are also useful for detecting the
CC	presence or absence of corresponding GPCRs. The antigenic peptides for
CC	GPCRs and antibodies are useful for diagnosing and designing drugs for
CC	treating immune-related diseases, growth-related diseases, cell
CC	regeneration-related disease, immunological-related cell proliferative
CC	diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC	atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC	osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC	inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC	disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC	anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC	loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, memory
CC	hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC	any other disorder in which GPCRs are involved. The antibodies may be
CC	used in immunoassays and immunodiagnosis. AB242553 to AB242869 encode
CC	GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC	exemplification of the present invention
XX	
XX	Sequence 1527 BP; 347 A; 439 C; 420 G; 321 T; 0 U; 0 Other;
Query Match	99.9%; Score 1525.4; DB 8; Length 1527;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 1526; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
0Y	1 ATAGACGTCACCTGACCAACAGACCGCGGAGAGTAAACGACGCCACAGCTGATGCC 60
Db	1 ATAGACGTCACCTGACCAACAGACCGCGGAGAGTAAACGACGCCACAGCTGATGCC 60
0Y	CTCTCCAAAATGCCCATCAGCTGAGCCGACGATCATCCGCTCAACCGTGTATC 120
Db	61 CTCTCCAAAATGCCCATCAGCTGAGCCGACGATCATCCGCTCAACCGTGTATC 120
0Y	121 TTCCTGCGCGCTTTTGTGCGCAATAGTGTGCGCTAGTGTGACGCGCAAGCCG 180
Db	121 TTCCTGCGCGCTTTTGTGCGCAATAGTGTGCGCTAGTGTGACGCGCAAGCCG 180
0Y	181 CAGCTGCTGACGAGTGAACCAACCTTTATCTTTAACTCTCTGACACGACTGCTGACG 240
Db	181 CAGCTGCTGACGAGTGAACCAACCTTTATCTTTAACTCTCTGACACGACTGCTGACG 240

XX Sequence 1527 BP, 347 A, 439 C, 420 G, 321 T, 0 U, 0 Other;
 Query Match 99.9%; Score 1525.4; DB 8; Length 1527;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCTCCACCTGCAACCAACAGCAGCGGAGAGTAAACAGACGCCACAGTGCATGCC 60
 DB 1 ATGAGCTCCACCTGCAACCAACAGCAGCGGAGAGTAAACAGACGCCACAGTGCATGCC 60
 QY 61 CTCTCCAAATGCCCCATCAGCCTGGGCCAAGGATATCCGCTCAACCGTGTGTATTC 120
 DB 61 CTCTCCAAATGCCCCATCAGCCTGGGCCAAGGATATCCGCTCAACCGTGTGTATTC 120
 QY 121 TTCCTGCGCGCCCTTTTCGTGGCAACATAGTCTGGCGCTAGTGTGAGCGCAAGCCG 180
 DB 121 TTCCTGCGCGCCCTTTTCGTGGCAACATAGTCTGGCGCTAGTGTGAGCGCAAGCCG 180
 QY 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTTAACCTCTGTCACCGACTGTGAC 240
 DB 181 CAGCTGCTCAGGTGACCAACCGTTTATCTTTAACCTCTGTCACCGACTGTGAC 240
 QY 241 ATTTGCGTGTGGCCCCCTGGGTGGTGGCCACTGTGCTCTCTTTCTGGCCCTCAAC 300
 DB 241 ATTTGCGTGTGGCCCCCTGGGTGGTGGCCACTGTGCTCTCTTTCTGGCCCTCAAC 300
 QY 301 AGCCACTTTCGACGCGGCCCTGGTTAGCTTCAACCCACTGTGGCCCTTCCGACGCTCAAC 360
 DB 301 AGCCACTTTCGACGCGGCCCTGGTTAGCTTCAACCCACTGTGGCCCTTCCGACGCTCAAC 360
 QY 361 ACCATTGTCTGTGTGTCAGTGTGCTACTTGTCCATCATCCACCCTCTCTCTACCCG 420
 DB 361 ACCATTGTCTGTGTGTCAGTGTGCTACTTGTCCATCATCCACCCTCTCTCTACCCG 420
 QY 421 TCCAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGAGCACTGGAATTGGCCATC 480
 DB 421 TCCAGATGACCCAGCGCGCGGTTACCTGCTCTCTATGAGCACTGGAATTGGCCATC 480
 QY 481 CTGCAAGAGCACTCTCACTCTACGCTGGGGGCAAGGCTGCTTATAGCGCCAAATGCT 540
 DB 481 CTGCAAGAGCACTCTCTCACTCTACGCTGGGGGCAAGGCTGCTTATAGCGCCAAATGCT 540
 QY 541 CTCTGCTCATGATCTGGGGGGGCAAGCCCAAGCTACATATCTCAGCGTGTCTTTC 600
 DB 541 CTCTGCTCATGATCTGGGGGGGCAAGCCCAAGCTACATATCTCAGCGTGTCTTTC 600
 QY 601 ATGCTATTCTCACTGATTTGTCATGATTGCTGCTACTCGTGTGTTCTGTGCAGCCGG 660
 DB 601 ATGCTATTCTCACTGATTTGTCATGATTGCTGCTACTCGTGTGTTCTGTGCAGCCGG 660
 QY 661 AGGCAAGCATGCTTGTGCTGTACATGTCACAGACACAGCTTGAAGTGGAGTCAAGAC 720
 DB 661 AGGCAAGCATGCTTGTGCTGTACATGTCACAGACACAGCTTGAAGTGGAGTCAAGAC 720
 QY 721 TGTGTGAGATGAGATGAGAGGAGGAGCAGAGAGAGAGAGTTCAGAGATGAGAT 780
 DB 721 TGTGTGAGATGAGATGAGAGGAGGAGCAGAGAGAGAGAGTTCAGAGATGAGAT 780
 QY 781 GAGTTTTCGCGCGCAGCATGAGGTGAGGTCAAGGCCAAGGAGGAGAAATGAAGCCAA 840
 DB 781 GAGTTTTCGCGCGCAGCATGAGGTGAGGTCAAGGCCAAGGAGGAGAAATGAAGCCAA 840
 QY 841 GAGCGAGAGCTTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGCC 900
 DB 841 GAGCGAGAGCTTGAAGGCCAAGAGAGAGAGAGAGAGAGAGAGAGTGTGAGAGCC 900
 QY 901 AGGCGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 960
 DB 901 AGGCGAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGT 960
 QY 961 AAGGAAGGAGAGCAAAAGTTGAGAGAAACAGATGAAGCAGAAAGGTCGACAGAG 1020
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Search completed: December 10, 2005, 00:23:45
 Job time : 665 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 10, 2005, 00:09:47 ; Search time 214 Seconds

(without alignments)
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Title: US-10-712-615-1

Perfect score: 1527

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1522.4	99.7	2781	3	US-10-314-048A-103
3	1520.6	99.6	1527	3	US-10-314-048A-91
4	103.8	6.8	7218	2	US-08-332-463-14
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6	98.4	6.4	1776	2	US-08-722-001-29
7	98.4	6.4	2002	2	US-09-016-434-1172
8	98.4	6.4	2140	2	US-08-334-698-1
9	98.4	6.4	2140	2	US-08-228-932-1
10	98.4	6.4	2140	2	US-08-468-939-1
11	98.4	6.4	2140	2	US-08-406-855A-1
12	98.4	6.4	2140	2	US-08-722-190-1
13	98.4	6.4	2140	3	US-08-244-354-1
14	98.4	6.4	2140	3	US-09-206-899-1
15	98.4	6.4	2140	3	US-09-444-783-1
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26	92.2	6.0	3083	3	US-08-693-308-1	Sequence 1, Appl
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44	84	5.5	2004	2	US-08-722-001-11	Sequence 11, Appl
45	84	5.5	2290	3	US-09-016-434-1368	Sequence 1368, Ap

ALIGNMENTS

RESULT 1
US-10-314-048A-15
Sequence 15, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unetl, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
APPLICANT: Choi, Bryan
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
FILE REFERENCE: 22, US6, CIP
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: US/10/314,048A
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/995,543
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/404,761
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 1527
TYPE: DNA
ORGANISM: Homo sapiens
US-10-314-048A-15
Query Match 99.9%; Score 1525.4; DB 3; Length 1527;
Best local Similarity 99.9%; Pred. No. 0;
Matches 1526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 301 AGCCACTTCTGACGCGCGCTGTGAGCTGACCTCAACCTGTGTGCGCTGTGCGCGCTCAAC 360
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Db 781 GAGTTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
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Db 1021 GTCAACGAGTGCATTTGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
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Db 1081 AATTTCAGTGAAGATGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140

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Db 1141 GGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
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RESULT 2
US-10-314-048A-103
Sequence 103, Application US/10314048A
Patent No. 6902902
GENERAL INFORMATION:
APPLICANT: Unetec, David J.
APPLICANT: Chen, Ruoping
APPLICANT: Richman, Jeremy
APPLICANT: Connolly, Daniel
APPLICANT: Dang, Huong T.
APPLICANT: Choi, Bryan
APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
FILE REFERENCE: 22, US6, CIP
CURRENT APPLICATION NUMBER: US/10/314, 048A
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 10/096, 511
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/995, 543
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399, 917
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/404, 761
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/410, 747
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 2781
TYPE: DNA
ORGANISM: Homo Sapiens and Rat
US-10-314-048A-103
Query Match 99.7%; Score 1522.4; DB 3; Length 2781;
Best Local Similarity 99.9%; Pred. No. 0;

US-10-314-048A-91

Query Match 99.6%; Score 1520.6; DB 3; Length 1527;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1523; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1441 GAAGATGACCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
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DB 1501 TCCTACGATTCGTACTTTTCTTGA 1527

RESULT 4
US-08-233-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PTGPT-Fls
US-08-232-463-14

Query Match 6.8%; Score 103.8; DB 2; Length 7218;
Best Local Similarity 3.8%; Pred. No. 2,4e-16;
Matches 15; Conservative 264; Mismatches 116; Indels 0; Gaps 0;

QY 686 TCAGAGACACAGCTTGGAAGTCCAGATGAGAGTTCGCCGCCAGCATGAAGTG 745
DB 1458 TAAAGAGATAGAGAAATTTGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1399
QY 746 GAGCAGAGAGAGAGAGAGATTCCAGATGAGAGTTCGCCGCCAGCATGAAGTG 805
DB 1398 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1339
QY 806 AGTCAGAGCCAGAGAGAGAGATGAGAGCCAGAGCCAGAGCCAGAGAGAG 865
DB 1338 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1279
QY 866 GAGCAGCGGAGACAGATGAGTGTAGAGCCAGGAGCCAGAGAGTCAAGAGA 925
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DB 1218 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1159
QY 986 AGAAGCAGTGAAGCAGAGAGAGGTCGAGCAGAGAGTCAAGCATGACTTGG 1045
DB 1158 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1099
QY 1046 GTGAAGATGACATGAGATTGTAAGACAGCATC 1080
DB 1098 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1064

RESULT 5
US-08-722-001-13
Sequence 13, Application US/08722001
Patent No. 5760054
GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huif, Joel R.
APPLICANT: Nerembey, Jennie B.
APPLICANT: Lee, Hee-Yoon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHALC ADRENALGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001

FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138625
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULAR TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-13

Query Match 6.4%; Score 98.4; DB 2; Length 1621;
Best Local Similarity 50.7%; Pred. No. 3e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCCAGGATATCCGCTCAACCGTGTGTTATCTTCTGCGCCCTTTCTGCGC 144
DB 209 GCGCAGGGGCTGGGCGTCTTCTGCGAGCCCTTATGAGCCCTGCGAGGT 268
QY 145 AACATAGTCTGCGCTAGTGTGACAGCGCAGCCAGCTGCTGAGTGACCAACGT 204
DB 266 AACCTGTTGTATCTTCAAGTGCCTGCAACCGCAGCTGACAGCTGACCACTAT 328
QY 205 TTATCTTTAATCTCTCTGTCACCGACCTGTGACAGATTTGCTGCGCCCTGCGTG 264
DB 322 TTATCTGTAACCTGCGCGTGGCCGACCTGCTGAGAGCGACCGTACTGCGCTTCTG 388
QY 265 GTGGCCACTCTGTGCTCTCTTTTGGCCCTTCAACAGCACTTGTGACGCGCCTGTT 324
DB 389 GCCACATGAGAGTTCTGGGCTTCTGGGCTTGGCCGCGCTTCTGCGACGTATGGGCGC 448
QY 325 AGCCTCACCCACTGTTGCGCTTGGCCAGCGCTCAACCATGCTGTGCTGTCAGTGAT 384
DB 449 GCCGTGACGTGCTGTGCGACGCGCTTCACTTCAAGCTTGTGACCATCTTCCGTGAC 508
QY 385 CGCTACTGTCCATCATCCACCCTCTCTCTCAACCGCTCCAAAGATGACCGAGCGCGT 444
DB 509 CGGTACGTGGGCGTGGCCACTCACTCAAGTACCCAGCATGATACCGAGCGCAAGGG 568
QY 445 TACTGCTCTCTATGACCACTGATGTGGCACTCTGACAGAGCACTTCCACTTAC 504
DB 569 GCCGCATCTGCGCTGCTGTGGTGTGAGCGCTGAGTGTGAGTGTGAGGCGCCCTGCTG 628
QY 505 GCGTGGGCGCAGCGCTTGTATAGAGCCATGCTCTGCTCATATATCTGGGGGGCC 564
DB 629 GCGTGAAGAGCCCGTGGCCCTTGA---CGAGCGCTTGTGGATATCAAGAGAG--- 683
QY 565 AGCCCGAGTACATATTCTCAGCGTGTGCTTCACTGATTCATTCATTCATGATTCATG 624
DB 684 -----CGGCTACGCTGTCTTCTCTCCGTGTGCTCTTCTTACTGCGCATGGCGGTATC 739
QY 625 ATGCTGCTACTCCGTGTGTCTGTGTGACGCGGAG 662
DB 740 GTGTCACTACTGCGCGTGTGACGTGTGCGGCGCAG 777

RESULT 6
US-08-722-001-29
Sequence 29, Application US/08722001
Patent No. 5760054

GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel R.
APPLICANT: Nerenberg, Jennie B.
APPLICANT: Lee, Hee-yeon
APPLICANT: Bell, Ian M.
TITLE OF INVENTION: ALPHALC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,001
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,276
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Appollina, Mary A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19169Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEFAX: (908) 594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-29

Query Match 6.4%; Score 98.4; DB 2; Length 1776;
Best Local Similarity 50.7%; Pred. No. 3.1e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCACGGCATCATCGCTCAACCGGCTGCTTATCTTCCTGCGCGCTCTTTCGTGGC 144
DB 337 GGGCAGGGGCTGGGCGCTGCGCTTCTCTGCGAGCTTATCTTATGCGCGAGGT 396
QY 145 AACATAGTGTGGCGTACTGTGTCAGCGCAAGCCGCACTGCTGAGGTGACCAACGT 204
DB 397 AACGTGCTGTATCTCTCAAGTGGCGTCAACCGGCACTGAGACCGTCAACATAT 456
QY 205 TTTATCTTAACTCTCTGTACACGACCTGCTGCAATTTGCTGTGGCCCCCTGGGGT 264
DB 457 TTCATCTGTAACTGTGCGCGTGTGCGCACTGTCTGAGCGCACCTTACTGTGCTTCTG 516
QY 265 GTGGGCACTGTGTGCTCTCTTTCGGGCGGCTCAACAGGCACTTTCGACGCGCGCTGT 324
DB 517 GCCACCATGAGGTTTGGGCTTCTGGGCTTTCGGGCGGCTTTCGCACTGATGGGCC 576
QY 325 AGCCTACCCACCTGTTCCCTTTCGCGCAGCTCAACACCATTTCTTGGTGTAGTGAAT 384
DB 577 GCGGTGAGAGTGTGTGCTGCAAGCGCTCATCTCTAGCTTCTGACACATCTTCCGTGAG 636
QY 385 GCGTACTTGTTCATCATCAACCTCTCTCTTACCCGCTTCAAGATGACCCAGCGCGCGGT 444
DB 637 CCGTACGTGGGGTGGCGCACTCACTCAAGTACCCAGCATCATGACGAGCGCAAGCGG 696

QY 445 TACTGTCTCTATAGCACTGATTTGSCCATCTCTGACAGACATCTTCCACTTAC 504
DB 697 GCCGCATCTGAGCCCTGCTGAGTCTGATCCCTGAGTGTCCGTAGAGGCCCTGCTG 756
QY 505 GCGTGGGGCCAGCGCTTGTGATGAGCGCAATGTCTCTGCTCATCATCATCTGAGGGCC 564
DB 757 GCGTGAAGAGAGCCGTCGCCCTGA--CGAGGCTTCTCGGTATACCGAGAGG-- 811
QY 565 AGCCCACTACATATTCTGAGCGTGTCTTTCATGTCATTCATTCATGATTTGATG 624
DB 812 ----CGGCTAGCGTGTCTTCTCCGCTGTCTCTTCTACCTGCGCATGCGGCTATC 867
QY 625 ATTGCTCTACTCCGCTGTCTTCTGTCAGCCCGGAG 662
DB 868 GTGTCTAGTACTGCGCGGTATCGTGTCCGCGCAG 905

RESULT 7
US-09-016-434-1172
Sequence 1172, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1172:
SEQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g177806
US-09-016-434-1172

Query Match 6.4%; Score 98.4; DB 3; Length 2002;
Best Local Similarity 50.7%; Pred. No. 3.3e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCACGGCATCATCGCTCAACCGTGTGCTTATCTTCTGCGCGCTCTTTCGTGGC 144
DB 209 GCGCAGGGGCTGGGCGTGTCTTCTCTGCGAGCTTATCTTATGAGCCGTGCGAGGT 268

QY 145 AACATAGTCTGCGCTAGTGTTCAGACGCAAGCCGAGCTGTGAGGTGACCAACCGT 204
DB 269 AACCTGCTTGTCACTCTCTCAGTGGCTGTGCAACGCGACCTGGAGACCGTCACTAT 328
QY 205 TTATCTTTAATCTCTCTGTCACCGAAGCTGTGCAATTTGCTGTGGCCCTTGGGTG 264
DB 329 TTCTATGTGAACCTGTGGCGGACCTGTCTGTGAGCCGACCGTATCTGCTTCTCG 388
QY 265 GTGGCAACCTGTGCTCTCTCTGAGCCCTTCAAGCAGCACTTGTGCAAGCCGTGTT 324
DB 389 GCCACCATGAGGTTCTGGGCTTCTGGGCTTGTGGCCGCTTCTGCAAGTATGGGCC 448
QY 325 AGCCTCAACCACTGTGTGCTTGTGCGGAGCTCAACCACTGTGTGTGTGATGAT 384
DB 449 GCGGTGAGAGTGTGTGCTGCAAGGCTCATCTGAGCTGTGCAACCATCTCGTGGAC 508
QY 385 CGCTACTTGTTCATTCACCACTCTCTCTCAACCGTCAAGATGACCAAGCCCGCGT 444
DB 509 CGGTACGTGGGCGGTGGCGCACTCACTCAAGTACCAAGCCATCATGACCGAGCGCAAGCG 568
QY 445 TACTGCTCTCTATGAGCACTGAGTGTGGCATCTGTGAGAGCACTCTCACTCTAC 504
DB 569 GCGGCATCTGTGCGCTCTGTGTGTGAGCCCTGTGTGTCTGTGAGGCGCTGTG 628
QY 505 GCGTGGGCGAGGCTGCTTGTGATGAGCGCATGCTCTGTCTCATGATCTGGGGGCGC 564
DB 629 GGTGAGAGAGCGCGTGGCGCCCTGA---GAGCGCTTCTGCGGTATACCGAGAGG-- 683
QY 565 AGCCCACTACATATTTCTGAGCGGTGTCTTCACTGTCAATTCAGTATGTCATG 624
DB 684 ---CGGGCTACCTGTCTCTCTCTGCTCTCTTCACTGCGCCATGAGGCGGTATC 729
QY 625 ATTGCTGTACTCCGTGTGTGTGTGTGAGCCCGAG 662
DB 740 GTGTGATGTACTGCGCGGTGTGAGTGTGCGCGAG 777

RESULT 8
US-08-334-698-1
; Sequence 1, Application US/08334698
; Patent No. 5556753
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrennergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/334,698
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/952,798
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 376901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525

TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:
US-08-334-698-1

Query Match 6.4%; Score 98.4; DB 2; Length 2140;
Best Local Similarity 50.7%; Pred. No. 3,4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCACGAGATCATCGGCTCAACCGGTGTATCTTCTGCGCGCTCTTCTGTCGCGC 144
DB 457 GCGCAGAGGCGTGGCGGTGGGCGCTTCTGTGGACCTTATCTTATGCGCGAGGT 516
QY 145 AACATAGTCTGCGCTAGTGTTCAGACGCAAGCCGAGCTGTGAGGTGACCAACCGT 204
DB 517 AACCTGCTTGTCACTCTCTCAGTGGCTGTGCAACGCGACCTGGAGACCGTCACTAT 576
QY 205 TTATCTTTAATCTCTCTGTCACCGAAGCTGTGCAATTTGCTGTGGCCCTTGGGTG 264
DB 577 TTCTATGTGAACCTGTGGCGGACCTGTCTGTGAGCCGACCGTATCTGCTTCTCG 324
QY 265 GTGGCAACCTGTGCTCTCTCTGAGCCCTTCAAGCAGCACTTGTGCAAGCCGTGTT 324
DB 637 GCCACCATGAGGTTCTGGGCTTCTGGGCTTGTGGCCGCTTCTGCAAGTATGGGCC 696
QY 325 AGCCTCAACCACTGTGTGCTTGTGCGGAGCTCAACCACTGTGTGTGTGATGAT 384
DB 697 GCGGTGAGAGGTTCTGGGCTTGTGAGCGCTCATCTCAAGCTGTGCAACCATCTCGTGGAC 756
QY 385 CGCTACTTGTTCATTCACCACTCTCTCTCAACCGTCAAGATGACCAAGCCCGCGT 444
DB 757 CGGTACGTGGGCGGTGGCGCACTCACTCAAGTACCAAGCCATCATGACCGAGCGCAAGCGC 816
QY 445 TACTGCTCTCTATGAGCACTGAGTGTGGCATCTGTGAGAGCACTCTCACTCTAC 504
DB 817 GCGGCATCTGTGCGCTCTGTGTGTGAGCCCTGTGTGTCTGTGAGGCGCTGTG 876
QY 505 GCGTGGGCGAGGCTGCTTGTGATGAGCGCAATGCTGTGCTCATGATCTGGGGGCGC 564
DB 877 GGTGAGAGAGCGCGTGGCGCCCTGA---GAGCGCTTCTGCGGTATACCGAGAGG-- 931
QY 565 AGCCCACTACATATTTCTGAGCGGTGTCTTCACTGTCAATTCAGTATGTCATG 624
DB 932 ---CGGGCTACCTGTCTCTCTCTGCTCTCTTCACTGCGCCATGAGGCGGTATC 987
QY 625 ATTGCTGTACTCCGTGTGTGTGTGTGAGCCCGAG 662
DB 988 GTGTGATGTACTGCGCGGTGTGAGTGTGCGCGAG 1025

RESULT 9
US-08-228-932-1
; Sequence 1, Application US/08228932
; Patent No. 5578611
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, Carlos C. Forray, George Chiu,
; APPLICANT: Theresa A. Branchek, John M. Weizel and Paul R. Hartig
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO TREAT BENIGN
; TITLE OF INVENTION: PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM

```
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,932
FILING DATE: 13-APR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41878-B/JPW/TEP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-228-932-1

Query Match
Best Local Similarity 50.7%; Score 98.4; DB 2; Length 2140;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
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QY 565 AGCCCACTACTATCTCAGCGTGTCTTTCATGCTCATTCACATGATGTCATG 624
DB 932 ----CGGCTACGCTGTCTTCTCTCCGTGTGCTTCTTACCTGCGCCATGCGCGTATC 987
QY 625 ATTGCTCTACTCCGCGTGTGTGTGTCAGCCCGGAG 662
DB 988 GTGCTCATGTACTGCGCGGTATGCTGTGCGCGGAG 1025
```

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RESULT 10
US-08-468-939-1
Sequence 1, Application US/08468939
Patent No. 5714381
GENERAL INFORMATION:
APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA: US/08/468,939
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41337-1B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-468-939-1
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Query Match
Best Local Similarity 50.7%; Score 98.4; DB 2; Length 2140;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;
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QY 85 GCCCAGGCATATCCGCTCAACCGTGTGTTATCTTCTGCGCGCTCTTTGCTGCGC 144
DB 457 GCGCAGGCGGTGGCGGTGGCGCTCTTCTGCGAGCCTTATCTTATGCGCGTGAAGGT 516
QY 145 AACATAGTCTGCGCGTGTGTGCAAGCGCAGCGCAGCTGCTGAGGTGACCAACGT 204
DB 517 AACGCTGTGTATCTCTCACTGAGTGGCTGCAACCGCAGCTGCAACCTCACTCACTAT 576
QY 205 TTTATCTTAACTCTCTGCTCAACCGACTGCTGCAAGATTGCTGCGCGCTGCGGTG 264
DB 577 TTCATGTGAACCTGCGCGCTGCGCAGCTGCTGAGCGCAACGTAAGCTTCTGCG 636
QY 265 GTGGCCACCTCTGTGCTCTTCTTGGGCCCCCAAGACCATTTCTGACAGCGCCCTGTT 324
DB 637 GGCACCTAGGAGGTTCTGGGCTTCTGGGCTTCTTGGCGCGCTTCTGCAAGTATGAGGCC 696
QY 325 AGCCTCACCCACTGTTGCGCTTTCGCAAGCGTCAACACCATTTGCTTGGTGTCAAGTAT 384
DB 697 GCGGTGAGAGTGTGTGCTGCAAGCGCTCACTCACTGAGCTTCAAGCTTCTGCAAGCTTCT 756
QY 385 GCGTACTGTGCTCATATCCACCTCTCTTCAACCGCTGCAAGATGACCCAGCGCGCGGT 444
DB 757 CGGTACGTGGGCGTGGCGCACTCACTCAAGTACCCAGCATATGACGAGGCAAGGCG 816
QY 445 TACCTGCTCTCTATAGGACCTGAGATTGGCCATCTTCAAGACACTCTTCACTCTAC 504
DB 817 GCGGCATCTCTGCGCTGTGGTGTGAGCGCTGTGAGTGTCTGAGGCGCGCTGCTG 876
QY 505 GCGTGGGCGAGGCTGCTTGTATGAGCGCAATGCTGCTGCTCAATGATCTTGGGCGCGC 564
DB 877 GCGTGAAGAGACCGCTGTGCGCCCTGA---GAGCGCTTCTGCGGTATCAACGAGAGAG-- 931
QY 265 GTGGCCACCTCTGTGCTCTTCTTCTGCGCCCTCAACGCAACTTCTGACAGCGCGCTGTT 324
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Db 637 GCCACCATGAGAGTCTTGGAGCTTCTGGGCTTTGGCCCTTTCGCGACGATATGGGCC 696
Qy 325 AGCCATACCCACCTGTTTCGCTTCGCGAGCGTACACCATATGTCGTGTCAGTGGAT 384
Db 697 GCGGTGAGATGCTGTGCTGCGACAGCGCTTCATCTCAAGCTTCGACCAATCTCCGTGAC 756
Qy 385 CGCTACTTTCATCATCAACCTCTCTCTACCCGTCGAAGATGACCCGCGCGGT 444
Db 757 CGGTACGTGGGGGTGGCCACTCAGTCAAGTACCAAGCATATGACCGAGCGCAAGGG 816
Qy 445 TACCTGCTCTCTATGACACCTGATGATGCGCATCTCGACAGCACTCTCTCATCTAC 504
Db 817 GCGGCAATCTGCGCCCTGCTGGGTGATGACCTGATGATCCGTAGGGGCCCTGCTG 876
Qy 505 GCGTGGGGGCGAGCTGCTTTGATGATGACCGCATCTCTGCTCCCATGATGCGGGGGCC 564
Db 877 GCGTGAAGAGAGCCGCTGCCCTGTA--CGAGCGCTTCGCGGTATCAACGAGGAG-- 931
Qy 565 AGCCCGAGCTACATATTCATGACCGGTGTCCTTCATGTCATTCACATGATTCATG 624
Db 932 ----GCGGCTAGCGCTCTCTCTCTCCGTGTGCTCTCTTACCTGCGCATGCGGTCTATC 987
Qy 625 ATTCCTGCTACTCGGTGTGTGTGTGACGCCGAG 662
Db 988 GTGCTATGTACTGCGCGGTGATGATGTCGCGGAG 1025

RESULT 11
US-08-406-855A-1
Sequence 1, Application US/08406855A
Patent No. 5861309

GENERAL INFORMATION:

APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,855A

FILING DATE: 21-AUG-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0526

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2140 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

FEATURE: NAME/KEY: CDS

LOCATION: 178..1893

OTHER INFORMATION:

US-08-406-855A-1

Query Match 6.4%; Score 98.4; DB 2; Length 2140;

Best Local Similarity 50.7%; Pred. No. 3 4e-15;

Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

Qy 85 GCCACCGCATATCGCTCAACCGTGTGATATCTTCGCGCCCTTTTCGTGGC 144
Db 457 GCGAGGGCGGTGGGGGTGGCGCTTCCTCGGACCTTATCTTATGACCGGTGAGGT 516
Qy 145 AACATAGTCTGCGCTTAATGTCAGGCGCAAGCCGAGCTCTGAGTACCAACGT 204
Db 517 AACCTGCTGTATCTCTCAAGTGTGACCGCAACCGCACTTCAACACCTTCAACTAT 576
Qy 205 TTTATCTTAACCTCTCTGTCACACCGATCTGACAGATTCGTCGTGGCCCGCGGGT 264
Db 577 TTCTATGTAACTTGGCCGTGGCCGACCTGCTGTGAGGCGCACCGTACTGCTCTTCTG 636
Qy 265 GTGGCCACCTGTGTGCTCTCTCTGACCCCTCAACAGCCACTTTCGACGCGCCGTGTT 324
Db 637 GCACCATGAGAGTTCGTGGGCTTTCGGGCTTTCGGGCGGCTTTCGACGATAGGGCC 696
Qy 325 AGCTTCACCCACTGTTGCGCTTCGCGACCGTCAACACCATTTGTTGATGATGAT 384
Db 697 GCGGTGAGAGTGTGTGCTGACAGCGCTTCATCTCAGCTTCGACCACTTCCTCGGAC 756
Qy 385 CGCTACTGTGCATATCAACCTCTCTCTCAACCGGTCCAGATGACCGAGCGCGGT 444
Db 757 CGGTACGTGGGGGTGGCGCCACTCACTCAAGTACCAAGCATATGACCGAGGAGCG 816
Qy 445 TACCTGCTCTCTATGACACCTGATGATGCGCATCTTCGACAGCACTCTCACTTAC 504
Db 817 GCGGCAATCTGCGCCCTGCTGTGGGTGATGACCTGTGATTCGTTAGGGCCCTGCTG 876
Qy 505 GCGTGGGCGAGCGCTGCTTATGACCGCAATGCTCTGCTCCATGATTCGCGGGGCC 564
Db 877 GCGTGAAGAGAGCCGTCGCCCTGTA--CGAGCGCTTCGCGGTATCAACGAGGAG-- 931
Qy 565 AGCCCGAGCTACATATTCATGACCGGTGTCCTTCATGTCATTCACATGATTCATG 624
Db 932 ----GCGGCTAGCGCTCTCTCTCTCCGTGTGCTCTCTTACCTGCGCATGCGGTCTATC 987
Qy 625 ATTCCTGCTACTCGGTGTGTGTGTGACGCCGAG 662
Db 988 GTGCTATGTACTGCGCGGTGATGATGTCGCGGAG 1025

RESULT 12

US-08-722-190-1

Sequence 1, Application US/08722190

Patent No. 5980128

GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, Carlos C. Forray, George

Chiu, Theresa A. Branche, John M. Wetzel and Paul R. Hartig

TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO

TREAT BENIGN PROSTATIC HYPERPLASIA

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: COOPER & DUNHAM LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722,190

FILING DATE: 4-APR-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 41878-D-PCT/JPM/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-722-130-1

Query Match 6.4%; Score 98.4; DB 2; Length 2140;
Best Local Similarity 50.7%; Pred. No. 3.4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCCAGCGCATCATCGCTCAACCGTGTATCTTCGCGCCCTCTTTCGTCGCG 144
DB 457 GCGCAGGGGCGTGGGCGTGGCGCTTCTCGGACGCTTATCTTATGGCCGTGCAAGT 516
QY 145 AACATAGTGTGCGCGCTAGTGTGACGCGCAAGCGGACGTCTGACAGTGAACACCT 204
DB 517 AACCTGCTGTATCTCTCACTGAGCTGCAACCGCACCTGACAGCCGTCAACATAT 576
QY 205 TTTATCTTTAACTCTCTCTCAACCGTGTATCTTCGTCGCGCCCTCTTTCGTCGCG 264
DB 577 TTCATGTGAACCTGCGCTGCGCGACCTGCTGAGGCGCAAGCTACTGCTTCTGCG 636
QY 265 GTGGCACCCTGTGCGCTCTTCTGCGCCCTCAACAGCAGCTTGTGACGCGCCCTGTT 324
DB 637 GCCACATGAGAGTCTGCGGCTTCTGCGGCTTGGCGGCGCTTCTGCGACGTATGGCG 696
QY 325 AGCCTCACCACCTGTGCGCTTCTGCGCGACGCTCAACACCATTTGTTGTGATGAT 384
DB 697 GCGGTGAGAGTGTGCTGTGACGAGCGCTCATCTCAGCTCTGACCATCTCCGTGAC 756
QY 385 CGCTACTGTGCATCATCAACCTCTCTCTCAACCGTGTATCTTCGCGCCCTCTTTCGTCGCG 444
DB 757 CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCGACCATCATGACGAGCGCAAGGCG 816
QY 445 TACCTGCTCTGTATGAGCACTGATTTGCGCATCTGACAGCACTCTCCACTCTAC 504
DB 817 GCGGCGATCTGCGGCGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 876
QY 505 GCGTGGGCGCAGAGCTGCTTGTGAGCGCAATGCTCTCTCTCAATGATCTTGGGGGCGC 564
DB 877 GCGTGAAGAGAGCGCTGCGCCCTGTA---GAGCGCTCTGCGGTATCAACGAGGAG-- 931
QY 565 AGCCCGAGTACATATTTCTCAAGCGTGTCTTATGTCATTTGCACTGATTTGTCAG 624
DB 932 ---CGGGCTACGCTGTCTTCTCTCCGAGTGTCTTCTTACCTGCGACGCGTCAATC 987
QY 625 ATGCTGCTACCTCGGTGTGTTCTGTCGAGCGCGAG 662
DB 988 GTGCTCATGTATGCGCGGTGATGAGTGTGCGCGAG 1025

RESULT 13
US-08-244-354-1
Sequence 1, Application US/08244354
Patent No. 6015819
GENERAL INFORMATION:

APPLICANT: Charles Gluchowski, et al.
TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
TREAT BENIGN PROSTATIC HYPERPLASIA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,354
FILING DATE: April 1, 1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28, 678
REFERENCE/DOCKET NUMBER: 41878-D-PCT-US/JPM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2140 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-08-244-354-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;
Best Local Similarity 50.7%; Pred. No. 3.4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCCAGCGCATCATCGCTCAACCGTGTATCTTCGCGCCCTCTTTCGTCGCG 144
DB 457 GCGCAGGGGCGTGGGCGTGGCGCTTCTCGGACGCTTATCTTATGGCCGTGCAAGT 516
QY 145 AACATAGTGTGCGCGCTAGTGTGACGCGCAAGCGGACGTCTGACAGTGAACACCT 204
DB 517 AACCTGCTGTATCTCTCACTGAGCTGCAACCGCACCTGACAGCCGTCAACATAT 576
QY 205 TTTATCTTTAACTCTCTCTCAACCGTGTATCTTCGTCGCGCCCTCTTTCGTCGCG 264
DB 577 TTCATGTGAACCTGCGCTGCGCGACCTGCTGAGGCGCAAGCTACTGCTTCTGCG 636
QY 265 GTGGCACCCTGTGCGCTCTTCTGCGCCCTCAACAGCAGCTTGTGACGCGCCCTGTT 324
DB 637 GCCACATGAGAGTCTGCGGCTTCTGCGGCTTGGCGGCGCTTCTGAGAGTATGGCGC 696
QY 625 AGCCTCACCACCTGTGCGCTTCTGCGCGACGCTCAACACCATTTGTTGTGATGAT 384
DB 697 GCGGTGAGAGTGTGCTGTGACGAGCTCTCACTCTGACACCATCTCCGTGAC 756
QY 385 CGCTACTGTGCATCATCAACCTCTCTCTCAACCGTGTATCTTCGCGCCCTCTTTCGTCGCG 444
DB 757 CGGTAGTGGGCGTGGCGCACTCACTCAAGTACCGACCATCATGACGAGCGCAAGGCG 816
QY 445 TACCTGCTCTGTATGAGCACTGATTTGCGCATCTGACAGAGCATCTCTCACTCTAC 504

Db 817 GCCGCATCTGGCCCTGCTCTGGGTGTAGACCCCTGCTGTCTCCGAGGCCCCCTGCTG 876
QY 505 GGGTGGGCGCAGGCTGCTTGTATGAGCGCAATGCTCTGTCTCATGATCTGGGGGCC 564
Db 877 GGGTGGAGGAGCCCGGCGCCCTGA---CGAGGCTTTCGGGATACCGAGGAG--- 931
QY 565 AGCCCCAGCTACATATTCTCAGCGGTGTCTTCTTATGCTCATTTCCATGATTTGATC 624
Db 932 ---CGGGCTACGCTGCTCTCTCTCCGCTGTCTCTTCACTGCGCCATGGCGGTATC 987
QY 625 ATTCCTGTACTCCGCTGTGTCTGTGAGCCCGAG 662
Db 988 GTGCTATGTACTGCCCGGTGTAGTGTGCGCGCAG 1025

RESULT 14

US-09-206-899-1
; Sequence 1, Application US/09206899
; Patent No. 6083705
; GENERAL INFORMATION:
; APPLICANT: Jonathan A. Bard et al.
; TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
; TITLE OF INVENTION: Receptors and Uses Thereof
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/206,899
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,855
; FILING DATE: 21-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41337-A-PCT-US/JPW/KDB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: N
; ANTI-SENSE: N
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 178..1893
; OTHER INFORMATION:
US-09-206-899-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;
Best Local Similarity 50.7%; Pired. No. 3,4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

QY 85 GCCCAGGATCATCCGCTCAACCGTCTGTTATCTCTCCGCGCTTTCTGTCGCGC 144
Db 457 GCCCAGGCGCTGAGCGCTCTCTCTCTGCGACCTTCACTTATGCGCGTGGCAGGT 516

QY 145 AACATAGTCTGGCGCTTAAGTTGTGACGCCCAAGCCGACGCTGTGACAGTACCAACCGT 204
Db 517 AACCTCTTGATCTCTTCAAGTGGCTGCAACCGCACCTGACAGACCTTCAACATAT 576
QY 205 TTATCTTTAAGCTCTCTGTCACCGACCTGTCAGATTTGCGTGGGCCCTTGGGTT 264
Db 577 TTATGTGAACCTGGCCGCTGGCGACCTGTGCTGAGGCCACCTACTGCTCTTCTCG 636
QY 265 GTGGCAGCTGTGTGCTCTTCTGAGCCCTTCAACAGCACTTGTGACAGGCGCTGTGT 324
Db 637 GCCACATAGAGGTTCTGGGCTTCTGGGCTTTGGCGGCGCTTCTGCAAGATAGGGCC 696
QY 325 AGCTTACCACTGTTGGCTTTCGCCAGCGTCAACCAATGTTCTTGTGTGATGTGAT 384
Db 697 GCGGTGAGAGTGTGTGTGACAGGCGCTCCATCTCAGCCTGTGACATCTCCGTGAC 756
QY 385 CGCTATTGTTCATATCAACCTCTCTCTCTCAACCCGTCCAAGATGACCAAGCGCCGGT 444
Db 757 CGGTAGTGGCGGTGGCCACTCACTCAAGTACCCAGCATATGACGAGCGCAAGGCG 816
QY 445 TACCTGCTCTTATGAGCACTGATTTGGCCATCTGCAAGCACTCTCCACTTAC 504
Db 817 GCCGCATCTGGCCCTGCTGTGGTGTGAGCCCTGTGTGTCTGAGGCCCCCTGCTG 876
QY 505 GGGTGGGCGCAGGCTGCTTGTATGAGCGCAATGCTCTGTCTCATGATTTGGGGGCC 564
Db 877 GGGTGGAGGAGCCGCTGCCCCCTGA---CGAGCGTTCTGGGGATACCGAGGAG--- 931
QY 565 AGCCCCAGCTACATATTCTCAGCGGTGTCTTCTTATGCTCATTTCCATGATTTGATC 624
Db 932 ---CGGGCTACGCTGCTCTCTCTCTCCGCTGTCTCTTCACTGCGCCATGGCGGTATC 987
QY 625 ATTCCTGTACTCCGCTGTGTCTGTGAGCCCGAG 662
Db 988 GTGCTATGTACTGCCCGGTGTAGTGTGCGCGCAG 1025

RESULT 15

US-09-444-783-1
; Sequence 1, Application US/09444783
; Patent No. 6420389
; GENERAL INFORMATION:
; APPLICANT: Charles Gluchowski, et al.
; TITLE OF INVENTION: USE OF ALPHA-1C SPECIFIC COMPOUNDS TO
; TITLE OF INVENTION: TREAT BENIGN PROSTATIC HYPERPLASIA
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/444,783
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41878-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2140 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 178..1893
OTHER INFORMATION:
US-09-444-783-1

Query Match 6.4%; Score 98.4; DB 3; Length 2140;

Best Local Similarity 50.7%; Pred. No. 3.4e-15;
Matches 293; Conservative 0; Mismatches 276; Indels 9; Gaps 2;

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QY 85 GCCCAGGCGATCATCCGCTCAACCGTGTGCTGTTATCTTCGCGCGCTTCTTCGTCGGC 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 457 GCGCAGGCGGTGGGCGTGGGCGCTTCTTCGCGCGCTTATCTTATGCGCGTGGCAGGT 516

QY 145 AACATAGTGTGCGCTGCTAGTGTGACGCGCAAGCCGACGCTGCGAGGTGACCAACCGT 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 517 AACGTGCTGTATCATCTCTCAAGTGGCTGCAACCGCACCTGGAAGCGTCAACCACTAT 576

QY 205 TTTATCTTAACTCTCTGCTACACGACCTGCTGCAAGTTGCGTGGCCCCCTGGGTG 264
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 577 TTCATCGTAACTGTGCGCTGCGCCGACCTGTGCTGAGCGCACCGTACTGCGCTTCTCG 636

QY 265 GTGGCCACCTGTGTGCTCTTCTTGGCCCCCTCAACAGCCACTTGTGACAGGCCCTGTGTT 324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 637 GCCACCTAGAGGTTCTGGGCTTCTGGGCTTGGGCGGCTTGTGCAAGTATGAGGCC 696

QY 325 AGCCTCACCACCTGTGTGCGCTTGGCGACGTCACACCATGTGTGTCAGTGAT 384
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 697 GCCGTGAGAGTGTGTGCTGCAAGGCGCTCATCTCTCAGCCTGTGACCATCTCCGTGAC 756

QY 385 CGCTACTTGTCAATCATCCACCTCTCTCTACCGGTCCAAGATGACCAAGCGCGCGGT 444
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Db 757 CGGTAGTGGGCGTGGCCACTCACTCAATCCAGCCATCATGACCGAGCGCAAGGCG 816

QY 445 TACCTGCTCTCTATGAGCAGCTGATTTGGCCATCTGTGACAGCAGCTCTCCACTCTAC 504
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 817 GCTGCGATCTTGCGCTGCTGTGGTGTGAGCCCTGTGTGTCTAGAGGCCCTGTG 876

QY 505 GCGTGGGCGCAGGCTGCTTTGATGAGCGCAATGCTTGTGTCATGATCTGGGGGCGC 564
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Db 877 GCGTGAAGAGAGCCGCTGCCCTGA--CGAGCGCTCTGGCGTATCACCGAGAGG-- 931

QY 565 AGCCCCAGTACATATTCTCAAGCGTGTCTCTTATGTCATTCATTCACCTGATTGTATG 624
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QY 625 ATTGCTGTACTCGGTGTGTTCTGTGAGCCGGAG 662
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Db 988 GTGCTATATCTGCGCGGTATCGTGTGCGGCGAG 1025
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Search completed: December 10, 2005, 03:07:08
Job time : 218 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:00 ; Search time 113.714 Seconds

(without alignments)
1437.373 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967
Sequence: 1 MEHTHAHLAANSLSWSPG.....NDSKSYOPEDAGICAVIIL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1967	100.0	372	4 AAU10067	Chemokine
2	1967	100.0	372	5 AAE18645	Human G-P
3	1967	100.0	372	6 ABR62521	Human G-P
4	1967	100.0	372	7 ADD18023	Human G-P
5	1967	100.0	372	7 ADJ87767	G-coupled
6	1967	100.0	372	8 ADI79323	AD179323
7	1962	99.7	372	8 ADO56002	Human NOV
8	1939.5	98.6	369	6 ABR62522	Adf65522
9	1864	94.8	591	7 ADF70485	Orphan re
10	1857	94.4	353	5 AAU76416	Novel G-P
11	1857	94.4	353	5 ABU74075	Human G P
12	1857	94.4	353	5 ABB79517	Human che
13	1857	94.4	353	6 ABR62524	Human AXO
14	1857	94.4	353	6 ABR44437	Human G P
15	1857	94.4	353	6 ABR82499	Human TGR
16	1857	94.4	353	8 ADR16434	Human KOR
17	1853	94.2	353	7 AAU10068	Chemokine
18	1853	94.2	353	7 ADJ87769	G-coupled
19	1853	94.2	353	8 ADI79325	NOV11 pro
20	1853	94.2	353	8 ADO56004	Human NOV
21	1853	94.2	353	8 ADO28954	Human nov
22	1829	93.0	353	5 AAE29236	Human 7TM
23	1829	93.0	353	6 ABG71163	Novel hum
24	1829	93.0	353	6 ABU09571	Human pro

25	1741	88.5	345	6 ABR82508	Mouse TGR
26	1741	88.5	345	8 ADO28956	Mouse nov
27	1628	82.8	318	7 ADJ87772	G-coupled
28	1628	82.8	318	8 ADI79348	NOV10b pr
29	1628	82.8	318	8 ADO56027	Human NOV
30	1623	82.5	333	5 AAE17081	Human NOV
31	1623	82.5	333	7 ABW00814	Human G-P
32	1623	82.5	343	5 ABR79519	Human GPC
33	1623	82.5	356	5 ABR79518	Human che
34	1623	82.5	385	5 ABR95606	Human GPC
35	1623	82.5	388	8 ADO89946	Antagonis
36	1611	81.9	333	5 AAE17229	Human tly
37	1471	74.8	287	4 AAU25559	Human G P
38	1421	72.2	321	7 ADC12696	Human GPC
39	1317	67.0	265	6 ABR81706	Human G P
40	1317	67.0	265	6 ABR62524	Human G-P
41	912.5	46.4	313	4 AAU25556	Human G P
42	742	37.7	340	8 ADO28936	Human nov
43	742	37.7	348	6 ABR82431	Murine 1s
44	737	37.5	374	5 ABU04070	Human G P
45	737	37.5	374	5 AAM49155	Human G P

ALIGNMENTS

RESULT 1	AAU10067	standard; protein; 372 AA.
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AC	AAU10067	
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XX		
DT	14-FEB-2002	(first entry)
XX		
DE	Chemokine receptor family related protein, NOV10.	
XX		
XX	NOV, cytostatic; psoriasis; noctropic; neuroprotectant;	
KW	cerebroprotective; hepatic; antiinflammatory; diabetes; anaemia;	
KW	haemostatic; atherosclerosis; gene therapy; neurogenesis; motility;	
KW	differentiation; proliferation; haematopoiesis; wound healing;	
KW	angiogenesis; cystic fibrosis; congenital myotonia; acute pancreatitis;	
KW	haemophilia; allergy; Pendered syndrome; skeletal dysplasia;	
KW	ischaemic injury; neuroepithelial disorder; hepatitis; heart failure;	
KW	chemokine receptor; chromosome 1.	
XX		
OS	Homo sapiens.	
XX		
XX		
EH	Key	Location/Qualifiers
FT	Peptide	1..47
FT	Protein	/label= Signal_peptide
FT		48..372
FT		/note= "Mature chemokine receptor related protein, NOV10"
XX		
XX	WO200170978-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	20-MAR-2001; 2001WO-US000993.	
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PR	20-MAR-2000; 2000US-0190768P.	
PR	20-MAR-2000; 2000US-0190835P.	
PR	22-MAR-2000; 2000US-0190972P.	
PR	22-MAR-2000; 2000US-0191199P.	
PR	24-MAR-2000; 2000US-0191947P.	
PR	28-MAR-2000; 2000US-0192657P.	
PR	28-MAR-2000; 2000US-0192664P.	
PR	28-MAR-2000; 2000US-0192665P.	
PR	28-MAR-2000; 2000US-0192984P.	
PR	29-MAR-2000; 2000US-0192836P.	
PR	31-MAR-2000; 2000US-0193843P.	
XX		
XX		
XX		
XX	(CURA-) CURAGEN CORP.	

CC and their encoding polynucleotides. GCRC is useful as an immunogen for
 CC preparing monoclonal and polyclonal antibodies. GCRC is useful for
 CC diagnosing, treating and preventing a cell proliferative disorder (e.g.,
 CC hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy,
 CC Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's
 CC disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension,
 CC myocardial infarction), gastrointestinal disorder (e.g., gastritis,
 CC cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g.,
 CC acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma,
 CC rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity,
 CC osteoporosis), and viral infections. GCRC is useful in a number of drug
 CC screening techniques, and to analyse the proteome of a tissue or cell
 CC type. GCRC is useful for creating knockin humanised animals or
 CC transgenic animals to model human diseases, in somatic or germ-line gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion, etc., among normal, carrier or affected individuals, and as
 CC hybridisation probes for mapping naturally occurring genomic sequences.
 CC GCRC is useful in Southern or northern analysis, dot blot or other
 CC membrane-based technologies, in PCR technologies, in dipstick, pin,
 CC multifactor enzyme linked immunosorbant (ELISA)-like assays, and in
 CC microarrays utilising fluids or tissues from patients to detect altered
 CC GCRC expression. The present sequence is human GCRC-6

XX Sequence 372 AA;

SQ Query Match 100.0%; Score 1967; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERTAHNLANSLSLSWSPGSAAGLGFVYVYVYSLLCGLPANILVTIILSQLVARQK 60
 DB 1 MERTAHNLANSLSLSWSPGSAAGLGFVYVYVYSLLCGLPANILVTIILSQLVARQK 60

QY 61 SSVNYLLAAADILVLPFTVDFLEBFLMOMPOVPDKIIVLESSIHITSITV 120
 DB 61 SSVNYLLAAADILVLPFTVDFLEBFLMOMPOVPDKIIVLESSIHITSITV 120

QY 121 PTIDRYIAVCHPLKHTVSYPARTRKIVSVYITCFLTSPYPMWPNWTEDYISTSVH 180
 DB 121 PTIDRYIAVCHPLKHTVSYPARTRKIVSVYITCFLTSPYPMWPNWTEDYISTSVH 180

QY 181 HVLIWHCFVTVLVPISIFILNSIIVYKLRKSNRFLRGYSTGKTTAIFTTISFATL 240
 DB 181 HVLIWHCFVTVLVPISIFILNSIIVYKLRKSNRFLRGYSTGKTTAIFTTISFATL 240

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 DB 241 WAPRIIMILYHLYGAPIQNRWLVHMSDIANMLALNTAINPFLYCFISKRFPTMAATL 300

QY 301 KAPFKQKQPOVQYTNHNSITSSPWPISANSHCIKMLVYVDKNGKPIKSRNDSKSYO 360
 DB 301 KAPFKQKQPOVQYTNHNSITSSPWPISANSHCIKMLVYVDKNGKPIKSRNDSKSYO 360

QY 361 FEDATGACVITL 372
 DB 361 FEDATGACVITL 372

RESULT 3
 ABR62521
 ID ABR62521 standard; protein; 372 AA.

XX ABR62521;
 AC 06-NOV-2003 (first entry)

DE Human G-protein coupled receptor HGRPMY34.

XX HGRPMY34; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
 KW human; neuroprotective; nootropic; tranquilizer; antidiarrhoeal;
 KW neuroleptic; antianemic; antidepressant; anticonvulsant; antiparkinsonian;
 KW cyostatic; cardiant; hypotensive; antidiarrhoeal; analgesic; anorectic;

KW anti-HIV; antiaesthetic; osteopathic; uropathic; antitumor; antiallergic;
 KW gene therapy.

XX Homo sapiens.
 OS Homo sapiens.

PH Key Location/Qualifiers
 FT Domain 16..36
 FT /label= TM1
 FT /note= "transmembrane domain 1"

FT Domain 65..87
 FT /label= TM2
 FT /note= "transmembrane domain 2"

FT Domain 109..131
 FT /label= TM3
 FT /note= "transmembrane domain 3"

FT Domain 148..166
 FT /label= TM4
 FT /note= "transmembrane domain 4"

FT Domain 182..208
 FT /label= TM5
 FT /note= "transmembrane domain 5"

FT Domain 227..249
 FT /label= TM6
 FT /note= "transmembrane domain 6"

FT Domain 269..288
 FT /label= TM7
 FT /note= "transmembrane domain 7"

PN MO2003050256-A2.
 XX 19-JUN-2003.

PD 06-DEC-2002; 2002MO-US039290.
 XX 06-DEC-2001; 2001US-0338371P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Feder JN, Gopal S, Mintier GA, Ramanathan CS;
 PI WPI, 2003-577295/54.

DR N-PSDB; ACF05275.
 XX New nucleic acid molecule encoding a human G-protein coupled receptor,
 PT HGRPMY34, useful for diagnosing, preventing or treating diseases
 PT involving the receptor, for example Parkinson's disease, dementia,
 PT asthma, hypertension or cancer.

PS Claim 5; Fig 1A-B; 112pp; English.

XX The present sequence is the protein sequence of human HGRPMY34, a newly
 CC identified G-protein coupled receptor (GPCR) belonging to the group of
 CC 'Class A' GPCRs and showing homology to the Pfam model 7 transmembrane
 CC receptor, rhodopsin family. HGRPMY34, also referred to as GPCR-P14
 CC and/or GPCR-145, is highly expressed in brain (especially in the
 CC amygdala, caudate nucleus, corpus callosum, hippocampus, thalamus,
 CC substantia nigra), spinal cord and pituitary, indicating an association
 CC in neurological systems and conditions. It is also expressed in the bone
 CC marrow and testis. The invention provides HGRPMY34 polynucleotides,
 CC polypeptides and antibodies, expression vectors, host cells and antisense
 CC molecules, methods for screening for modulators of HGRPMY34 activity
 CC and/or function, and methods for diagnosing, treating, preventing and
 CC screening for disorders and diseases associated with abnormal HGRPMY34
 CC activity, including: a disorder related to aberrant G-protein coupled
 CC signalling; a disorder related to aberrant cell cycle regulation;
 CC neurological disorders; anxiety; headache; migraine; schizophrenia; manic
 CC depression; delirium; dementia; severe mental retardation and
 CC dyskinesias, such as Huntington's disease or Gilles de la Tourette's
 CC syndrome; Parkinson's disease; brain disorders; spinal cord disorders;
 CC affective disorders; neoplastic disorders; cardiovascular disorders;
 CC acute heart failure; hypotension; hypertension; angina pectoris;
 CC myocardial infarction; an immunological disorder; immune-related
 CC disorders; endocrinal diseases; growth disorders; neuropathic pain;

CC obesity; anorexia; HIV infections; cancers; bulimia; asthma; osteoporosis
 CC ; psychosis; metabolic disorders; pituitary disorders; urinary retention;
 CC ulcers; allergies; or benign prostatic hypertrophy (all claimed)
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 6; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGFGPVVYYSLLCLGIPANILTVIISQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGFGPVVYYSLLCLGIPANILTVIISQLVAROK 60
 QY 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIDRYAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEYISTSVH 180
 DB 121 PLTIDRYAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEYISTSVH 180
 QY 181 HVLWIHGFYVLPVCSIFFLINSIIYVKLRKSNFRGISTGKTALIFTISIFATL 240
 DB 181 HVLWIHGFYVLPVCSIFFLINSIIYVKLRKSNFRGISTGKTALIFTISIFATL 240
 QY 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINEFLYCFISKFRYMAAATL 300
 DB 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINEFLYCFISKFRYMAAATL 300
 QY 301 KAFKFCQKQPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 DB 301 KAFKFCQKQPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIACVYIIL 372
 DB 361 FEDAIACVYIIL 372

RESULT 4

ADD18023
 ID ADD18023 standard; protein; 372 AA.

AC ADD18023;

DT 15-JAN-2004 (first entry)

DE Human G-protein coupled receptor (GPCR) sequence Seq ID19.

XX G protein coupled receptor; GPCR; signal transduction pathway; G protein;
 KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
 KW colour blindness; retinal pigmentosa; aschma; depression; schizophrenia;
 KW sleeplessness; hypertension; anxiety; stress; renal failure;
 KW cardiovascular disorder; neural disorder; oncology disorder;
 KW immune disorder; neuroprotective; gene therapy.

XX Homo sapiens.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Misc-difference 347.351

PN WO2003016478-A2.

PD 27-FEB-2003.

PF 15-AUG-2002; 2002WO-US026017.

XX 20-AUG-2001; 2001US-0313658P.

PR 12-SEP-2001; 2001US-0316675P.

PR 30-OCT-2001; 2001US-0340703P.

PR 26-NOV-2001; 2001US-0333417P.

PR 06-DEC-2001; 2001US-0338367P.

PR 06-FEB-2002; 2002US-0355596P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Feder JN, Ramanathan CS, Gopal S, Muntler GA;

XX MPI, 2003-276556/27.

XX N-ESDB; ADD18120.

PR New nucleic acid, useful for manufacturing a medicament for preventing,

PR treating or ameliorating a medical condition e.g., neural disorder.

PS Example 1; SEQ ID NO 19; 251pp: English.

CC This invention relates to novel G protein coupled receptors (GPCRs) and
 CC their encoding nucleotide sequences. Many medically significant
 CC biological processes are mediated by proteins participating in signal
 CC transduction pathways involving G proteins. GPCRs are one of the largest
 CC receptor superfamilies known. These receptors are biologically important
 CC and malfunction of these receptors results in diseases such as
 CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
 CC pigmentosa and asthma. They are also involved in depression,
 CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
 CC failure and other cardiovascular, neural, oncology and immune disorders.
 CC A modulator of the GPCRs of the invention may have neuroprotective
 CC activity whilst the sequences of the invention may be useful for gene
 CC therapy. The invention may also be useful for manufacturing a medicament
 CC for preventing, treating or ameliorating a medical condition. The present
 CC sequence is the amino acid sequence of a human GPCR of the invention.

XX Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGFGPVVYYSLLCLGIPANILTVIISQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGFGPVVYYSLLCLGIPANILTVIISQLVAROK 60
 QY 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVLFVDFLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIDRYAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEYISTSVH 180
 DB 121 PLTIDRYAVCHPLKHYTVSPARTKRVIVSVYITCFLTSIPYWMPIWTEYISTSVH 180
 QY 181 HVLWIHGFYVLPVCSIFFLINSIIYVKLRKSNFRGISTGKTALIFTISIFATL 240
 DB 181 HVLWIHGFYVLPVCSIFFLINSIIYVKLRKSNFRGISTGKTALIFTISIFATL 240
 QY 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINEFLYCFISKFRYMAAATL 300
 DB 241 WAPRIIMLYLHGYAPIONRWLVHMSDIANMLALNTAINEFLYCFISKFRYMAAATL 300
 QY 301 KAFKFCQKQPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 DB 301 KAFKFCQKQPVQFYTNHNSITSSPWISPAISHCIKMLVYQYDKGKPIKSRNDSKSSYQ 360
 QY 361 FEDAIACVYIIL 372
 DB 361 FEDAIACVYIIL 372

RESULT 5

ADJ87767
 ID ADJ87767 standard; protein; 372 AA.

AC ADJ87767;

DT 06-MAY-2004 (first entry)

DE G-coupled protein receptor-related protein #56.
XX novel protein; G-coupled protein receptor-related protein;
XX cardiomyopathy; atherosclerosis; cell signal processing-related disorder;
KM metabolic pathway modulation-related disorder; diabetes; cancer; stroke;
KM Huntington's disease; epilepsy; anxiety; pain; hypercholesterolemia;
KM obesity; hypertension; Crohn's disease; systemic lupus erythematosus;
KM viral infections; bacterial infection; parasitic infection;
KM hyperthyroidism; hypothyroidism; Von Hippel-Lindau syndrome;
KM Alzheimer's disease; tuberosus sclerosis; hypercalcaemia; cerebral palsy.
XX
OS Unidentified.
XX
XX WO2002102321-A2.
XX
XX 27-DEC-2002.
XX
XX 18-JUN-2002; 2002WO-US019522.
XX
XX 18-JUN-2001; 2001US-0298994P.
PR 18-JUN-2001; 2001US-0299134P.
PR 04-OCT-2001; 2001US-00972446.
PR 06-JUN-2002; 2002US-00299134.
PR 07-JUN-2002; 2002US-00298994.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Anderson DW, Guo X, Gusev VY, Herrmann JL, Li L, Mezes PS;
PI Pena CER, Spaderna SK, Zhong M;
XX
XX WPI; 2003-167441/16.
DR N-PSDB; ADJ87766.
XX
XX New MOX polypeptides and polynucleotides, useful in gene therapy,
PT particularly for treating or preventing e.g. cardiomyopathy,
PT atherosclerosis, diabetes, adenoma, brain tumor, breast cancer, prostate
PT cancer, stroke or pain.
XX
XX
PS Claim 1; SEQ ID NO 202; 378bp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel G-
CC coupled protein receptor-related (MOL) proteins. The DNA and protein
CC sequences of the invention are useful for treating or preventing a MOL-
CC associated disorder, such as: cardiomyopathy, atherosclerosis, disorders
CC associated with cell signal processing and metabolic pathway modulation,
CC or diabetes. The DNA and protein sequences are also useful for the
CC treatment of: cancer, stroke, Huntington's disease, epilepsy, anxiety,
CC pain, hypercholesterolemia, obesity, hypertension, Crohn's disease,
CC systemic lupus erythematosus, viral infections, bacterial infections,
CC parasitic infections, hyperthyroidism, hypothyroidism, Von Hippel-Lindau
CC syndrome, Alzheimer's disease, tuberosus sclerosis, hypercalcaemia, or
CC cerebral palsy. The present amino acid sequence represents a MOL protein
CC of the invention.
SQ
SQ Sequence 372 AA;
Query Match 100.0%; Score 1967; DB 7; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.4e-209;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAIIPTTISFATL 240
QY WAPRIIMLYHLYSGPIQNRMLVHTMSDIANNALNTAINELKCFISKRRTPMAATL 300
DB 241 WAPRIIMLYHLYSGPIQNRMLVHTMSDIANNALNTAINELKCFISKRRTPMAATL 300
QY 301 KAFKFCQOPQVQFYNNHFSITSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYO 360
DB 301 KAFKFCQOPQVQFYNNHFSITSPWISPAHSHCIKMLVYQYDKNGKPIKSRNDSKSSYO 360
QY 361 FEDAIQACVITL 372
DB 361 FEDAIQACVITL 372
RESULT 6
AD179323
ID AD179323 standard; protein; 372 AA.
XX
XX AD179323;
AC
XX
DT 22-APR-2004 (first entry)
XX
XX NOV10a protein sequence, SEQ ID 20.
DE
XX
XX Cytostatic; Immunosuppressive; Anti-allergic; Antimicrobial; Vasotropic;
KM Respiratory; Hepatotropic; Vinicide; Gastrointestinal; Antidiabetic;
KM Ophthalmological; Antiproliferative; Neuroprotective; Nocotropic;
KM Antiarteriosclerotic; Hypotensive; Cardiant; Cerebroprotective;
KM Gene Therapy; NOX; human; cancer; myelogenous leukaemia;
KM congenital neonatal autoimmune thrombocytopenia; immunological disorder;
KM allergy; infection; asthma; lung disease; reproductive disorder;
KM haemangioma; deafness; liver cirrhosis; hepatitis C; gastric disorder;
KM diabetic retinopathy; psoriasis; multiple sclerosis; atherosclerosis;
KM hypertension; stroke; heart failure; chromosome 1; NOV10a;
KM chemokine receptor.
XX
XX Homo sapiens.
OS
XX
XX WO2004009635-A2.
XX
XX 29-JAN-2004.
XX
XX 04-OCT-2001; 2001WO-US031292.
PR
XX 20-MAR-2001; 2001US-00813432.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Taupier RJ, Majumder K, Spaderna SK, Smithson G, Mezes PS;
PI Vernet CAM;
XX
XX WPI; 2004-123380/12.
DR N-PSDB; AD179322.
XX
XX
PS Claim 1; Page 41; 158bp; English.
XX
XX The present invention relates to novel NOX proteins and their coding
CC sequences (AD179304-AD179327). The sequences are useful for the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease associated with the protein, or for diagnosing and treating
CC disorders associated with the NOX protein, such as cancer, myelogenous
CC leukaemia, congenital neonatal autoimmune thrombocytopenia,
CC immunological disorders, allergy and infection, asthma, lung diseases,
CC reproductive disorders, male and female reproductive diseases,
CC haemangioma, deafness, liver cirrhosis, hepatitis C, gastric disorders,
CC diabetic retinopathy, psoriasis, multiple sclerosis, atherosclerosis,
CC hypertension, stroke and heart failure. NOV10a represents a new member of
CC the chemokine receptor family and the gene is located on chromosome 1.
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1967; DB 8; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.4e-209;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGIFVPPVYYSLCLGLPANILTVIILSQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGIFVPPVYYSLCLGLPANILTVIILSQLVAROK 60
 QY 61 SSYNVLLAAADILVLFVIVDFLLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVLFVIVDFLLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIIRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSIPYMWPMIWTEDYISTSVH 180
 DB 121 PLTIIRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSIPYMWPMIWTEDYISTSVH 180
 QY 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLGYSTGKTTAILFTITSIFATL 240
 DB 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLGYSTGKTTAILFTITSIFATL 240
 QY 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRMAAATL 300
 DB 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRMAAATL 300
 QY 301 KAFKCCQKQPOVFTNNHFSITSSPWISPANSHCIKMLVYOYDKNGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCCQKQPOVFTNNHFSITSSPWISPANSHCIKMLVYOYDKNGKPIKSRNDSKSSYQ 360
 QY 361 FEDAGACVIIL 372
 DB 361 FEDAGACVIIL 372

RESULT 7
 ADO56002
 ID ADO56002 standard; protein; 372 AA.
 AC ADO56002;
 DT 15-JUL-2004 (first entry)
 XX
 DE Human NOVI0 polypeptide.
 XX
 KW human; cancer; obesity; diabetic nephropathy; acute pancreatitis; stroke;
 KW multiple sclerosis.
 XX
 OS Homo sapiens.
 XX
 PN US2004058862-A1.
 XX
 PD 25-MAR-2004.
 XX
 PF 18-SEP-2002; 2002US-00246583.
 XX
 PR 18-SEP-2002; 2002US-00246583.
 XX
 PA (MAJU/) MAJUMDER K.
 XX
 PI Majumder K;
 XX
 DR WPI, 2004-268835/25.
 DR N-PSDB; ADO56001.
 XX
 PT Novel NOVX polypeptides, useful for treating cancer, obesity, diabetic
 PT nephropathy, acute pancreatitis, strokes and multiple sclerosis.
 XX
 PS Claim 1; Page 27; 87pp; English.
 XX
 CC The invention relates to novel isolated NOVX nucleic acids and encoded
 CC polypeptides. The nucleic acids, polypeptides and antibodies raised
 CC against the polypeptides are useful for preventing or treating diseases
 CC associated with aberrant NOVX expression or activity e.g., cancer,
 CC obesity, diabetic nephropathy, acute pancreatitis, stroke, multiple

CC sclerosis. The present sequence represents a NOVX polypeptide of the
 CC invention.
 XX
 SQ Sequence 372 AA;

Query Match 99.7%; Score 1962; DB 8; Length 372;
 Best Local Similarity 99.7%; Pred. No. 4.9e-209;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSSLSWSPGACGIFVPPVYYSLCLGLPANILTVIILSQLVAROK 60
 DB 1 MEHTAHLAANSSLSWSPGACGIFVPPVYYSLCLGLPANILTVIILSQLVAROK 60
 QY 61 SSYNVLLAAADILVLFVIVDFLLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 DB 61 SSYNVLLAAADILVLFVIVDFLLEDFILNMQMPQVPDKIEVLEFSSIHISIMTV 120
 QY 121 PLTIIRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSIPYMWPMIWTEDYISTSVH 180
 DB 121 PLTIIRYIAVCHPLKHYTVSPARTRKIVSVYITCFLTSIPYMWPMIWTEDYISTSVH 180
 QY 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLGYSTGKTTAILFTITSIFATL 240
 DB 181 HVLIMHCFVTVLVPCSIFFILNSIIVYKLRKSNFRLGYSTGKTTAILFTITSIFATL 240
 QY 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRMAAATL 300
 DB 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRMAAATL 300
 QY 301 KAFKCCQKQPOVFTNNHFSITSSPWISPANSHCIKMLVYOYDKNGKPIKSRNDSKSSYQ 360
 DB 301 KAFKCCQKQPOVFTNNHFSITSSPWISPANSHCIKMLVYOYDKNGKPIKSRNDSKSSYQ 360
 QY 361 FEDAGACVIIL 372
 DB 361 FEDAGACVIIL 372

RESULT 8
 ABR62522
 ID ABR62522 standard; protein; 369 AA.
 AC ABR62522;
 DT 06-NOV-2003 (first entry)
 XX
 DE Human G-protein coupled receptor HGRBM734 variant.
 XX
 KW HGRBM734; G-protein coupled receptor; receptor; GPCR-P14; GPCR-145;
 KW human; neuroprotective; nociceptive; tranquilizer; antimalarial;
 KW neuroleptic; antitumor; antidepressant; anticonvulsant; antiparkinsonian;
 KW cytoskeletal; cardiac; hypotensive; antidiabetic; anorectic;
 KW anti-HIV; antitubercular; osteoporosis; uropathic; antileukemic;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PH Key
 PH Domain
 FT 16..37
 FT /label= TM1
 FT /note= "transmembrane domain 1"
 FT 65..87
 FT /label= TM2
 FT /note= "transmembrane domain 2"
 FT 109..131
 FT /label= TM3
 FT /note= "transmembrane domain 3"
 FT 148..166
 FT /label= TM4
 FT /note= "transmembrane domain 4"
 FT 182..208
 FT /label= TM5
 FT /note= "transmembrane domain 5"

```

FT      Domain                227, .249
FT      /label= TM6
FT      /note= "transmembrane domain 6"
FT      Domain                269, .288
FT      /label= TM7
FT      /note= "transmembrane domain 7"
XX
PN      WO2003050256-A2.
PD      19-JUN-2003.
XX
PF      06-DEC-2002; 2002WO-US039290.
XX
PR      06-DEC-2001; 2001US-0338371P.
XX
PA      (BRIM ) BRISTOL-MYERS SQUIBB CO.
PI      Feder JN, Gopal S, Mintier GA, Ramanathan CS;
XX
DR      WPI; 2003-577295/54.
XX      N-PSDB; ACF05276.
XX
PT      New nucleic acid molecule encoding a human G-protein coupled receptor,
PT      HGRPMY34, useful for diagnosing, preventing or treating diseases
PT      involving the receptor, for example Parkinson's disease, dementia,
PT      asthma, hypertension or cancer.
XX
PS      Claim 5; Fig 2A-B; 112pp; English.
XX
XX      The present sequence is the protein sequence of a variant of human
XX      HGRPMY34 (see ABR62521) containing a deletion of 3 amino acids but
XX      expected to share at least some of the expression patterns and function
XX      of HGRPMY34. HGRPMY34 is a newly identified G-protein coupled receptor
XX      (GPCR) belonging to the group of 'Class A' GPCRs and showing homology to
XX      the Pfam model 7 transmembrane receptor, rhodopsin family. HGRPMY34 (or
XX      GPCR-P14, GPCR-145) is highly expressed in brain (amygdala, caudate
XX      nucleus, corpus callosum, hippocampus, thalamus, substantia nigra),
XX      spinal cord and pituitary, indicating an association in neurological
XX      systems and conditions. It is also expressed in the bone marrow and
XX      testis. The invention provides HGRPMY34 polynucleotides, polypeptides
XX      and antibodies, expression vectors, host cells and antisense molecules,
XX      methods for screening for modulators of HGRPMY34 activity and/or
XX      function, and methods for diagnosing, treating, preventing and screening
XX      for disorders and diseases associated with abnormal HGRPMY34 activity,
XX      including: a disorder related to aberrant G-protein coupled signalling; a
XX      disorder related to aberrant cell cycle regulation; neurological
XX      disorders; anxiety; headache; migraine; schizophrenia; manic depression;
XX      delirium; dementia; severe mental retardation and dyskinesias, such as
XX      Huntington's disease or Gilles de la Tourette's syndrome; Parkinson's
XX      disease; brain disorders; spinal cord disorders; affective disorders;
XX      neoplastic disorders; cardiovascular disorders; acute heart failure;
XX      hypotension; hypertension; angina pectoris; myocardial infarction; an
XX      immunological disorder; immune-related disorders; endocrine diseases;
XX      growth disorders; neuropathic pain; obesity; anorexia; HIV infections;
XX      cancers; bulimia; asthma; osteoporosis; psychosis; metabolic disorders;
XX      pituitary disorders; urinary retention; ulcers; allergies; or benign
XX      prostatic hypertrophy (all claimed)
XX
SQ      Sequence 369 AA;

```

```

DB      121 PLTIDRYIAVCHPLKXHTVSYPARTRKVIYSYITCFLISIPYMWPNITBEDYISTSVH 180
QY      181 HYLWIFHCFTYLVPCISPEFINSIIVYLRKRSNRLRAGYSTGKTALIFTTISFATL 240
DB      181 HYLWIFHCFTYLVPCISPEFINSIIVYLRKRSNRLRAGYSTGKTALIFTTISFATL 240
QY      241 MAPRIIMILYHLYGAPIQNRWLVMISDIANNALALNTAINFELYCFISKRPRYMAATL 300
DB      241 MAPRIIMILYHLYGAPIQNRWLVMISDIANNALALNTAINFELYCFISKRPRYMAATL 300
QY      301 KAPFKQKQPVQVQFYTNHNSITSSPWISPAHSHCTMLVYQYDKGKPIKSRNDSKSSYQ 360
DB      301 KAPFKQKQPVQVQFYTNHNSITSSPWISPAHSHCTMLVYQYDKGK--KSRNDSKSSYQ 357
QY      361 FEDATGACVITL 372
DB      358 FEDATGACVITL 369

RESULT 9
ADP70485
ID      ADP70485 standard; protein; 591 AA.
XX
AC      ADP70485;
XX
DT      12-FEB-2004 (first entry)
XX
DE      Orphan receptor ligand-related human protein SegID108.
XX
KW      ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW      cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW      GFPuv; Enhanced GFP; EGFP; human.
XX
OS      Homo sapiens.
XX
PN      WO2003071272-A1.
XX
PD      26-AUG-2003.
XX
PF      21-FEB-2003; 2003WO-JP001901.
XX
PR      22-FEB-2002; 2002JP-00045728.
PR      23-JUL-2002; 2002JP-00213949.
PR      11-OCT-2002; 2002JP-00298237.
XX
PA      (TAKS ) TAKEDA CHEM IND LTD.
XX
PI      Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
DR      WPI; 2003-697654/66.
DR      N-PSDB; ADP70587.
XX
PT      Transformation of cells with a fusion protein of an orphan receptor
PT      protein with a fluorescent protein useful for identification of ligands
PT      to the orphan receptor.
XX
PS      Disclosure; SEQ ID NO 108; 594pp; Japanese.
XX
XX      This invention relates to a novel method of identifying ligands to an
XX      orphan receptor protein which comprises transforming cells with DNA
XX      encoding a fusion protein of the orphan receptor with a fluorescent
XX      protein, so that the fusion protein is expressed in the cells (or cell
XX      membranes isolated from them) and contacting the cells with the potential
XX      ligand to be tested. A suitable fluorescent protein for incorporation in
XX      the fusion protein is green fluorescent protein (GFP), for example GFP-1,
XX      wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
XX      identification of ligands binding to an orphan receptor protein.
XX
SQ      Sequence 591 AA;

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Query Match          94.8%; Score 1864; DB 7; Length 591;
Best Local Similarity 96.7%; Pred. No. 7; 5e-198;

```

Matches 353; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

QY 1 MEHTHAHAANSSLSWSPGACGIFVPPVYYSLLCGLPANILTYIIISQVARRQK 60
DB 1 MEHTHAHAANSSLSWSPGACGIFVPPVYYSLLCGLPANILTYIIISQVARRQK 60
QY 61 SSYNVLLAADAADIVLFFVDFVDFLEDFILNMQMPVDPKIEVLEFSSIHSTIWTV 120
DB 61 SSYNVLLAADAADIVLFFVDFVDFLEDFILNMQMPVDPKIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKVIVSYITCFLTSPYYMMPNIMTEDIYSTSVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKVIVSYITCFLTSPYYMMPNIMTEDIYSTSVH 180
QY 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
DB 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
QY 241 WAPRIIMTLVHLXGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
DB 241 WAPRIIMTLVHLXGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
QY 301 KAFKCKQKQVQVFTNNHFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKVSPPSKGREL 360
DB 301 KAFKCKQKQVQVFTNNHFSITSSPWISPAHSHCIKMLVYQYDKNGKPIKVSPPSKGREL 360
QY 361 FEDAI 365
DB 361 FTGVV 365

RESULT 10
AAU76416
ID AAU76416 standard; protein; 353 AA.
XX
AC AAU76416;
XX
DT 08-MAY-2002 (first entry)
XX
DE Novel G-protein coupled receptor TGR8.
XX
KM G-protein coupled; receptor; cardiovascular; immunomodulator; TGR8;
XX
KM cytoskeletal; antiinflammatory; antidiabetic; fetal brain;
XX
KM central nervous system disease; circulatory organ disorder; cancer;
XX
KM metabolic disease; immunological disease; gastrointestinal disease;
XX
KM gene therapy; transgenic animal; human.
XX
OS Homo sapiens.
XX
FN WO200194582-A1.
XX
PD 13-DEC-2001.
XX
PF 01-JUN-2001; 2001WO-0P004643.
XX
PR 02-JUN-2000; 2000JP-00170446.
XX
PR 23-JUN-2000; 2000JP-00194926.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Tereao Y, Matsui H, Shintani Y;
XX
DR WPI; 2002-164317/21.
XX
DR N-PSDB; ABK15562, ABK15563.
XX
PT Human fetal brain-originated G protein-coupled receptor protein TGR8 and
XX
PT encoding DNA, for developing drugs to treat e.g. diseases of the central
XX
PT nervous system or circulatory organs, cancer, and metabolic diseases.
XX
PS Claim 1; Fig 2; 102pp; Japanese.
XX
CC The invention describes a human fetal brain-originated G protein-coupled
XX
CC receptor protein, or its salt. The protein and encoded DNA are useful for

CC developing drugs to treat e.g. diseases of the central nervous system or
CC circulatory organs, cancer, metabolic diseases, immunological diseases
CC and gastrointestinal diseases. The invention also describes creation of a
CC probe for gene therapy and construction of a transgenic animal. This is
CC the amino acid sequence of the novel G-protein coupled receptor TGR8,
CC described in the method of the invention
XX
SQ Sequence 353 AA;
XX
Query Match 94.4%; Score 1857; DB 5; Length 353;
Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTHAHAANSSLSWSPGACGIFVPPVYYSLLCGLPANILTYIIISQVARRQK 60
DB 1 MEHTHAHAANSSLSWSPGACGIFVPPVYYSLLCGLPANILTYIIISQVARRQK 60
QY 61 SSYNVLLAADAADIVLFFVDFVDFLEDFILNMQMPVDPKIEVLEFSSIHSTIWTV 120
DB 61 SSYNVLLAADAADIVLFFVDFVDFLEDFILNMQMPVDPKIEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKVIVSYITCFLTSPYYMMPNIMTEDIYSTSVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKVIVSYITCFLTSPYYMMPNIMTEDIYSTSVH 180
QY 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
DB 181 HVLIMHCFVTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
QY 241 WAPRIIMTLVHLXGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
DB 241 WAPRIIMTLVHLXGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRTMAAATL 300
QY 301 KAFKCKQKQVQVFTNNHFSITSSPWISPAHSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFKCKQKQVQVFTNNHFSITSSPWISPAHSHCIKMLVYQYDKNGKPIK 350

RESULT 11
ABJ04075
ID ABJ04075 standard; protein; 353 AA.
XX
AC ABJ04075;
XX
DT 11-OCT-2002 (first entry)
XX
DE Human G protein coupled receptor hRUP35.
XX
KM Human; G-protein coupled receptor; GPCR; hRUP28; hRUP29; hRUP30; hRUP31;
XX
KM hRUP32; hRUP33; hRUP34; hRUP35; hRUP36; hRUP37.
XX
OS Homo sapiens.
XX
FN WO200242461-A2.
XX
PD 30-MAY-2002.
XX
PF 26-NOV-2001; 2001WO-US044386.
XX
PR 27-NOV-2000; 2000US-0253404P.
XX
PR 12-DEC-2000; 2000US-0253366P.
XX
PR 20-FEB-2001; 2001US-0270266P.
XX
PR 20-FEB-2001; 2001US-0270286P.
XX
PR 06-APR-2001; 2001US-0282032P.
XX
PR 06-APR-2001; 2001US-0282356P.
XX
PR 06-APR-2001; 2001US-0282358P.
XX
PR 06-APR-2001; 2001US-0282365P.
XX
PR 14-MAY-2001; 2001US-0290917P.
XX
PR 31-JUL-2001; 2001US-0309208P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Chu ZL, Dang HT, Lowitz KP, Pride C;

```
XX MPI, 2002-566565/60.
DR N-PSDB; ABT04873.
XX Novel endogenous and non-endogenous versions of G protein-coupled
PT receptor useful for identification of candidate compounds as receptor
PT agonists or antagonists for use as therapeutic agents.
XX Claim 29; Page 70-72; 84pp; English.
XX The present invention provides the protein and coding sequences of
CC several human G-protein coupled receptors (GPCRs). These can be used in
CC the identification of candidate compounds as receptor agonists or inverse
CC agonists having applicability as therapeutic agents. The present sequence
CC is a GPCR protein of the invention
XX
SQ Sequence 353 AA;
Query Match 94.4%; Score 1857; DB 5; Length 353;
Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSSLLCIGLPANILTVIILSQVAROK 60
DB 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSSLLCIGLPANILTVIILSQVAROK 60
QY 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
DB 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYMWPNMTEDYSTVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYMWPNMTEDYSTVH 180
QY 181 HVLIMHCTVYLVPCSIFFILNSIIVYKLRRKSNFRLGYSTGKTTALFTTTSIFATL 240
DB 181 HVLIMHCTVYLVPCSIFFILNSIIVYKLRRKSNFRLGYSTGKTTALFTTTSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQRMLVHIMSDIANMLALNTAINFLYCFISKRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQRMLVHIMSDIANMLALNTAINFLYCFISKRRTMAAATL 300
QY 301 KAFKCOQOPVOFTYNNHFSITSSPMISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFKCOQOPVOFTYNNHFSITSSPMISPANSHCIKMLVYQYDKNGKPIK 350
RESULT 12
ABB79517
ID ABB79517 standard; protein; 353 AA.
XX
AC ABB79517;
XX
DT 23-SEP-2002 (first entry)
XX
DE Human chemokine-like receptor.
XX
KM Chemokine-like receptor; G-protein coupled receptor; receptor; human;
KM HIV infection; cardiovascular disease; asthma;
KM chronic obstructive pulmonary disease; cardiac; antiasthmatic;
KM vasodilator; hypotensive; antiarrhythmic; thrombolytic; anticoagulant;
KM antiinflammatory; antiallergic; immunomodulator; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200246358-A2.
XX
PD 20-JUN-2002.
XX
PF 12-DEC-2001; 2001WO-EP014571.
XX
PR 14-DEC-2000; 2000US-0255150P.
PR 02-APR-2001; 2001US-0280110P.
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PR 21-JUN-2001; 2001US-0299474P.
XX
XX (FARB ) BAYER AG.
XX
PI Smolyar A, Zhu Z, Encinas J, Watanabe S, Okigami H;
XX MPI, 2002-547858/58.
DR N-PSDB; ABN84269, ABN84273.
XX
XX New isolated polynucleotide encoding a chemokine-like receptor
PT polypeptide for treating e.g. asthma, myocardial infarction, human
PT immunodeficiency virus infection, or chronic obstructive pulmonary
PT disease.
XX
PS Claim 25; Fig 2; 114pp; English.
XX
CC The present sequence is the protein sequence of a novel human chemokine-
CC like receptor of 353 amino acids. The chemokine-like receptor has 7
CC putative transmembrane domains, consistent with the structure of a G-
CC protein coupled receptor. Its closest human homologue is C-C chemokine
CC receptor 3. The novel receptor is expressed at low levels in most
CC tissues. It is expressed at a high level in phytohemagglutinin-
CC stimulated CD8+ cells, but in none of the other immune cells tested. It
CC may act as a receptor of chemottractant molecules on activated
CC lymphocytes and be involved in cell trafficking and homing to sites of
CC infection, inflammation or tissue injury. Regulation of activity of the
CC novel receptor can therefore be used to treat cardiovascular,
CC immunological and inflammatory diseases, including asthma and chronic
CC obstructive pulmonary disease (COPD). The receptor may also be a target
CC for viruses that reside in the nervous system. Regulating the binding of
CC ligands, e.g. chemottractant molecules or virus particles, to the
CC receptor can therefore be used to modulate the immune response to inhibit
CC viral infections, including HIV infection. A claimed method of reducing
CC activity of the receptor involves contacting a cell with a reagent
CC (preferably an antibody, antisense oligonucleotide or ribozyme) to a
CC product (preferably RNA or a polypeptide) encoded by a polynucleotide
CC encoding the human chemokine-like receptor in vivo or in vitro. A claimed
CC method of treating a chemokine-like receptor dysfunction related disease
CC selected from HIV infection, a cardiovascular disorder, asthma or COPD
CC uses a reagent that modulates a function of the receptor
XX
SQ Sequence 353 AA;
Query Match 94.4%; Score 1857; DB 5; Length 353;
Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSSLLCIGLPANILTVIILSQVAROK 60
DB 1 MEHTAHLAANSSLSWSPGACGLGFVPPVYVYSSLLCIGLPANILTVIILSQVAROK 60
QY 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
DB 61 SSVNYLLAAADIIIVLPFIVDFLEDFILNMQMPQVDPDKIEVLEFSSIHSTWITV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYMWPNMTEDYSTVH 180
DB 121 PLTIDRYAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYMWPNMTEDYSTVH 180
QY 181 HVLIMHCTVYLVPCSIFFILNSIIVYKLRRKSNFRLGYSTGKTTALFTTTSIFATL 240
DB 181 HVLIMHCTVYLVPCSIFFILNSIIVYKLRRKSNFRLGYSTGKTTALFTTTSIFATL 240
QY 241 WAPRIIMILYHLYGAPIQRMLVHIMSDIANMLALNTAINFLYCFISKRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQRMLVHIMSDIANMLALNTAINFLYCFISKRRTMAAATL 300
QY 301 KAFKCOQOPVOFTYNNHFSITSSPMISPANSHCIKMLVYQYDKNGKPIK 350
DB 301 KAFKCOQOPVOFTYNNHFSITSSPMISPANSHCIKMLVYQYDKNGKPIK 350
RESULT 13
```

ABP98724
ID ABP98724 standard; protein; 353 AA.
XX
AC ABP98724;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human AXOR-57 protein.
XX
KW Antibacterial; antifungal; antiviral; antiproteolytic; analgesic;
KW cytoskeletal; antidiabetic; anorectic; anabolic; anticholinergic; antagonist;
KW antiparkinsonian; cardiant; hypotensive; hypertensive; nephrotoxic;
KW osteoprotective; antianxiety; antitumor; antidiabetic; agonist;
KW antiepileptic; neurotrophic; tranquilizer; neuroprotective; antidepressant;
KW vaccine; gene therapy; G-protein coupled receptor; receptor; infection;
KW pain; cancer; diabetes; obesity; anorexia; bulimia; asthma; stroke;
KW Parkinson's disease; osteoporosis; angina pectoris; ulcer; allergy;
KW vomiting; schizophrenia; depression; dementia; Huntington's disease.
XX
OS Homo sapiens.
XX
PN GB2365009-A.
XX
PD 13-FEB-2002.
XX
PE 11-APR-2001; 2001GB-00009018.
XX
PR 11-APR-2001; 2001GB-00009018.
XX
PA (SMIX) SMITHKLINE BEECHAM CORP.
XX (SMK) SMITHKLINE BEECHAM PLC.
XX
PI Elshourbagy N, Gattu M, Michalovich D, Shabon U;
XX
DR WPI; 2003-203569/20.
DR N-PSDB; ACC44115.
XX
PT New G-protein coupled receptor; AXOR 57, for diagnosing and treating
PT diseases, such as, pain, cancer, diabetes, obesity, anorexia, asthma,
PT Parkinson's disease, hypotension, hypertension, urinary retention, and
PT osteoporosis.
XX
PS Claim 1; Page 27-28; 32pp; English.
XX
CC The invention relates to the isolation of a novel G-protein coupled (7TM)
CC receptor AXOR 57 (this sequence) or a DNA fragment encoding a polypeptide
CC having at least 95% identity with AXOR-57 protein. The protein has been
CC shown to have homology to the human chromosome 16 clone CTRB-H1_036x2
CC (AC008785). The protein and polynucleotides encoding the protein are used
CC in screening for compounds that stimulate or inhibit the function or
CC level of the polypeptide or polynucleotides, such as, agonists and
CC antagonists. The protein, polynucleotides, and antibodies to the protein
CC are used in diagnostic kits, to diagnose a disease. Polynucleotides
CC encoding the protein are used for chromosome localization studies, or for
CC tissue expression studies. The protein and nucleic acids encoding the
CC protein are used in vaccines for treating diseases such as, bacterial,
CC fungal, protozoal, and viral infections, pain, cancer, diabetes, obesity,
CC anorexia, bulimia, asthma, Parkinson's disease, acute heart failure,
CC hypotension, hypertension, urinary retention, osteoporosis, angina
CC pectoris, myocardial infection, stroke, ulcer, allergy, benign prostatic
CC hypertrophy, migraine, vomiting, anxiety, schizophrenia, depression,
CC delirium, dementia, severe mental retardation, or Huntington's disease
XX
SQ Sequence 353 AA;
Query Match 94.4%; Score 1857; DB 6; Length 353;
Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANGSLSSWSPGSAAGLGFVGVVYYSLLCLGLPANITVTIISQLVARROK 60
DB 1 MEHTAHLAANGSLSSWSPGSAAGLGFVGVVYYSLLCLGLPANITVTIISQLVARROK 60

QY 61 SSNYLLAALAAADILVLFYIVDFLLEDFLLNMQMPVDPKITEVLEFSSIHSTIWTV 120
DB 61 SSNYLLAALAAADILVLFYIVDFLLEDFLLNMQMPVDPKITEVLEFSSIHSTIWTV 120
QY 121 PLTIDRYAVGCHPLKHYTVSPARTRKIVSVYITCFITSIPYMMENIMEDYISTSVH 180
DB 121 PLTIDRYAVGCHPLKHYTVSPARTRKIVSVYITCFITSIPYMMENIMEDYISTSVH 180
QY 181 HVLIMHCFYTVLVPCGIFPLINSIYVKLRKSNFRLRGYSTGKTTAILETITSIFATL 240
DB 181 HVLIMHCFYTVLVPCGIFPLINSIYVKLRKSNFRLRGYSTGKTTAILETITSIFATL 240
QY 241 WAPRIIMLVHLYGAPIONRMLVHIMSDIANMLLNTAINFELICYFSKFRMAAATL 300
DB 241 WAPRIIMLVHLYGAPIONRMLVHIMSDIANMLLNTAINFELICYFSKFRMAAATL 300
QY 301 KAFPCOKOPQVPTNNHFSITSSPMISPAHSHCIKMLVVOYDNGKPIK 350
DB 301 KAFPCOKOPQVPTNNHFSITSSPMISPAHSHCIKMLVVOYDNGKPIK 350

RESULT 14
ABR44437
ID ABR44437 standard; protein; 353 AA.
XX
AC ABR44437;
XX
DT 25-JUL-2003 (first entry)
XX
DE Human G protein-coupled receptor #SEQ ID 2.
XX
KW Human, G protein-coupled receptor; anorectic; eating disorder; obesity.
XX
OS Homo sapiens.
XX
PN WO2003027142-A1.
XX
PD 03-APR-2003.
XX
PE 19-SEP-2002; 2002WO-JP009626.
XX
PR 21-SEP-2001; 2001JP-00288278.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Matsumoto S, Takasaki J, Kurama T, Saito T, Kamohara M, Soga T;
PI HiYama H;
XX
DR WPI; 2003-333291/31.
DR N-PSDB; ACC71785.
XX
PT New G protein-coupled receptor and encoded gene, useful in screening
PT preventives or remedies for eating disorders or obesity.
XX
PS Claim 1; Page 34-35; 48pp; Japanese.
XX
CC The invention relates to a novel G protein-coupled receptor. The protein
CC and its encoded gene are useful for screening preventives or remedies for
CC eating disorders or obesity. The current sequence represents a G protein
CC coupled receptor sequence
XX
SQ Sequence 353 AA;
Query Match 94.4%; Score 1857; DB 6; Length 353;
Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTAHLAANGSLSSWSPGSAAGLGFVGVVYYSLLCLGLPANITVTIISQLVARROK 60
DB 1 MEHTAHLAANGSLSSWSPGSAAGLGFVGVVYYSLLCLGLPANITVTIISQLVARROK 60
QY 61 SSNYLLAALAAADILVLFYIVDFLLEDFLLNMQMPVDPKITEVLEFSSIHSTIWTV 120

Db 61 SSYNTLLALAAADILVLPFIVVDLLEDFILNMQMPQVDPKIEVLEFSSIHSTIWTV 120
QY 121 PLTIIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYWMNPINWTDYISTSVH 180
Db 121 PLTIIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYWMNPINWTDYISTSVH 180
QY 181 HVLIMIHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALIFTTISIFATL 240
Db 181 HVLIMIHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALIFTTISIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRRTMAAATL 300
QY 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPA NSHCIMLVYQYDKXGKPIK 350
Db 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPA NSHCIMLVYQYDKXGKPIK 350

RESULT 15

ABB82499
ID ABB82499 standard; protein; 353 AA.

AC ABB82499;

DT 22-JAN-2003 (first entry)

DE Human TGR20 polypeptide.

KM G-protein coupled receptor; GPCR; antipsoriatic; antiinflammatory;
KW antileptic; nootropic; neuroprotective; antianemic; antidiabetic; human;
KW antiparkinsonian; antileptic; TGR20; receptor.

OS Homo sapiens.

PN WO200277001-A2.

PD 03-OCT-2002.

PF 08-MAR-2002; 2002WO-US007171.

PR 09-MAR-2001; 2001US-00802803.

PR 16-MAR-2001; 2001US-0276649P.

PA (TULA-) TULARIK INC.

PI Tian H, Zhao J, Chen J, Cutler G;

DR WPI; 2003-018881/01.

DR N-PSDB; ABV73364.

PT New G-protein coupled receptor polypeptides and polynucleotides useful
PT for identifying compounds for treating a TGR-associated disorder, e.g.
PT psoriasis, inflammatory bowel disease, hyperlipidemia, Parkinson's
PT disease, anemia.

PS Claim 15; Page 63; 87pp; English.

CC The invention relates to G-protein coupled receptor (GPCR) polypeptides
CC and encoding polynucleotides selected from TGR20, TGR35, TGR36, TGR83,
CC TGR341, TGR211, TGR216 and TGR79. The polypeptides and nucleic acids are
CC useful for identifying compounds for treating a TGR-associated disorder,
CC such as psoriasis, inflammatory bowel disease, hyperlipidemia,
CC Parkinson's disease, Huntington's disease, anemia, immune and blood
CC disorders, ulcerative colitis, Crohn's disease or spleen enlargement.
CC They are also useful for identifying cells such as kidney, liver,
CC hypothalamus, colon, adipose, or spleen cells, for forensics and
CC paternity determination, diagnosing diseases and examining signal
CC transduction. The present sequence represents a human TGR20 polypeptide
CC
SQ Sequence 353 AA;

Query Match

94.4%; Score 1857; DB 6; Length 353;

Best Local Similarity 100.0%; Pred. No. 2,2e-197;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEHTAHLAANSLSWSPGACGLFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
Db 1 MEHTAHLAANSLSWSPGACGLFVPPVYYSLLCLGLPANILTVIISQLVARROK 60
QY 61 SSYNTLLALAAADILVLPFIVVDLLEDFILNMQMPQVDPKIEVLEFSSIHSTIWTV 120
Db 61 SSYNTLLALAAADILVLPFIVVDLLEDFILNMQMPQVDPKIEVLEFSSIHSTIWTV 120
QY 121 PLTIIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYWMNPINWTDYISTSVH 180
Db 121 PLTIIDRYIAVCHPLKXHTVSPARTRKIVSVYITCFLTSIPYWMNPINWTDYISTSVH 180
QY 181 HVLIMIHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALIFTTISIFATL 240
Db 181 HVLIMIHCTVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTALIFTTISIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFELYCFISKRRRTMAAATL 300
QY 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPA NSHCIMLVYQYDKXGKPIK 350
Db 301 KAFPKCQKQPVQFYTNHNFSTSSPWISPA NSHCIMLVYQYDKXGKPIK 350

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OM protein - protein search, using sw model

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(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

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2	238.5	12.1	398	1	US-08-288-663A-1
3	232	11.8	415	2	US-09-545-944-2
4	232	11.8	415	2	US-10-215-619-2
5	231.5	11.8	355	1	US-08-012-988A-2
6	231.5	11.8	355	1	US-08-450-393A-5
7	231.5	11.8	355	2	US-08-446-669-5
8	231.5	11.8	355	2	US-09-239-938-1
9	231.5	11.8	355	2	US-09-886-319A-14
10	231.5	11.8	355	2	US-10-039-659A-13
11	231.5	11.8	355	2	US-09-961-068-1
12	231.5	11.8	355	2	US-09-625-573-5
13	231.5	11.8	355	2	US-09-960-547-1
14	231.5	11.8	355	4	PCT-US95-00476-5
15	228	11.6	412	2	US-09-949-016-10101
16	228	11.6	415	1	US-08-875-076-12
17	226.5	11.5	398	2	US-08-288-663A-15
18	226	11.5	415	2	US-09-341-016A-1
19	225	11.4	357	2	US-09-693-746-4
20	225	11.4	357	2	US-08-833-746-8
21	223.5	11.4	355	2	US-08-833-752-9
22	223.5	11.4	355	2	US-09-938-719-9
23	223.5	11.4	355	2	US-09-938-726B-9
24	223.5	11.4	355	2	US-09-938-703B-9
25	223	11.3	352	2	US-09-029-027B-2
26	222.5	11.3	347	1	US-08-118-270-47
27	222.5	11.3	347	4	PCT-US93-08528-47

28	219	11.1	353	1	US-08-118-270-45	Sequence 45, Appl
29	219	11.1	353	4	PCT-US93-08528-45	Sequence 45, Appl
30	219	11.1	367	1	US-08-149-093A-4	Sequence 4, Appl
31	219	11.1	367	1	US-08-911-245-4	Sequence 4, Appl
32	219	11.1	367	1	US-08-553-058C-4	Sequence 4, Appl
33	219	11.1	367	1	US-08-514-451A-4	Sequence 4, Appl
34	219	11.1	367	2	US-09-170-331-4	Sequence 4, Appl
35	219	11.1	367	2	US-09-510-473-4	Sequence 4, Appl
36	219	11.1	367	2	US-09-048-916B-4	Sequence 4, Appl
37	219	11.1	384	2	US-09-071-434-3	Sequence 4, Appl
38	218	11.1	378	2	US-09-045-583-5	Sequence 5, Appl
39	218	11.1	378	2	US-09-534-185-5	Sequence 5, Appl
40	217	11.0	355	2	US-09-045-583-53	Sequence 53, Appl
41	217	11.0	355	1	US-09-534-185-53	Sequence 53, Appl
42	217	11.0	367	2	US-08-454-549-2	Sequence 2, Appl
43	217	11.0	367	2	US-08-454-552-2	Sequence 2, Appl
44	217	11.0	367	2	US-08-147-592A-6	Sequence 6, Appl
45	217	11.0	367	2	US-08-889-108-17	Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-07-629-1041-3
; Sequence 3, Application US/076291041
; Patent No. 5288621
; GENERAL INFORMATION:
; APPLICANT: Gershengorn, Marvin C
; APPLICANT: Straub, Richard E
; TITLE OF INVENTION: PITUITARY TRH RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 3.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/629,1041
; FILING DATE: 19901214
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26, 824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-629-1041-3

Query Match      12.3%; Score 241; DB 1; Length 393;
Best Local Similarity 22.1%; Pred. No. 1e-13;
Matches 81; Conservative 75; Mismatches 123; Indels 88; Gaps 15;

QY      19 PSACGLGF-VPVVYYSLLC-IGPANIILYIISOLVARQKSSV-N-YLLAAAPIL 75
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      16 PQAAVALRQYVITLLVYIIGLGIQVGNIMVTVLMR--TKMRPTTCYLVSLVADIM 73
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      76 VLFIVFVDFLEDFILNMQMPQVDPKI-----IEVLFSSHSHTSIWTVPL 122
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```

Db      VL-----VAAGLPNITSIIGSWYGVGCLITVLYGLGNASSCSITAF 119
Qy      123 TIDRIANCHPLKHTHTVSYPARTRKIVYVYITCELTSPYVW-----PNWT-EDYIS 176
      120 TIERIALICHIPKAOFLCTSPBRKKIITVMA--FTSIYCNMLPFLDLNISTYKNAV 176
Qy      177 TSVHVLWIMHCFVTVLPBCSIFFLINSI---IVY-----208
Db      177 VSCGYKISRNYSPIYLMDFGVFYVVPMLATVGLFIARILEPNIPSPDKENSKMMKN 236
Qy      209 -KLARKSNPRLEG-----YSTCKTALLETITISIPATLMAR-RIMILYHLYGAP 257
Db      237 DSIHONKINLWATNRCENSTVSSRKQVKMLAAVVILFPLLMPPRTLVVAVSPSSPF 296
Qy      258 ONRWLVHIMSDIANMLALNTAINTAFYLCFISKRPRTMAATLKAEFFCKQOPVQPYTN 317
Db      297 GENWFLL----PCRICIYLSAINPIVYIMLSQKFR-----AAPRKLCNCKQKTEKAANY 348
Qy      318 NFSITSS 324
Db      349 SVALNYS 355

```

RESULT 2
US-08-288-663A-1
; Sequence 1, Application US/08288663A
; Patent No. 5879896

1 APPLICANT: HIMMA, Shuji
2 APPLICANT: HOSOYA, Masaki
3 APPLICANT: ONDA, Haruo
4 TITLE OF INVENTION: HUMAN TSH RECEPTOR, ITS PRODUCTION
5 TITLE OF INVENTION: AND USE
6 NUMBER OF SEQUENCES: 15
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
9 STREET: 130 Water Street

```

1  COUNTRY: USA
2  ZIP: 02109
3  COMPUTER READABLE FORM:
4  MEDIUM TYPE: Diskette
5  COMPUTER: IBM Compatible
6  OPERATING SYSTEM: DOS
7  SOFTWARE: FASTSO for Windows Version 2.0
8  CURRENT APPLICATION DATA:
9  APPLICATION NUMBER: US/06/288.663A
10 FILING DATE: 09-AUG-1994

```

APPLICATION NUMBER: 198309/1993
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: 286886/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 325215/1993
FILING DATE: 22-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44612
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

```

; INFORMATION FOR SEQ ID NO: 1
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 398 amino acids
;
; TYPE: amino acid
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
US-08-288-663A-1

```

Query Match	12.1%;	Score 238.5;	DB 1;	Length 398;
Best Local Similarity	22.4%;	Pred. No. 1.8e-13;		
Matches	80;	Conservative	70;	Mismatches 120;
			Indels	87;
			Gaps	13;

```

28 VPRVYVYSLLC-LGIPANILTVIISQVARRQKSSYN-YLLALAADIILVLFIVPVD 85
      | : ||| | : ||| : : : : : ||| ||| ||| |||
26 VVITILLVITICGLIGINIMVLLVMR--TKMRIPTCIVLSLVADLMVL----- 75

```

```

86 LLEDFLNNQMPQVPDKI-----IEVLEFSSHSITWITPLRIDRYAVCH 132
      : : : | : : : | : : : | : : : |
76 -----VAAGLPNITDSIGSWVYGCGCTCTTQYLGINASSCSPTAFITERIYAICH 129

```

133 PLCKHTVSYPABTRKIVSVVITCELTSPYVMA-----PNIWT-EDYISTSVHHLWI 186
| : : : | : : : | : : : | : : :
130 PIAGELCTFSAPAKIIIFVMA---FTSLYCMLEFFLLDINISYXDAIVISCGYISRN 186

```

187 HCFYVLVPCSEFFILNSIIYKL-----RRKSN- 215
      : :|: :|:| :|:| :|:| :|:| :|:|
187 YSPPIILMDGVFVYVPMILATVLGFIARILFLNPSPDPKENSITKNDSTHONTNLN 246

```

```

216 -----FLKRGSTGKTTAIIFTTSFATIMAD-RIMILIIYHKGAPIDQRKLVHIMS 267
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
247 VNTSNCFNSTVSSRKQVTKMLAVVILFALLIMEPYRILVVNSPLSSSPQENMFL--- 303

```

268 DIANMLALNTAANFELYCFISKPRMTAAATLKAFKCKQKQPVQFTNNHSITSS 324
 304 -FCRICYLSAINPVIYMLSQKR----AAFRKCNCKQKPTKRPANYSVALNYS 355

RESULT 3
US-09-545-944-2
; Sequence 2, Application US/09545944
; Patent No. 6461836
; GENERAL INFORMATION:

? APPLICANT: AMES, ROBERT
 ? APPLICANT: ELSHOURBAGY, NABIL
 ? APPLICANT: MICHALOVICH, DAVID
 ? APPLICANT: SARAU, HENRY
 ? APPLICANT: SHABON, USMAN
 ? APPLICANT: VAMTER, LISA
 ? TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
 ? TITLE OF INVENTION: (AXOR34) AND SCREENING METHODS THEREOF
 ? FILE REFERENCE: GP70657-1

```

CURRENT APPLICATION NUMBER: 05/09/545,944
CURRENT FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: US 09/435,384
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2

```

```

; LENGTH: 415
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-545-944-2

```

Query Match	11.84; Score 232; DB 2; Length 415;
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Best Local Similarity 22.4%; Pred. No. 7.3e-13;
Matches 79; Conservative 77; Mismatches 112; Indels 84; Gaps 15;

```

27 FVEV-VYXSLLCGLPANILTVIILSQLVARRÖKSSYNLALAAADIVLEFFIVEVD 85
    | : ||| : :||| : :||| : :||| : :||| :
4E E DVENIDVIDEVUICUTCNIT VCI VTI ÖHUMREPNVV -VI ECJ AVET I TV -----T C M 90

```

86 LLEDFILNNQMP-----QVPDKIEEVEFSSIHSTIWTVPLTIDRYIAVACHPLKXH 137

100 PLEVYEMRNPNYPFLGPGVGCYFKTALFETVCPSI---LSITT-VSVERVVALHPFRAK 155
138 TVSGPARTRKVIISVYITCELTSP-----YYMMPN-----IWTEDY 174

156 LGSTRRLALRLIGIVMGFVSFLSLENTSIHGKIFHIFPNSGLVPGSATCTVIKPMW---- 211

TITLE OF INVENTION: PROTEIN RECEPTORS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleson & T
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/450,393A
 FILING DATE: May 25, 1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Caesar, Luann
 REGISTRATION NUMBER: 31,822
 REFERENCE/DOCKET NUMBER: UCAAL-237/02US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5165
 TELEFAX: 415-8857-0663
 TELEX: 380816CcoaleypA
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 355 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 US-08-450-393A-5

```
APPLICANT: LeukoSite, Inc.
TITLE OF INVENTION: ANTI-CCR1 ANTIBODIES AND METHODS OF USE
FILE REFERENCE: LKS97-13
CURRENT APPLICATION NUMBER: US/09/239,938
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 1
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapien
US-09-239-938-1
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```
Query Match      11.8%; Score 231.5; DB 2; Length 355;
Best Local Similarity 26.3%; Pred. No. 6,7e-13;
Matches 81; Conservative 57; Mismatches 105; Indels 65; Gaps 13;
```

```
QY 22 ACGLGFVPVYVYSLILCGLPANILTVIILSQVVAROKSSVNYLLAALADIVLFFIV 81
DB 31 AFGAQLPPL-YSLVFGVIGLVGNILVVLVQYKRLKNTSI-YLLNLAIISDLFLFTLP 88
QY 82 F-VDF-LLEDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTVPITIDRYIYVCH---PLKY 136
DB 89 FWIDYKLDWDVFGDAM---CKILSGFYTGYSIEIFIIILLITDRYIAIYHAAVAPALRA 144
QY 137 HTVSYPARTRKIVSVYITCPLTSLP-YVWMPNITWEDYISTSVH-----181
DB 145 RVTGVTISIIIMALAI---LASMPGLYFSKTQWEPHTHTCSLHPHESLREWKLFQAL 201
QY 182 -----VLIWHCFVYVLPSCIFPILNSIIVYKLRKSNFRLRGYSTGKTTALIF 231
DB 202 KNLPLGLVPLVLMVICY-----GIKILLRPNE-----KSKAVRLIF 242
QY 232 TTTSIFATLMAPRIIMILVHLGAPY-----QNRMLVHIMSDIANMLALTAINFLY 285
DB 243 VMIIFPLEWTPYNTILISVQDPLFTHCEQSRHL-DLAQVTEVIAIYTHCCVNPVY 301
QY 286 CFISKRFR 293
DB 302 AFGGERFR 309
```

RESULT 9

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US-09-886-319A-14
Sequence 14, Application US/09886319A
Patent No. 6586185
GENERAL INFORMATION:
APPLICANT: Wolf, Eckard
APPLICANT: Werner, Sabine
APPLICANT: Halle, Jörn-Peter
APPLICANT: Regenbogen, Johannes
APPLICANT: Goppelt, Andreas
TITLE OF INVENTION: Use of Polypeptides or Nucleic Acids for
TITLE OF INVENTION: the Diagnosis or Treatment of Skin Disorders and Wound
TITLE OF INVENTION: Healing and for the Identification of Pharmacologically
FILE REFERENCE: 50125/014002
CURRENT APPLICATION NUMBER: US/09/886,319A
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 60/222,081
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: DE 10030149.5
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for windows version 4.0
SEQ ID NO 14
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-09-886-319A-14
```

```
Query Match      11.8%; Score 231.5; DB 2; Length 355;
```

```
Best Local Similarity 26.3%; Pred. No. 6,7e-13;
Matches 81; Conservative 57; Mismatches 105; Indels 65; Gaps 13;
```

```
QY 22 ACGLGFVPVYVYSLILCGLPANILTVIILSQVVAROKSSVNYLLAALADIVLFFIV 81
DB 31 AFGAQLPPL-YSLVFGVIGLVGNILVVLVQYKRLKNTSI-YLLNLAIISDLFLFTLP 88
QY 82 F-VDF-LLEDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTVPITIDRYIYVCH---PLKY 136
DB 89 FWIDYKLDWDVFGDAM---CKILSGFYTGYSIEIFIIILLITDRYIAIYHAAVAPALRA 144
QY 137 HTVSYPARTRKIVSVYITCPLTSLP-YVWMPNITWEDYISTSVH-----181
DB 145 RVTGVTISIIIMALAI---LASMPGLYFSKTQWEPHTHTCSLHPHESLREWKLFQAL 201
QY 182 -----VLIWHCFVYVLPSCIFPILNSIIVYKLRKSNFRLRGYSTGKTTALIF 231
DB 202 KNLPLGLVPLVLMVICY-----GIKILLRPNE-----KSKAVRLIF 242
QY 232 TTTSIFATLMAPRIIMILVHLGAPY-----QNRMLVHIMSDIANMLALTAINFLY 285
DB 243 VMIIFPLEWTPYNTILISVQDPLFTHCEQSRHL-DLAQVTEVIAIYTHCCVNPVY 301
QY 286 CFISKRFR 293
DB 302 AFGGERFR 309
```

RESULT 10

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US-10-039-659A-13
Sequence 13, Application US/10039659A
Patent No. 6723520
GENERAL INFORMATION:
APPLICANT: Wang, Wei
APPLICANT: Gish, Kurt C.
APPLICANT: Schall, Thomas J.
APPLICANT: Vicari, Alain P.
APPLICANT: Zlocnik, Albert
TITLE OF INVENTION: Antibodies that bind chemokine TRCK
FILE REFERENCE: DX0589K1B US
CURRENT APPLICATION NUMBER: US/10/039,659A
CURRENT FILING DATE: 2002-01-03
PRIOR APPLICATION NUMBER: US 08/887,977
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 60/021,664
PRIOR FILING DATE: 1996-07-05
PRIOR APPLICATION NUMBER: US 60/028,329
PRIOR FILING DATE: 1996-10-11
PRIOR APPLICATION NUMBER: US 60/048,593
PRIOR FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-659A-13
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```
Query Match      11.8%; Score 231.5; DB 2; Length 355;
Best Local Similarity 26.3%; Pred. No. 6,7e-13;
Matches 81; Conservative 57; Mismatches 105; Indels 65; Gaps 13;
```

```
QY 22 ACGLGFVPVYVYSLILCGLPANILTVIILSQVVAROKSSVNYLLAALADIVLFFIV 81
DB 31 AFGAQLPPL-YSLVFGVIGLVGNILVVLVQYKRLKNTSI-YLLNLAIISDLFLFTLP 88
QY 82 F-VDF-LLEDFILNMQMPQVDPKIIIEVLEFSSIHSTIWTVPITIDRYIYVCH---PLKY 136
DB 89 FWIDYKLDWDVFGDAM---CKILSGFYTGYSIEIFIIILLITDRYIAIYHAAVAPALRA 144
QY 137 HTVSYPARTRKIVSVYITCPLTSLP-YVWMPNITWEDYISTSVH-----181
DB 145 RVTGVTISIIIMALAI---LASMPGLYFSKTQWEPHTHTCSLHPHESLREWKLFQAL 201
```



```

QY 182 -----VIMIHCFVYLVPCGFPIIASIIYKLRKSNFRLRGSTGKTAILE 231
      : : : : :
Db 202 KLNIEGLVPLVIMICYT-----GIKILLRRPE-----KSKAVRLIF 242
      : : : : :
QY 232 TITSIFATIMABRIIMILYHLGYAPI-----QNRWVHIMSDIANMLLAINPEFY 285
      | | | | : : : : :
Db 243 VIMIIIFELFWIDYNTLILISVFQDFLEHCEOSRHL-DLAVQTEVIAYTHCCNPVIT 301
      : : : : :
QY 286 CFISKRRFR 293
      | : : |
Db 302 AFVGERFR 309

```

```

RESULT 11.068-1
US-09-961-068-1
: Sequence 1, Application US/09961068
: Patent No. 673570
: GENERAL INFORMATION:
: APPLICANT: Qin, Shixin
: APPLICANT: Newman, Walter
: APPLICANT: Kassam, Naim
: TITLE OF INVENTION: ANTICCR1 ANTIBODIES AND METHODS OF USE
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1855.1048-011
: CURRENT APPLICATION NUMBER: US/09/961,068
: CURRENT FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: US 09/239,938
: PRIOR FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 355
: TYPE: prt
: ORGANISM: Homo sapiens
US-09-961-068-1

```

Query Match	11.8%	Score 231.5;	DB 2;	Length 355;
Best Local Similarity	26.3%	Pred. No. 6.7e-13;		
Matches	81;	Conservative	57;	Mismatches 105;
		Indels	65;	Gaps 13;

```

Qy 22 ACGGFGVPPVYVYSLSLCLGELRPNILVTIILISQVARKQSSNYUALLAADAIDLVEFTV 81
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 AFGAGLBPPL-YSLVFGVIGVGNITLVVLVQYKRKKMNTS-I-YLLNLASIDLLFLFTLP 88
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 82 F-VDF-LLEDFLNNQMGPVDPDKIIEVLEBSSTHTSIWITVPLTIDRYAVCH---PLKY 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 FVIDKYLKDDMWFGDAM---CIIISGFEYTGYSSEIFITLLTIDRYALVAHVAPALRA 144
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 137 HTVSYPATRKAKIVSVYITCFPLTSIP-YWMPPIWIEDYDISTSVNH-----181
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 RTVTEGVTISIIIMALAI---LASMGLYFSKQWMEFTNHTGSLNHPHESREMKLEQAL 201
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 182 -----VLIWIGHCTVVLVPCGSIFFILNSIIYUKLRKSNFRLRGYSTGKTAAILF 231
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 KLNLFGLVPLRLTWICICTY-----GIKILLRRPNE-----KSKSAVRLIF 242
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 232 TITSIFATIMARIRIMILYHLYGAPL-----QNRKLVNHSIMSIANMLALNLTALINEFLY 285
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 VIMIFFPLFWETFEYNLTILISVFODPLFTHCEQSRHL-DLAVQVTEVIATYHCCVNPVIX 301
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 286 GFSIKRFR 293
      : : : : :
Db 302 AFVGERFR 309

```

RESULT 12
US-09-625-573-5
; Sequence 5, Application US/09625573
; Patent No. 6730301
; GENERAL INFORMATION:
; APPLICANT: Charco, Israel
; Coughlin, Shaun

TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOTACTANT
 PROTEIN RECEPTORS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
 STREET: 5 Palo Alto Square
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94306-2155
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/625,573
 FILING DATE: 25-Jul-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/446,669
 FILING DATE: May 25, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Neeley, Richard
 REGISTRATION NUMBER: 30,092
 REFERENCE/DOCKET NUMBER: UCAL-237/01US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-5000
 TELEFAX: 415-857-0663
 TELEX: 380816CooleyPA
 INFORMATION FOR SEQ ID NO: 5:

ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-09-625-573-5

Query Match	11.8%	Score 231.5	DB 2	Length 355
Best Local Similarity	26.3%	Pred. No. 6.7e-13		
Matches	81	Conservative 57	Mismatches 105	Indels 65
				Gaps 13
QY	22	ACGGFAPVYVYSLTCLGCPANLTITVITIIISQVAPARQKSSVYNVLTAAADITLVEPIV	81	
DB	31	AFGGQLPPLVSLVFIYIGLVGNLTVALVLYQKRLKNMTSI-VLTNLASDILFELTLP	88	
QY	82	F-VDF-LLEDFILNMQPOVDKKEIVLEFSSIHSTSIWITVPLTIDRYIVACH---	136	DLKY
DB	69	FMIDYKXKDDVPEGDAM-----CKLGGFYITGLYSELFIIILITIDRYIAIVHAVPFLRA	144	
QY	137	HTVSVPARTKRVISVYITCFELTSP-VYWMPIWTEDYISTSVNH-----	181	
DB	145	RTVTFGVITSIILWALAI---IASMPGLYESTKQWTEFHTHTCSDPHPHESLREWKLFQAL	201	
QY	182	-----VLTIHCFYTVLVVSCSIFFLINSIIVYKLRKNSFRLRGISTGKTIALF	231	
DB	202	KLNDFGLVLPALVWIIICYT-----GIKILTLRRPNE-----KKSAYVRLIF	242	
QY	232	TITSIPATIMAPRILIMLIYHLYGAPI-----QNRMLVHMSDANMLALNTAINFELY	285	
DB	243	VIMTIFLFWPVPVYLLISVFQDLFTTHCEGSRHU-DIAVOQTEVIAIYTHCCVNPVY	301	

Db 302 AFVGERFR 309

RESULT 13
US-09-960-547-1
; Sequence 1, Application US/09960547


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Db 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Qy 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Db 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Qy 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Qy 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372

RESULT 2
US-10-219-834-19
; Sequence 19, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
; FILE REFERENCE: D0191 NP
; CURRENT APPLICATION NUMBER: US/10/219, 834
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/313, 658
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340, 703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318, 675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355, 596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333, 417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338, 367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-834-19

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Qy 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Db 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Qy 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Db 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Qy 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Qy 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372
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Qy 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372

RESULT 3
US-10-314-076-2
; Sequence 2, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY34, AND VARIANTS A
; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314, 076
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338, 371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-2

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.8e-173; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Db 1 MEHTAHLAANSSLSWSPGSAAGLGFVAVVYSSLLCLGLPANILTVIILISQVARRQK 60
Qy 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Db 61 SSYNVLLAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIEVLEFSSIHSTISWTV 120
Qy 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHTVSPARTRKIVSVYITCFILTSIPYWMWPNITWEDYISTSVH 180
Qy 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTTISIPATL 240
Qy 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Db 241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLCYCFISKRFRMAAATL 300
Qy 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCOQOPVOFTNNHFSITSSPWISPA NSHCKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Qy 361 FEDAGACVITL 372
Db 361 FEDAGACVITL 372

RESULT 4
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US-10-174-364-20
: Sequence 20, Application US/10174364
: Publication No. US20030216308A1
: GENERAL INFORMATION:
:   APPLICANT: Anderson et al.
:   TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
:   FILE REFERENCE: 15966-729CIP2
:   CURRENT APPLICATION NUMBER: US/10/174,364
:   CURRENT FILING DATE: 2002-06-17
:   PRIOR APPLICATION NUMBER: 60/190,835
:   PRIOR FILING DATE: 2000-03-20
:   PRIOR APPLICATION NUMBER: 60/190,768
:   PRIOR FILING DATE: 2000-03-20
:   PRIOR APPLICATION NUMBER: 60/190,972
:   PRIOR FILING DATE: 2000-03-22
:   PRIOR APPLICATION NUMBER: 60/191,199
:   PRIOR FILING DATE: 2000-03-22
:   PRIOR APPLICATION NUMBER: 60/191,947
:   PRIOR FILING DATE: 2000-03-24
:   PRIOR APPLICATION NUMBER: 60/192,665
:   PRIOR FILING DATE: 2000-03-28
:   PRIOR APPLICATION NUMBER: 60/192,657
:   PRIOR FILING DATE: 2000-03-28
:   PRIOR APPLICATION NUMBER: 60/192,984
:   PRIOR FILING DATE: 2000-03-28
:   PRIOR APPLICATION NUMBER: 60/192,664
:   PRIOR FILING DATE: 2000-03-28
:   PRIOR APPLICATION NUMBER: 60/192,836
:   PRIOR FILING DATE: 2000-03-29
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 128
:   SOFTWARE: PatentIn Ver. 2.1
:   SEQ ID NO 20
:   LENGTH: 372
:   TYPE: PRT
:   ORGANISM: Homo sapiens
:   US-10-174-364-20

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Query Match	100.0%	Score	1967	DB 4	Length	372			
Best Local Similarity	100.0%	Pred. No.	3,86-173						
Matches	372	Conservative	0	Mismatches	0	Indels	0	Gaps	0
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Db	1	MEHTAHIAANSSISWSPGSACGLGFVPVYYIIILLCGLPANIITVYIISQVARRQK	60						
QY	61	SSYNYTLAAADILVLFPIVVDLDEFLINMOMPOVDDKIEIVLESSIHSTIWTY	120						
Db	61	SSYNYTLAAADILVLFPIVVDLDEFLINMOMPOVDDKIEIVLESSIHSTIWTY	120						
QY	121	PLTIDRYIAYVCHPLKHTVSYEPARTKIVSYVYITCFPLTSPYYMMPNIMTEDYISTSVH	180						
Db	121	PLTIDRYIAYVCHPLKHTVSYEPARTKIVSYVYITCFPLTSPYYMMPNIMTEDYISTSVH	180						
QY	181	HVLIMIHOFYIYLVPCSLFPIINSLIYVKLRKSNPRJRGSTGKTALPFTTISIPATL	240						
Db	181	HVLIMIHOFYIYLVPCSLFPIINSLIYVKLRKSNPRJRGSTGKTALPFTTISIPATL	240						
QY	241	WAPRIIMILYHLYGAPIONRWLVHIMSDIANMALNTAINFELCFISKRETYAAATL	300						
Db	241	WAPRIIMILYHLYGAPIONRWLVHIMSDIANMALNTAINFELCFISKRETYAAATL	300						
QY	301	KAFFKQOPQOQFYNNHNPSTSSWISPANSHCIKMLVYQYDKNGKPKIKSNDSSSYQ	360						
Db	301	KAFFKQOPQOQFYNNHNPSTSSWISPANSHCIKMLVYQYDKNGKPKIKSNDSSSYQ	360						
QY	361	FEDAIGACVITL	372						
Db	361	FEDAIGACVITL	372						

```

Sequence 6, Application US/10333946
Publication No. US20040023252A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
APPLICANT: BURFORD, Neil; YUE, Henry
APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
APPLICANT: HARFALLA, April J A.; YAO, Monique G.
APPLICANT: LU, Yan; TRIBOULET, Catherine M.
APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
APPLICANT: GRAU, Richard C.; WARREN, Bridget A.
APPLICANT: LEE, Ernestine A.; DING, Li
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0176 USN
CURRENT APPLICATION NUMBER: US/10/333,946
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: PCT/US01/23433
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: US 60/221,478
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/223,268
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 60/227,054
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 60/331,121
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: US 60/232,243
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: US 60/232,691
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/235,146
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PERL Program
SEQ ID NO 6
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040023252A1 7474767CD1
US-10-333,946-6

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	Query Match	100.0%;	Score 1967;	DB 4;	Length 372;
	Best Local Similarity	100.0%;	Pred. No. 3.8e-173;		
	Matches 372;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0.
QY	1 MEHTHAHLAANSLSLWMSPGSACGLGVPPVYVYSLLLCLGLPAILITVYILISQLVAROK	60			
Db	1 MEHTHAHLAANSLSLWMSPGSACGLGVPPVYVYSLLLCLGLPAILITVYILISQLVAROK	60			
QY	61 SSNYVLLALAADIIVLPFIVFVDFLEDFILNMQMPQVPDKITEVLEFSSIHTSIMTV	120			
Db	61 SSNYVLLALAADIIVLPFIVFVDFLEDFILNMQMPQVPDKITEVLEFSSIHTSIMTV	120			
QY	121 PLITDRYIACHPLKPKHTVSYPATRKIVISVYTCTFLTSIPYMMWPMIMEDIYSTVH	180			
Db	121 PLITDRYIACHPLKPKHTVSYPATRKIVISVYTCTFLTSIPYMMWPMIMEDIYSTVH	180			
QY	181 HVLIMHICFWYVLVPCGISIFPLINSIIYVKLKRKSNFRLRGVSTGKTALIFLTITSIPATL	240			
Db	181 HVLIMHICFWYVLVPCGISIFPLINSIIYVKLKRKSNFRLRGVSTGKTALIFLTITSIPATL	240			
QY	241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLLNTAINFELCYCFISKFRMAAATL	300			
Db	241 WAPRIIMILYHLYGAPIONRWLVHIMSDIANMLLNTAINFELCYCFISKFRMAAATL	300			
QY	301 KAPKCKCKOPQOPFTNNFSLTSSPWLSPANSHCIKMLVVOYDNGKPKIRKRNDSKSYQ	360			
Db	301 KAPKCKCKOPQOPFTNNFSLTSSPWLSPANSHCIKMLVVOYDNGKPKIRKRNDSKSYQ	360			

Oy 361 FEDAIGACVITL 372
Db 361 FEDAIGACVITL 372

RESULT 6
US-10-246-583-20
; Sequence 20, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15366-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-20

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3,8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQVARRQK 60
Db 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQVARRQK 60
Oy 61 SSYNVLLAAADILVLFYIVFDLLEDFILNMOPVDPKILEVESSIHHSIMITV 120
Db 61 SSYNVLLAAADILVLFYIVFDLLEDFILNMOPVDPKILEVESSIHHSIMITV 120
Oy 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Oy 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Oy 181 HVLIMHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLIMHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Oy 241 WAPRITMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Db 241 WAPRITMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Oy 301 KAFKCKQKOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCKQKOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Oy 361 FEDAIGACVITL 372

Db 361 FEDAIGACVITL 372

RESULT 7
US-10-689-832-20
; Sequence 20, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Majmuder, Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15366-729DIV1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-832-20

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3,8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQVARRQK 60
Db 1 MEHTAHLAANSSLSWSPGACGIGFVPPVYYSLLCLGLPANILTVIISQVARRQK 60
Oy 61 SSYNVLLAAADILVLFYIVFDLLEDFILNMOPVDPKILEVESSIHHSIMITV 120
Db 61 SSYNVLLAAADILVLFYIVFDLLEDFILNMOPVDPKILEVESSIHHSIMITV 120
Oy 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Oy 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKHYTVSPARTRKIVSVYITCFILTSIPYWMWPNIMWEDYISTSVH 180
Oy 181 HVLIMHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Db 181 HVLIMHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTTISIFATL 240
Oy 241 WAPRITMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Db 241 WAPRITMILYHLYGAPIONRWLVHIMSDIANMLALNTAINFPLYCFISKRFRTMAAATL 300
Oy 301 KAFKCKQKOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Db 301 KAFKCKQKOPVOFTYNNHFSITSSPWISPANSHCIKMLVYQYDKNGKPIKSRNDSKSSYQ 360
Oy 361 FEDAIGACVITL 372

Db 361 FEDAGACV11L 372

RESULT 8
US-10-712-615-103
; Sequence 103, Application US/10712615
; Publication No. US20040214317A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY8, EXPRESSED
; FILE REFERENCE: D0047A-CIP
; CURRENT APPLICATION NUMBER: US/10/712,615
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: U.S. 09/992,238
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/248,285
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: U.S. 60/268,581
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/308,285
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: U.S. 60/317,166
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 134
; SOFTWARE: Patent version 3.2
; SEQ ID NO 103
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-712-615-103

Query Match 100.0%; Score 1967; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 3,8e-173;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHTHAHLAANSSLSWSPGSAACGLGFVVVYSSLLCLGLPANILTVIILSQLVAROK 60
Db 1 MHTHAHLAANSSLSWSPGSAACGLGFVVVYSSLLCLGLPANILTVIILSQLVAROK 60
Qy 61 SSYNVTLAALAAADILVLFPIVFDLLEDFILNMQPVDPDKIEVLEFSSIHSTIWTIV 120
Db 61 SSYNVTLAALAAADILVLFPIVFDLLEDFILNMQPVDPDKIEVLEFSSIHSTIWTIV 120
Qy 121 PLTIDRYIANVCHPLKXHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Db 121 PLTIDRYIANVCHPLKXHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Qy 181 HVLWICHFTVYLVPCSIFFILNSIIYVGLRRKSNFRLRGYSTGKTTAILFTTISFATL 240
Db 181 HVLWICHFTVYLVPCSIFFILNSIIYVGLRRKSNFRLRGYSTGKTTAILFTTISFATL 240
Qy 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFLYCFISKRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFLYCFISKRRTMAAATL 300
Qy 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360
Db 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360
Qy 361 FEDAGACV11L 372
Db 361 FEDAGACV11L 372

RESULT 9
US-10-314-076-4
; Sequence 4, Application US/10314076
; Publication No. US20030152977A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY34, AND VARIANTS A
; METHODS OF USE THEREOF

; FILE REFERENCE: D0197NP
; CURRENT APPLICATION NUMBER: US/10/314,076
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: U.S. 60/338,371
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent version 3.1
; SEQ ID NO 4
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-314-076-4

Query Match 98.6%; Score 1939.5; DB 4; Length 369;
Best Local Similarity 99.2%; Pred. No. 1.3e-170;
Matches 369; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MHTHAHLAANSSLSWSPGSAACGLGFVVVYSSLLCLGLPANILTVIILSQLVAROK 60
Db 1 MHTHAHLAANSSLSWSPGSAACGLGFVVVYSSLLCLGLPANILTVIILSQLVAROK 60
Qy 61 SSYNVTLAALAAADILVLFPIVFDLLEDFILNMQPVDPDKIEVLEFSSIHSTIWTIV 120
Db 61 SSYNVTLAALAAADILVLFPIVFDLLEDFILNMQPVDPDKIEVLEFSSIHSTIWTIV 120
Qy 121 PLTIDRYIANVCHPLKXHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Db 121 PLTIDRYIANVCHPLKXHTVSPARTKRVISVYITCFLSIPYMWPNMTEDYISTSVH 180
Qy 181 HVLWICHFTVYLVPCSIFFILNSIIYVGLRRKSNFRLRGYSTGKTTAILFTTISFATL 240
Db 181 HVLWICHFTVYLVPCSIFFILNSIIYVGLRRKSNFRLRGYSTGKTTAILFTTISFATL 240
Qy 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFLYCFISKRRTMAAATL 300
Db 241 WAPRIIMILYHLYGAPIQNRMLVHMSDIANNLALNTAINFLYCFISKRRTMAAATL 300
Qy 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 360
Db 301 KAFKQKOPVOFYTNHNSITSSPWISPAHSHCIKMLVYQYDKNGKPKSRNDSKSYQ 357
Qy 361 FEDAGACV11L 372
Db 358 FEDAGACV11L 369

RESULT 10
US-10-505-486-108
; Sequence 108, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
; APPLICANT: Takeda Chemical Industries, Ltd.
; TITLE OF INVENTION: Determination of a ligand
; FILE REFERENCE: P03-0006PCT
; CURRENT APPLICATION NUMBER: US/10/505,486
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: JP 2002-45728
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: JP 2002-213949
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: JP 2002-298237
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 108
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Human
US-10-505-486-108

Query Match 94.8%; Score 1864; DB 5; Length 591;
Best Local Similarity 96.7%; Pred. No. 2.1e-163;
Matches 353; Conservative 1; Mismatches 11; Indels 0; Gaps 0;

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Db 1 MEHTHAHLAANSSLSWSPSGACGIFPVVYVYSSLLCLGEPANLITVITIIISQVARROK 60
QY 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPVDPKIIIEVLFSSIHSTIWTIV 120
Db 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPVDPKIIIEVLFSSIHSTIWTIV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTKVIIVSYITCFLTSPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKXHTVSPARTKVIIVSYITCFLTSPYWMWPNIMWEDYISTSVH 180
QY 181 HVLWIHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFELYCFISKFRITMAAATL 300
Db 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFELYCFISKFRITMAAATL 300
QY 301 KAFKCOQOPVOFYTNHNFISITSSPWISPAISHCIKMLVYQYDKXGKPIKSHNDSKSYQ 360
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QY 361 FEDAI 365
Db 361 FTGVV 365
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RESULT 11
US-09-813-432-60
; Sequence 60, Application US/09813432
; Publication No. US20030148485A1
; GENERAL INFORMATION:
; APPLICANT: Taupier Jr., Raymond J
; APPLICANT: Majmuder, Kamud
; APPLICANT: Spaderna, Steven K
; APPLICANT: Smithson, Glenda
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20030148485A1 Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729
; CURRENT APPLICATION NUMBER: US/09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/193,843
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-813-432-60
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Query Match 94.4%; Score 1857; DB 3; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEHTHAHLAANSSLSWSPSGACGIFPVVYVYSSLLCLGEPANLITVITIIISQVARROK 60
Db 1 MEHTHAHLAANSSLSWSPSGACGIFPVVYVYSSLLCLGEPANLITVITIIISQVARROK 60
QY 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPVDPKIIIEVLFSSIHSTIWTIV 120
Db 61 SSYNVLLAAADIVLFFIYFVDFLEDFILNMQMPVDPKIIIEVLFSSIHSTIWTIV 120
QY 121 PLTIDRYAVCHPLKXHTVSPARTKVIIVSYITCFLTSPYWMWPNIMWEDYISTSVH 180
Db 121 PLTIDRYAVCHPLKXHTVSPARTKVIIVSYITCFLTSPYWMWPNIMWEDYISTSVH 180
QY 181 HVLWIHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
Db 181 HVLWIHCFYTVLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAILFTITSIFATL 240
QY 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFELYCFISKFRITMAAATL 300
Db 241 WAPRIIMLYHLYGAPIONRMLVHIMSDIANMLALNTAINFELYCFISKFRITMAAATL 300
QY 301 KAFKCOQOPVOFYTNHNFISITSSPWISPAISHCIKMLVYQYDKXGKPIKSHNDSKSYQ 360
Db 301 KAFKCOQOPVOFYTNHNFISITSSPWISPAISHCIKMLVYQYDKXGKPIKSHNDSKSYQ 360
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RESULT 12
US-10-174-364-60
; Sequence 60, Application US/10174364
; Publication No. US20030216308A1
; GENERAL INFORMATION:
; APPLICANT: Anderson et al.
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2
; CURRENT APPLICATION NUMBER: US/10/174,364
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,836
; PRIOR FILING DATE: 2000-03-29
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-364-60
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Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEHTAHLAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
QY 61 SSYNLLAALAAADILVLFVIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
DB 61 SSYNLLAALAAADILVLFVIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
QY 121 PLTIIRYIAVCHPLKXHTVSPARTRKIVSVYITCFILTSIPYWMNPINWEDYSTSVH 180
DB 121 PLTIIRYIAVCHPLKXHTVSPARTRKIVSVYITCFILTSIPYWMNPINWEDYSTSVH 180
QY 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTISIFATL 240
DB 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTISIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALNTAINFLVCFISKRRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALNTAINFLVCFISKRRRTMAAATL 300
QY 301 KAFPCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKXGKPIK 350
DB 301 KAFPCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKXGKPIK 350

RESULT 13
US-10-246-583-60
; Sequence 60, Application US/10246583
; Publication No. US20040058862A1
; GENERAL INFORMATION:
; APPLICANT: Majumder
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-729CIP2CON1
; CURRENT APPLICATION NUMBER: US/10/246,583
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 2002-06-17, 364
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-246-583-60

Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEHTAHLAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
QY 61 SSYNLLAALAAADILVLFVIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
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DB 61 SSYNLLAALAAADILVLFVIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
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DB 121 PLTIIRYIAVCHPLKXHTVSPARTRKIVSVYITCFILTSIPYWMNPINWEDYSTSVH 180
QY 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTISIFATL 240
DB 181 HVLIMHCFVTYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILFTISIFATL 240
QY 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALNTAINFLVCFISKRRRTMAAATL 300
DB 241 WAPRIIMILYHLYGAPIQNRMLVHIMSDIANMLALNTAINFLVCFISKRRRTMAAATL 300
QY 301 KAFPCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKXGKPIK 350
DB 301 KAFPCQKOPVOFYTNHNSITSSPWPISPANSHCIKMLVYOYDKXGKPIK 350

RESULT 14
US-10-689-832-60
; Sequence 60, Application US/10689832
; Publication No. US20040121380A1
; GENERAL INFORMATION:
; APPLICANT: Kamud
; TITLE OF INVENTION: Novel Polypeptides and Amino Acids Encoding Same
; FILE REFERENCE: 15966-729D1V1
; CURRENT APPLICATION NUMBER: US/10/689,832
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: 09/813,432
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,835
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,768
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/190,972
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,199
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/191,947
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,665
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,657
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,984
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 60/192,664
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 60
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-832-60

Query Match 94.4%; Score 1857; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 5,1e-163;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEHTAHLAANSSLSWSPGSAACGFGFVVVYYSLLCLGLPANILTVIISQVARROK 60
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DB 61 SSYNLLAALAAADILVLFVIVVDLLEDFILNMQMPQVPDKIEVLEFSSIHSTISWTV 120
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Db 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTSIPYWMWPNWTEYISTSVH 180
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 Db 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILEFTISIFATL 240
 Qy 241 WAPRIIMLYHLXGAPIONRMLVHIMSDIANMLALNTAINFPLYCFISKFRPTMAAATL 300
 Db 241 WAPRIIMLYHLXGAPIONRMLVHIMSDIANMLALNTAINFPLYCFISKFRPTMAAATL 300
 Qy 301 KAFFKCKQKQPVQFYTNHNFSTSSPMISPAISHCIRKMLVYQYDKNGKPIK 350
 Db 301 KAFFKCKQKQPVQFYTNHNFSTSSPMISPAISHCIRKMLVYQYDKNGKPIK 350

RESULT 15
 US-09-995-225-16
 ; Sequence 16, Application US/09995225
 ; Publication No. US20020193584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Chu, Zhi Liang
 ; APPLICANT: Dang, Huang T.
 ; APPLICANT: Lowitz, Kevin P.
 ; APPLICANT: Priddy, Cameron
 ; TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions of Human C
 ; FILE REFERENCE: AREN-0308
 ; CURRENT APPLICATION NUMBER: US/09/995,225
 ; PRIOR FILING DATE: 2001-11-26
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: PCT/US99/23938
 ; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: 60/253,404
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/255,366
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: 60/270,286
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/282,365
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/270,266
 ; PRIOR FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 60/282,032
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,358
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282,356
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/290,917
 ; PRIOR FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: 60/309,208
 ; PRIOR FILING DATE: 2001-07-31
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 353
 ; TYPE: prt
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: No. US20020193584A1 Sequence
 US-09-995-225-16

Query Match 94.4%; Score 1857; DB 3: Length 353;
 Best Local Similarity 100.0%; Pred. No. 5.2e-163;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEHTAHLAANSLSWMSPGSACGLGFVYVYVYSLLCGLPANITLVIILSQLVARROK 60
 Db 1 MEHTAHLAANSLSWMSPGSACGLGFVYVYVYSLLCGLPANITLVIILSQLVARROK 60
 Qy 61 SSNYLLALAAADILVLFIVDFVLEDFILNMQMPQVDPKIEVLEFSSIHSTIWTIV 120

Db 61 SSNYLLALAAADILVLFIVDFVLEDFILNMQMPQVDPKIEVLEFSSIHSTIWTIV 120
 Qy 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTSIPYWMWPNWTEYISTSVH 180
 Db 121 PLTIDRYAVCHPLKHTVSYPARTRKIVSVYITCFLTSIPYWMWPNWTEYISTSVH 180
 Qy 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILEFTISIFATL 240
 Db 181 HVLIMHCFYVYLVPCSIFFILNSIIYVKLRKSNFRLRGYSTGKTTAILEFTISIFATL 240
 Qy 241 WAPRIIMLYHLXGAPIONRMLVHIMSDIANMLALNTAINFPLYCFISKFRPTMAAATL 300
 Db 241 WAPRIIMLYHLXGAPIONRMLVHIMSDIANMLALNTAINFPLYCFISKFRPTMAAATL 300
 Qy 301 KAFFKCKQKQPVQFYTNHNFSTSSPMISPAISHCIRKMLVYQYDKNGKPIK 350
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Search completed: December 3, 2005, 06:55:38
 Job time : 98.65 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:36:57 ; Search time 5.07273 Seconds
(without alignments)
351.144 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967
Sequence: 1 MEHTRAHLAANSLSWSPG.....NDSKSYQFEDAIGACVILL 372

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1471	74.8	287	6	US-10-980-388-66 Sequence 66, App1
2	912.5	46.4	313	6	US-10-980-388-63 Sequence 63, App1
3	205	10.4	355	7	US-11-068-686-4 Sequence 4, App1
4	202.5	10.3	352	7	US-11-068-686-20 Sequence 20, App1
5	199.5	10.1	352	7	US-11-068-686-2 Sequence 2, App1
6	176	8.9	417	6	US-10-992-577-44 Sequence 44, App1
7	158	8.0	430	6	US-10-992-577-8 Sequence 8, App1
8	156	7.9	358	6	US-10-980-388-96 Sequence 96, App1
9	156	7.9	389	6	US-10-980-388-116 Sequence 116, App
10	154.5	7.9	420	6	US-10-992-577-6 Sequence 6, App1
11	154.5	7.9	522	6	US-10-510-018-2 Sequence 2, App1
12	151.5	7.7	432	6	US-10-992-577-2 Sequence 2, App1
13	151	7.7	409	6	US-10-627-633-4 Sequence 4, App1
14	149.5	7.6	415	6	US-10-627-633-2 Sequence 2, App1
15	145.5	7.4	352	6	US-10-627-633-6 Sequence 6, App1
16	138.5	7.0	360	6	US-10-851-667A-26 Sequence 26, App1
17	134	6.8	353	7	US-11-067-884-6 Sequence 934, App
18	132	6.7	485	6	US-10-821-234-934 Sequence 119, App
19	126.5	6.4	323	6	US-10-980-388-119 Sequence 1085, App
20	125.5	6.4	339	6	US-10-821-234-1085 Sequence 2, App1
21	121.5	6.2	364	7	US-11-067-884-2 Sequence 114, App
22	120.5	6.1	333	6	US-10-980-388-114 Sequence 91, App
23	119.5	6.1	333	6	US-10-980-388-91 Sequence 118, App
24	112.5	5.7	342	6	US-10-980-388-118 Sequence 117, App
25	112	5.7	340	6	US-10-980-388-117

26	105	5.3	351	7	US-11-067-884-4 Sequence 4, App1
27	103.5	5.3	313	7	US-11-095-093-2 Sequence 2, App1
28	103	5.2	211	6	US-10-980-388-97 Sequence 97, App1
29	100.5	5.1	508	6	US-10-980-388-112 Sequence 112, App
30	97	4.9	473	6	US-10-467-657-1874 Sequence 1874, App
31	96	4.9	440	6	US-10-502-893-2 Sequence 2, App1
32	94.5	4.8	419	7	US-11-067-884-8 Sequence 8, App1
33	92.5	4.7	347	6	US-10-131-826A-18 Sequence 18, App1
34	91	4.6	272	6	US-10-793-626-1308 Sequence 1308, App
35	87.5	4.4	143	6	US-10-793-626-370 Sequence 370, App
36	87	4.4	604	6	US-10-485-517-168 Sequence 168, App
37	86.5	4.4	321	6	US-10-793-626-2816 Sequence 2816, App
38	84.5	4.3	351	7	US-11-095-624-5 Sequence 5, App1
39	84	4.3	336	6	US-10-980-388-110 Sequence 120, App
40	82.5	4.2	337	6	US-10-980-388-115 Sequence 115, App
41	82.5	4.2	926	6	US-10-841-129-2 Sequence 2, App1
42	82	4.2	308	6	US-10-793-626-2446 Sequence 2446, App
43	81.5	4.1	275	7	US-11-110-977-4 Sequence 4, App1
44	81	4.1	350	6	US-10-502-145-1 Sequence 1, App1
45	80.5	4.1	433	7	US-11-082-389-332 Sequence 332, App

ALIGNMENTS

RESULT 1
US-10-980-388-66
Sequence 66, Application US/10980388
PUBLICATON No. US20050255490A1
GENERAL INFORMATION:
APPLICANT: Vogeli, Gabriel
APPLICANT: Parodi, Luis A.
APPLICANT: Hiebach, Ronald R.
APPLICANT: Lind, Peter
APPLICANT: Kayes, Paul S.
APPLICANT: Huff, Valerie
APPLICANT: Huff, Rita M.
APPLICANT: Wood, Linda S.
TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App.
FILE REFERENCE: 00325.US1
CURRENT FILING DATE: US/10/980,388
PRIOR FILING DATE: 2004-11-02
PRIOR APPLICATION NUMBER: US/09/791,932
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/184,305
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,304
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,303
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,397
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/184,247
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/188,880
PRIOR FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: 60/217,369
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/217,370
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/218,492
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 184
SOFTWARE: PatentIn version 3.0
SEQ ID NO 66
LENGTH: 287
TYPE: PRT
ORGANISM: Homo sapiens
US-10-980-388-66
Query Match 74.8%; Score 1471; DB 6; Length 287;
Best local Similarity 99.6%; Pred. No. 1.2e-123;

Matches 281; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 43 ANILTVIILSQLVAROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPK 102
Db 6 ANILTVIILSQLVAROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQMPQVDPK 65
Qy 103 IIEVEFSSISHTSIITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYTCTLSIP 162
Db 66 IIEVEFSSISHTSIITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYTCTLSIP 125
Qy 163 YWMNNTEDYISVHHVLIWHCFVYLVPCSIFFILNSIIYKLRKSNFRLRGS 222
Db 126 YWMNNTEDYISVHHVLIWHCFVYLVPCSMFFILNSIIYKLRKSNFRLRGS 185
Qy 223 TGTALIFTTISIPATLWAPRIIMILYHLYGAPIONRMLVHMSDIANMLALTAINF 282
Db 186 TGTALIFTTISIPATLWAPRIIMILYHLYGAPIONRMLVHMSDIANMLALTAINF 245
Qy 283 FLYCFISGRFRTMAAATLKAFKCKOKOPVQFYTNHNSITSS 324
Db 246 FLYCFISGRFRTMAAATLKAFKCKOKOPVQFYTNHNSITSS 287

RESULT 2

US-10-980-388-63
; Sequence 63, Application US/10980388
; Publication No. US2005025490A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayles, Paul S.
; APPLICANT: Huff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325. US1
; CURRENT APPLICATION NUMBER: US/10/980.388
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791.932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184.305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184.247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188.880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217.369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217.370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218.492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patent version 3.0
; SEQ ID NO 63
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-63

Query Match 46.4%; Score 912.5; DB 6; Length 313;
Best Local Similarity 76.8%; Pred. No. 3.4e-74;
Matches 185; Conservative 6; Mismatches 21; Indels 29; Gaps 3;

Qy 5 HAHLAANSLSWMBD--GSACGLGFVPPVYVSYLL-----LC----- 38
Db 61 HLSWLCNISTIKYPLVGAICNAEVEVQKFNHFHSGAKTYAGPHRSQRSHLCFRAX 120
Qy 39 ---GLPANITLVIIISQVARROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQ 95
Db 121 PVFLSTNNILTVIILSQLVAROKSSVNYLLAALADIVLFFIVFDLLEDFILNMQ 180
Qy 96 MPQVDPKIIIEVEFSSISHTSIITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYT 155
Db 181 MPQVDPKIIIEVEFSSISHTSIITVPLTIDRIYAVCHPLKHTVSPARTRKIVSVYT 240
Qy 156 CFLSISIPYWMNNTEDYISTVHHVLIWHCTVYLVPCSIFFILNSIIYKLRKSN 215
Db 241 CFLSISIPYWMNNTEDYISTVHHVLIWHCTVYLVPCSIFFILNSIIYKLRKSN 300
Qy 216 F 216
Db 301 F 301

RESULT 3

US-11-068-686-4
; Sequence 4, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweickart, Vicky L.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068.686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Grete E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "88-28 amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-068-686-4

Query Match 10.4%; Score 205; DB 7; Length 355;
Best Local Similarity 24.7%; Pred. No. 1.6e-11;
Matches 81; Conservative 65; Mismatches 144; Indels 38; Gaps 13;

Qy 27 FVPVYVYLLCLCTGPAIILTVIILSQLVAROKSSVNYLLAALADIVLFFIVFDL 85
Db 36 FVPPL-VSLVFTVGLGNVVVMIL--IKYRRRLRIMTNVILLNLAISDL--FLVTL 89

Qy 86 LL-----EDFILNMQPQVDPKIIIEVLEFSSIHSTSWITVPLTIDRYIAVCH---PLKXH 137
Db 90 WIHVYRGHWVFGHGM-----CKLLSGFYHTGLYSSEIFILLTIDRYLAIHAVFALBAR 145
Qy 138 TVSYARRKRVIVSVYITCFLTSPYMMPNITWETYSTVHH--VLWICHTVYL-V 194
Db 146 TVTFGVITISVTWGLAVLALPEEFIFETEELCEALYBEDTVSMRPHHTLRMTI 205
Qy 195 PCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAIFTTISIPATLMAPRIMILVH--- 251
Db 206 FCLVLPFLVMAICVGIITLRLCRSKKKYKAIRLFVJMAVFFIWTYVNAIILSSIQ 265
Qy 252 --LYGAPIONRWLVHIMSDIANMLALNTAINFFLYCFISKRPRTWAAATLKAFFKCQ-- 307
Db 266 SILFGNDGCRSHGLDLVMLVTEVIAVSHCCMPVIAVAFGERFRKY----LHNFHRL 321
Qy 308 ---KOPVOPTYNHNSITSSPWISPMNS 332
Db 322 WHLGRYIPLPSEKLERTSS--VSPSTA 347

RESULT 4

US-11-068-686-20
; Sequence 20, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-11-068-686-20

Query Match 10.3%; Score 202.5; DB 7; Length 352;
Best Local Similarity 24.8%; Pred. No. 2,6e-11;
Matches 78; Conservative 48; Mismatches 121; Indels 67; Gaps 12;
Qy 33 YSLLLCLGIPANILVTIISQVLRKSSYN-YLLALAADIIVLFFIVFVDFLEDP 91
Db 37 YSLVIFPGVGNILVLLI--INCKRLKSMTDIYLLNLAIISDL---FLITVFPMAHYAA 91
Qy 92 LNMQMPQVDPKIIIEVLEFSSIHSTSWITVPLTIDRYIAVCH---PLKXHTVSYPARTRKY 148

Db 92 AQMGFNTMQLLTGLYFPGFSSGIFPILLTIDRYLAIHAVFALKARTVFGVNTS-- 149
Qy 149 IYSVITCFLTSP-----YYMPPNITWEDYSTSVHVL 184
Db 150 -VITWVAVFAVSLPGLIFTRSORBGLHTTCSHFYSQYQFPAKNTQ-----LKMVL 201
Qy 185 WICHTVYLVPCSIFFILNSIIVYKLRKSNFRLRGYSTGKTTAIFTTISIPATLMADR 244
Db 202 GL-----VLPLVWVICVSGILKTLRLCRNEKKR-----HRAVRLIFTIMIVFLMABY 251
Qy 245 IIMIL-----YHLYGAPIONRWLVHIMSDIANMLALNTAINFFLYCFISKRPRTMA 297
Db 252 NIVLLNTFOEFGGNNSSNR--LDQAMQVETELGHTHCINDIYAVFGEKFRNYLL 309
Qy 298 A-----TLKAPFKC 306
Db 310 VFQGHIAKRFCKC 323

RESULT 5

US-11-068-686-2
; Sequence 2, Application US/11068686
; Publication No. US20050260565A1
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; Raport, Carol J.
; TITLE OF INVENTION: Chemokine Receptor Materials and Methods
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/068,686
; FILING DATE: 28-Feb-2005
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: /= "88C amino acid sequence"
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-11-068-686-2

Query Match 10.1%; Score 199.5; DB 7; Length 352;
Best Local Similarity 24.2%; Pred. No. 4,8e-11;
Matches 76; Conservative 46; Mismatches 125; Indels 67; Gaps 11;
Qy 33 YSLLLCLGIPANILVTIISQVLRKSSYN-YLLALAADIIVLFFIVFVDFLEDP 91
Db 37 YSLVIFPGVGNVLLIIL--INCKRLKSMTDIYLLNLAIISD---LFFILTVFPMAHYAA 91


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Qy 92 LNMQMPQVDPKIEVLEFSSIHSTWITVPLTIDRYAVCH---PLKXHTVSYPARTKV 148
Db 92 AOMDFGNTMCCQLLTGLYFIFGFGSIFILITLIDRYLAVHAVFALPKARTYFEGVTS-- 149
Qy 149 IVSVYITCFELTSIP-----YYMMPNITWEDYISTSVHVL 184
Db 150 -VITMVAVVAFSLPFIITFRSQKEGLAHTCSHFYSQVQFQAKNQTILKIVILGL----- 203
Qy 185 WIHCTVYVLPQSIFFIINSIIVYKLRRKSNFRLGSGTGKTTALFTTISFEATLMA 244
Db 204 -----VLPLLVAVICSGILKTLRLCRNEKKR-----HRAVRLIFITMIYVFLFMA 251
Qy 245 IIMIL-----YHLYGAPICQRMVHIMSDIANMLALNTALINFELCFISKPRMTAA 297
Db 252 NIVLLNTFQEFEGFINNCSSNR--LDAQOVTEITLGMTHCCINPIIYAFVGEKFRNYLL 309
Qy 298 A-----TLKAFPKC 306
Db 310 VFQKHIAKRFCKC 323

RESULT 6
US-10-992-577-44
; Sequence 44, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide PF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT FILING DATE: 2004-11-18
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-992-577-44

Query Match 8.9%; Score 176; DB 6; Length 417;
Best Local Similarity 22.7%; Pred. No. 7e-09; Mismatches 142; Indels 102; Gaps 18;
Matches 89; Conservative 59;

Qy 10 ANSSLSW---WSPG-----SACGLGF-----VPVY---YSLLCLGLPANILT 47
Db 7 SNSSGSMWHINSNGNTQHPWYSDINITWNNYLLHQPHYAVFISSYFLIFCWMGN--T 64
Qy 48 VIIISQVARKOKSSYN-YLALAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIEV 106
Db 65 VVCFVAVNRKYMHTYTNFFIFMLAISDLVGFICMPIT-LLDNIITAGWPFSSMCKISGL 123
Qy 107 LEFSSIHSTWITVPLTIDRYAVCHPLKYHTVSPARTK-----VIVSVYITCFELT 159
Db 124 VQGISVAASVFTLVAIVADRFRCVYPRK-----PKLTIVKTAFWIYIIGLALITMTP 177
Qy 160 SI-----PYW---WPNIWEDYISTSVHVLIMHCFIVYL 193
Db 178 SAIMLHVOEKYRVRLSHNKTSIVYWCREDMPN-----QEMRRITYTLVLRATIVYL 229
Qy 194 VPCSIFFIINSIIVYKLRRKSNFRLGSGTG-----KTTALFTTISIPAT 239
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Db 230 APLSI-----VIMARIASLFTTSAHSTGKQLEBOMHNSKKQKQYIKMLIVALLFIL 284
Qy 240 LMAPRIIMILYHLG--APICNRMLVHIMSDIANMLALNTALINFELCFISKPRMTAA 297
Db 285 SWLPLMTLMMSDVAADSPNKLAVINIYVYFPAHMLAFCNSSVPIIYGFENENFR---S 341
Qy 298 ATLKAFPKCK--QPVQFY---TNNFSITSS 324
Db 342 GFODAFQFCQKKVXQEAAYGLRAKRNLDINTS 373

RESULT 7
US-10-992-577-8
; Sequence 8, Application US/10992577
; Publication No. US20050260687A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; APPLICANT: Craig, Douglas A.
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide PF (NPFF) Receptors
; FILE REFERENCE: 57155-D/JPM
; CURRENT FILING DATE: 2004-11-18
; PRIOR FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/09/538,036
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/405,558
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: 09/255,368
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-577-8

Query Match 8.0%; Score 158; DB 6; Length 430;
Best Local Similarity 21.7%; Pred. No. 2.8e-07; Mismatches 133; Indels 76; Gaps 14;
Matches 76; Conservative 66;

Qy 3 HTHAHLANSSLSW---SPGSAAGLGFVPPVYVYSLILCLGLPANILTVIILQVARR 58
Db 21 NTEATPATNLTFFSSYYQHTSPVAA-----MFIYVYALIFLLCWMGNTLVCFIV--LKNRH 73
Qy 59 QKSSYN-YLALAAADIVLFFIYFVDFLEDFILNMQMPQVDPKIEVLEFSSIHSTIW 117
Db 74 MHTYTNMILMLANSDDLVGIFCM-PTLVVNLTLMGPFDAATCKMSGVLQGSVASVF 132
Qy 118 ITVPLTIDRYAVCHPLKYHTVSPARTKVIISVYITCFELT----- 159
Db 133 TLVAIAVERFCIYVPRFKLT-----LRKALVTIAVIMALALIMCPASAVTLVTREH 187
Qy 160 -----SIPIYWMMPNITWEDYISTSVHVLIMHCFIVYVLPQSIFFIINSIIVYKL 210
Db 168 HPMVDARNRSYPLVSCWAMEKGM-RRVYTTVLFSSH--LYLAPLALIVMVYARIARL 243
Qy 211 -----RRKSNFRLGSGTGKTTALFTTISFEATLMAPRIMIYHLYGA 255
Db 244 COAREPAPGGEAADPRASRRRAVYHMLVWVAFLEFITS--WLPDMA-LLLIDYGOLSA 300
Qy 256 PIONRMVLHINS---DIANNALNTALINFELCFISKPRMTAAATLKA 302
Db 301 F-----QHLVTYVAAFPPAHMLAFNNSANDIIGYFENENFRRGQAAAFRA 346

RESULT 8
```

```
US-10-980-388-96
; Sequence 96, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325. US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-96

Query Match          7.9%; Score 156; DB 6; Length 358;
Best Local Similarity 22.7%; Pred. No. 3.5e-07;
Matches 71; Conservative 54; Mismatches 120; Indels 68; Gaps 12;

QY 11 NSSLSWSPGSAAGFVPPVYYSLTCLGIPANILTYIIS-QLVARROKSSNYLLAL 69
DB 10 NETLSWTSRATYGAFL-----LLAALLGLPGNGFVWSLGMWRPARGRPLAATLVHL 64
QY 70 AAADILVLEFI-VFVDLFLEDFILNMOMQOVDPDKIIEVLEFSSIHSTIWITPLTIDRYI 128
DB 65 ALADGAVILLPLFLFAFLTRQ---AMPFGQAGCKAVYYVCALSMYASVLLTGLSLQKCL 121
QY 129 AVCHPLKHTVSYPARTRKVIYSVYITCFLTSIPYWMNITWEDYIS---TSVHHVL- 183
DB 122 AVTRFPLARLRSPLARLLAWLALAVPAAYVRHLMRDVQCQLCHPSPVHAAAH 181
QY 184 IWIHCFYVLYVPCSFIFLINSIIYVKLRKSNFRLRG--YSTGKTTA---ILPITYTSIF 237
DB 182 LSELTLTAFVLPFGMLGCGYSVTL-----ARLKGARWGSGRGARVGRLSAIVLAF 233
QY 238 ATLWAPRIIMLYHLYGAPIQNRWLVIHMSDIAMN-----LA 274
DB 234 GLWMAF-----YH-----AVNLLQAVAAALAPPEGALAKUGAGQARAGTTALA 277
QY 275 LNTAINPFLYCF 287
DB 278 FFSSSVNPVLYVF 290
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RESULT 9
US-10-980-388-116
; Sequence 116, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kayes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325. US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 116
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-116

Query Match          7.9%; Score 156; DB 6; Length 389;
Best Local Similarity 22.7%; Pred. No. 3.8e-07;
Matches 71; Conservative 54; Mismatches 120; Indels 68; Gaps 12;

QY 11 NSSLSWSPGSAAGFVPPVYYSLTCLGIPANILTYIIS-QLVARROKSSNYLLAL 69
DB 41 NETLSWTSRATYGAFL-----LLAALLGLPGNGFVWSLGMWRPARGRPLAATLVHL 95
QY 70 AAADILVLEFI-VFVDLFLEDFILNMOMQOVDPDKIIEVLEFSSIHSTIWITPLTIDRYI 128
DB 96 ALADGAVILLPLFLFAFLTRQ---AMPFGQAGCKAVYYVCALSMYASVLLTGLSLQKCL 152
QY 129 AVCHPLKHTVSYPARTRKVIYSVYITCFLTSIPYWMNITWEDYIS---TSVHHVL- 183
DB 123 AVTRFPLARLRSPLARLLAWLALAVPAAYVRHLMRDVQCQLCHPSPVHAAAH 212
QY 184 IWIHCFYVLYVPCSFIFLINSIIYVKLRKSNFRLRG--YSTGKTTA---ILPITYTSIF 237
DB 213 LSELTLTAFVLPFGMLGCGYSVTL-----ARLKGARWGSGRGARVGRLSAIVLAF 264
QY 238 ATLWAPRIIMLYHLYGAPIQNRWLVIHMSDIAMN-----LA 274
DB 265 GLWMAF-----YH-----AVNLLQAVAAALAPPEGALAKUGAGQARAGTTALA 308
QY 275 LNTAINPFLYCF 287
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Db      313  ---TlTlTWISPFSSASKPTLYSLYNNANFPRGMKETFCMSMKC-----YRSNATlTlT 362
QY      324  SPMWISpan 331
        |  ::  |
Db      363  SSRMAKNN 370

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RESULT 15
US-10-627-633-6
: Sequence 6, Application US/10627633
: Publication No. US20050250720A1
: GENERAL INFORMATION:
: APPLICANT: Charles, Andrew David
: APPLICANT: Brennand, John Charles
: APPLICANT: Hart, Kevin Anthony
: TITLE OF INVENTION: Novel Compound
: FILE REFERENCE: 1991-221
: CURRENT APPLICATION NUMBER: US/10/627,633
: CURRENT FILING DATE: 2003-07-28
: PRIOR APPLICATION NUMBER: 09/722,342
: PRIOR FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: 60/172,146
: PRIOR FILING DATE: 1999-12-17
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 6
: LENGTH: 352
: TYPE: prt
: ORGANISM: Rattus norvegicus
US-10-627-633-6

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Query Match	7.4%	Score 145.5;	DB 6;	Length 352;
Best Local Similarity	21.1%;	Pred. No. 2.9e-06;		
Matches 76;	Conservative 68;	Mismatches 154;	Indels 63;	Gaps 18;

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0Y      1 MENTAHJALANSSLSW~WSPGSACGJFVPVYVYLLCLGLGJLANITLTVILISOLVARQ 59
      2 LSEBSHMSNRDLQYELNPGEVA---TASIFGALMEFISIGNSLVCVJYH--SRRT 55
Db
0Y      60 KSSYNVL~LALAAADILVLF---FIVVDLFLEDEFLNMQMBQVPDKIIEVLEFSSJHT 114
      56 OSTNYVLVYSMACADLLISVASSTPFVY~IQFTTGRWTLGSAM---CKVRYFOYLTPGV 110
Db
0Y      115 SWITIVPELTDIXYANCHPLKHTYVSPARTKVIYS~VYITGFLNSIP~----- 163
      111 QIVYLLSTICIDRFYITVYLP~F~KVSREKAKEMIAASWIIDAAFTVPVFFPGSNDSDHC 169
0Y      164 ~YWMENIMTEDYISTSVHVLVIMHGFYVLVCSIFFL~NSIYV-----KLR 211
      170 NYFLPSPW~EGTAYTVIH-----FLVGVLPSVAILLFYVKVILYIWRIGTGGTLR 220
Db
0Y      212 RKSNFLRCYSGTKTALFTITSIPATLWAPRIIMLYLWGLAPIONRWLVHIMSDIAN 271
      221 RRMNVLPR~TKVTKJMKFLFLNVLVFLSWLPRHVAQMLMHPHOEYRKSLSV---TAVT 275
Db
0Y      272 MIALINTAINFLYCFISKRFT~MAAATLKAFCKCQKQDQVQVYTNHNSITSSPWISPA 330
      276 WVSFSSSSASKPTLYSIYNANFRGMKETFCMSMKC-----YRSNAYVITITSSRWAKR 328
0Y      331 N 331
Db      329 N 329

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Search completed: December 3, 2005, 06:55:55
Job time : 6.07273 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 06:22:45 ; Search time 21.1364 Seconds
(without alignments)
1693.415 Million cell updates/sec

Title: US-10-712-615-103

Perfect score: 1967

Sequence: 1 MEHTAHLANSSLSWMSFG.....NDSKSSYQFEDAIGACVILL 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir80:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	242	12.3	411	2	156444
2	242	12.3	412	2	S23436
3	241	12.3	393	2	A39251
4	238.5	12.1	398	2	JN0708
5	231.5	11.8	355	2	A45177
6	226	11.5	352	2	JE0296
7	225	11.4	352	2	JC7319
8	225	11.4	423	2	JC7677
9	219.5	11.2	388	2	A47249
10	219	11.1	384	2	A47249
11	217.5	11.1	340	2	T18704
12	217.5	11.1	394	2	JC7209
13	217.5	11.1	658	2	JC8611
14	217	11.0	367	2	JC2421
15	217	11.0	367	2	I49022
16	217	11.0	367	2	I56520
17	214.5	10.9	595	2	JC8612
18	213.5	10.9	355	2	I49339
19	213	10.8	352	2	A45747
20	213	10.8	370	2	S43087
21	212	10.8	360	2	JC4629
22	212	10.8	360	2	T23063
23	211.5	10.8	376	2	T24368
24	211.5	10.8	380	2	JC2338
25	211.5	10.8	504	2	T29338
26	210.5	10.7	380	2	S36143
27	209	10.6	424	2	JH0164
28	208.5	10.6	477	2	JC7913
29	207.5	10.5	363	2	I57940

30	207.5	10.5	399	2	A46632	bombesin-like pept
31	207.5	10.5	428	2	JN0692	cholecystokinin ty
32	206.5	10.5	380	2	A48227	kappa opioid recep
33	206.5	10.5	380	2	JC2434	kappa opioid recep
34	206.5	10.5	391	2	A41795	somatostatin recep
35	206.5	10.5	391	2	C41795	somatostatin recep
36	205.5	10.4	353	2	JC2492	G protein-coupled
37	205.5	10.4	391	2	A39297	somatostatin recep
38	205	10.4	355	2	G02436	chemokine (C-C) re
39	205	10.4	355	2	JC5067	G protein-coupled
40	205	10.4	448	2	S59601	vasopressin recept
41	205	10.4	444	2	T27866	hypothetical prote
42	204.5	10.4	352	2	S60024	bradykinin B1 rece
43	204.5	10.4	380	2	A55259	kappa opioid recep
44	204	10.4	353	2	S28787	neuropeptide y/pep
45	204	10.4	372	2	I38532	delta opioid recep

ALIGNMENTS

RESULT 1		156444		thyrotrophin-releasing hormone receptor - mouse	
C:Species: Mus sp. (mouse)		C:Date: 26-Jul-1996		#sequence_revision 26-Jul-1996 #text_change 11-Jan-2000	
C:Accession: I56444		R:Sellar, R.E.; Taylor, P.L.; Lamb, R.F.; Zabavnik, J.; Anderson, L.; Elaine, K.A.		J. Mol. Endocrinol. 10, 199-206, 1993	
A:Title: Functional expression and molecular characterization of the thyrotrophin-releas		A:Reference number: I56444; PMID:93249585; PMID:8387312		A:Accession: I56444	
A:Status: preliminary; translated from GB/EMBL/DBJ		A:Molecule type: mRNA		A:Residues: 1-411 <RES>	
A:Cross-references: UNIPARC:UPI000170AE1; GB:S60053; NID:G300151; PIDN:AAB26491.1; PID		C:Superfamily: adenosine receptor A1			
Query Match		12.3% Score 242; DB 2; Length 411;			
Best Local Similarity 22.6%; Pred. No. 1.2e-12;		Matches 83; Conservative 71; Mismatches 125; Indels 86; Gaps 14;			
QY	19	PSACGLGF-VPVVVYSLLC-LGLPANILTVIISQLVARRQKSYN-YLLALAADIL 75			
DB	16	PQVAVALAEVQVTVILLVVICGLGIVGNIMVLLVMR-TKMRPATNCYLVSLAVADLM 73			
QY	76	VLPFTVFDPLLEDFILMOMQVDPDKI-----LEVEFSSIHSTITVPL 122			
DB	74	VL-----VAAGLPNITDSIYGSWVYGCLCTIYLGAINSSCSITAF 119			
QY	123	TIDRYAVCHPLKHTVSPARTRKIVSVYTCTFLTSIPYMW-----PNIMT-EDYIS 176			
DB	120	TIERIALICHPKIAQFLCTFSRAKIIIFVMA--FTSIYCMWFFLDLNIISTYKDAIV 176			
QY	177	TSVHVLIWICFTVYLVPCISIFILNSIIVKL----- 210			
DB	177	ISCGYKISNNYSPIYLMFGVYVMPMLAVLVGFIARILFLNPISDPKENSMTKKN 236			
QY	211	---RRKSNFRLG-----YSTGKTALLFTTTSIPATLMAP-RIIMILVHLGYADI 257			
DB	237	DSTHQKNNKNNLNTWRFCFNSVTSRKQVTKMLAVVILFALLMMPFRLTVVNSFLSSPF 296			
QY	258	QNRMLVHMSDANMLALNTAINPFLYCFISKRPRTMAALILKAFKQKQPVQVQYTTN 317			
DB	297	QNRWFL---FCRICIYLSAINPIVYLMQOKR---AARFKLCNCKOKPTEKAVNY 348			
QY	318	NFSITSS 324			
DB	349	SVALNYS 355			
RESULT 2		S23436			

thyrotropin receptor - rat
N:Alternate names: thyrotropin-releasing hormone receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S23436; E153279; A49168; P00326
R:de la Pena, P.; Delgado, L.M.; del Camino, D.; Barro, F.
Biochem. J. 284, 891-899, 1992
A:Title: Cloning and expression of the thyrotropin-releasing hormone receptor from GH(3)
A:Reference number: S23436; MUID:92322017; PMID:137915
A:Accession: S23436
A:Molecule type: mRNA
A:Residues: 1-412 <P&N>
A:Cross-references: UNIPROT:001717; UNIPARC:UPI0000137380; EMBL:X64630; NID:G57394; PIDN:
R:Kimura, N.; Arai, K.; Sahara, Y.; Suzuki, H.; Kimura, N.
Endocrinology 134, 432-440, 1994
A:Title: Estradiol transcriptionally and posttranscriptionally up-regulates thyrotropin-
A:Reference number: E153279; MUID:94102223; PMID:8275956
A:Accession: E153279
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-412 <RES>
A:Cross-references: UNIPARC:UPI0000137380; GB:D17469; NID:9464199; PIDN:BA04289.1; PID:
R:Zhao, D.; Yang, J.; Jones, K.E.; Gerald, C.; Suzuki, Y.; Hogan, P.G.; Chin, W.W.; Tash
Endocrinology 130, 3529-3536, 1992
A:Title: Molecular cloning of a complementary deoxyribonucleic acid encoding the thyrotr
A:Reference number: A49168; MUID:92283212; PMID:1317787
A:Accession: A49168
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12, 'D', '14-290, 'K', '292-412 <ZHA>
A:Cross-references: UNIPARC:UPI00001788B0
A:Experimental source: GH cells
A:Note: Sequence extracted from NCBI database (NCBIN:104788, NCBIPI:104795)
R:Yanada, M.; Monden, T.; Satoh, T.; Iizuka, M.; Murakami, M.; Iituchi, T.; Mori, M.
Biochem. Biophys. Res. Commun. 184, 367-372, 1992
A:Title: Differential regulation of thyrotropin-releasing hormone receptor mRNA levels b
A:Reference number: P00326; MUID:92231953; PMID:1373613
A:Accession: P00326
A:Molecule type: mRNA
A:Residues: 30-58, 'P', '60-222, 'T', '224-261 <YAM>
A:Cross-references: UNIPARC:UPI00001788B1
A:Experimental source: strain M18ter
A:Note: The authors translated the codon ACA for residue 88 as Ala
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; transmembrane protein
F:1-22/Domain: transmembrane #status predicted <TM1>
F:32-54/Domain: transmembrane #status predicted <TM2>
F:71-92/Domain: transmembrane #status predicted <TM3>
F:116-140/Domain: transmembrane #status predicted <TM4>
F:165-186/Domain: transmembrane #status predicted <TM5>

Query Match 12.3%; Score 242; DB 2; Length 412;
Best Local Similarity 22.6%; Pred. No. 1.2e-12;
Matches 83; Conservative 71; Mismatches 125; Indels 88; Gaps 14;

QY 19 PGACGLGF-VPVYYSLLC-LGLPNILTVIILSQLVARQKSSYN-YLLALAADIL 75
DB 16 PQAAVALEYQVTVILLVIIICGLGIVGNIMVAVMR--TKMRTATNCYLVSLAVADLM 73
QY 76 VLFFVFDVFLLEDPIILNQMPQVDPDKI-----IEVLFSSIHSTWITVPL 122
DB 74 VL-----VAAGLPNITDSIYGSWVGYGCLCTIYLYGGINASSCSITAF 119

QY 123 TIDRYAVCHPLKHTVSPARTKRVISVYITCFELSPYVWM-----PNIMT-EDYIS 176
DB 120 TIERIALCHPILKQFLCTFSRAKKIILFVMA---FTSIYCMLEFLLDLNISTYKDAIV 176
QY 177 TSVHVLWIMICFTVYLVPCSIFFILNSIIVKL----- 210
DB 177 ISCGKISRNYSPIYLMDFGVYVPMILATVVGFIARILFLNPISDPKSKMKN 236
QY 211 ---RKSKNRLRG-----YSTGKTTALIFTITSITATIMAP-RIMILYHLXGAPI 257

DB 237 DSTHONKMLNLTNRCPENSVSSRKQVTKLAAVVVLLFALLMMPYRTLVVNSFLSSPF 296
QY 258 QNRVLVHIMSDIANMLALNTAINFFLYCFISKFRMTAAATLAFKQKQPOVQFTNH 317
DB 297 QENNFL-----FCRICIYLNSAINPIVYNLMSOKFR---AARFLCNCCKQKPTKAKANY 348
QY 318 NFSITSS 324
DB 349 SVALNYS 355

RESULT 3
A39251
thyrotropin-releasing hormone receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1993 #sequence revision 22-Jan-1993 #text_change 09-Jul-2004
C:Accession: A39251
R:Straub, R.E.; Frech, G.C.; Joho, R.H.; Gerhengorn, M.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 9514-9518, 1990
A:Title: Expression cloning of a cDNA encoding the mouse pituitary thyrotropin-releasing
A:Reference number: A39251; MUID:91088548; PMID:2175902
A:Accession: A39251
A:Molecule type: mRNA
A:Residues: 1-393 <STR>
A:Cross-references: UNIPROT:P21761; UNIPARC:UPI000002930A; GB:M59811; GB:M37490; NID:G20
C:Superfamily: adenosine receptor A1
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 12.3%; Score 241; DB 2; Length 393;
Best Local Similarity 22.1%; Pred. No. 1.4e-12;
Matches 81; Conservative 75; Mismatches 123; Indels 88; Gaps 15;

QY 19 PGACGLGF-VPVYYSLLC-LGLPNILTVIILSQLVARQKSSYN-YLLALAADIL 75
DB 16 PQAAVALEYQVTVILLVIIICGLGIVGNIMVAVMR--TKMRTATNCYLVSLAVADLM 73
QY 76 VLFFVFDVFLLEDPIILNQMPQVDPDKI-----IEVLFSSIHSTWITVPL 122
DB 74 VL-----VAAGLPNITDSIYGSWVGYGCLCTIYLYGGINASSCSITAF 119

QY 123 TIDRYAVCHPLKHTVSPARTKRVISVYITCFELSPYVWM-----PNIMT-EDYIS 176
DB 120 TIERIALCHPILKQFLCTFSRAKKIILFVMA---FTSIYCMLEFLLDLNISTYKNAV 176
QY 177 TSVHVLWIMICFTVYLVPCSIFFILNSI---IYV----- 208
DB 177 VSCGKISRNYSPIYLMDFGVYVPMILATVVGFIARILFLNPISDPKSKMKN 236
QY 209 -KLRRKSNRLRG-----YSTGKTTALIFTITSITATIMAP-RIMILYHLXGAPI 257
DB 237 DSIHONKMLNLTNRCPENSVSSRKQVTKLAAVVVLLFALLMMPYRTLVVNSFLSSPF 296

QY 258 QNRVLVHIMSDIANMLALNTAINFFLYCFISKFRMTAAATLAFKQKQPOVQFTNH 317
DB 297 QENNFL-----FCRICIYLNSAINPIVYNLMSOKFR---AARFLCNCCKQKPTKAKANY 348

QY 318 NFSITSS 324
DB 349 SVALNYS 355

RESULT 4
JN0708
thyrotropin-releasing hormone receptor - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: S40682; JN0759; S50151; S50152; I38356; JN0708
R:Matre, V.; Karlsten, H.E.; Wright, M.S.; Lundell, I.; Fjeldheim, A.K.; Gabrielsen, O.S.
Biochem. Biophys. Res. Commun. 195, 179-185, 1993
A:Title: Molecular cloning of a functional human thyrotropin-releasing hormone receptor.
A:Reference number: S40682; MUID:93371401; PMID:8395824
A:Accession: S40682
A:Status: preliminary

Query Match	Similarity	Score	DB 2	Length	355
Beet local	26.3%	Pred. No. 7.7e-12			
Matches	81	Conservative	57	Mismatches	105
				Indels	65
				Gaps	13
22	ACGCGPVPVYSSLLCTG.PANILTVIISQVARRKSSVNYLALAAADILVFFIV	81			
31	AFGQGLPPL-YSLVPIVIGLVGNILVVLVQYRLKNMMSI-VLNLALASDLLFLFLP	88			
82	F-VDF-LLEDFILNMQPOVPDKIIEVLFSSHTSITWIVPLITDRIYAVCH--PLKY	136			
89	FMIDYKIKDMVWFGDM---CKILSGEYVYGLVSEIFILLITIDRYLAIIVHAVPALRA	144			
137	HTVSPARTKRVIYSVYITGFLSIP-YWMMPNITWEDYSTSVNH-----	181			
145	RTVTFGVYITSIYALAI---LASMPEGLYFSKTOMERTHTTCSLHFPHESIREKLFQAL	201			
182	-----VLWICFTVYLVPCSIFFILNHSIIVKLRKRSNFRLLRGYSTGTTALP	231			
202	KLNLFGLVLPDLWILICYT-----GIKILRLRPN-----KKSQAVRLIF	242			
232	TIISIPATLAAPRIIMLYHLYGAP-----QNRVLVHMSIDIANMLALNLAIFLY	285			
243	VIMIIIFLFTPTPVNLITLISVFDPLFTHCEGSRHL-DLAVQTEVIAYTHCCVNPVY	301			

Query 286 CFIKRRR 293
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Db 302 AFVGRFR 309

RESULT 6

JE0296
thyrotropin releasing hormone receptor - rat
CISpecies: Rattus norvegicus (Norway rat)
CDate: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
CAccession: JE0296
Ritadani, H.; Nakamura, T.; Itoh, J.; Iwasa, H.; Kanatani, A.; Borkowski, J.; Ihara, M.
Biochem. Biophys. Res. Commun. 250, 66-71, 1998
A>Title: Cloning and characterization of a new subtype of thyrotropin-releasing hormone
A.Reference number: JE0296; PMID:98407892; PMID:9735333
A.Accession: JE0296
A.Molecule type: mRNA
A.Residues: 1-352 <ITA>
A.Cross-references: UNIPROT:O88820; UNIPARC:UPI000000B6811; DDBJ:AB015645; NID:g360553;
GSuperfamily: adenosine receptor A1
F:26-48/Domain: transmembrane #status predicted <TM1>
F:58-80/Domain: transmembrane #status predicted <TM2>
F:97-118/Domain: transmembrane #status predicted <TM3>
F:142-165/Domain: transmembrane #status predicted <TM4>
F:188-209/Domain: transmembrane #status predicted <TM5>
F:252-273/Domain: transmembrane #status predicted <TM6>
F:282-304/Domain: transmembrane #status predicted <TM7>

Query Match 11.5%; Score 226; DB 2; Length 352;
Best Local Similarity 23.5%; Pred. No. 2,2e+11,
Matches 76; Conservative 61; Mismatches 104; Indels 82; Gaps 11;

QY 31 VYSLLLCGLPANILTVIILLSQLVARROKSSYN-YLALAADIIVLFPIVDPLLE 88
 ||:|||::|::|::|::|::|::|::|:
Db 26 VFVLVVLTGLIGVANAVLV--LTSRDHPTPCNYLSALADLDLV----- 72
 ::::::|::|::|::|::|::|::|:
89 DFLLNQMPQVPDKI-----IEVLESISTHTITVTPLTDRIYAACHPK 135
 :|||::|::|::|::|::|::|:
Db 73 ---LAAGFLPVSDSLVGHWIYGACLGITFYQYLGINVSFSIIAFTERYATAIChPur 129
 |||||::|::|::|::|::|::|:
136 YHTSVSPARTRKYVSYYTICFLTGISPYWPMNMTEDVISYHHNVLIWHCFYLYNP 195
 |||||::|::|::|::|::|::|:
Db 130 AQTCVCVAARKRIIAGIWGTSTLCYMFLVLDVNDRQLCEGYKVRLYPITYILD 189
 |||||::|::|::|::|::|::|:
196 CSIFPI---DNSIIVVKL-----BRKSNFRLR 219
 ::|||::|::|::|::|::|::|:
190 FAYVFEGPLLVTLVLYGLIRILFGSPLSQEAWKERQHGSSEAPNGCSRAKS---- 244
 ::|||::|::|::|::|::|::|:
220 GVSTGKTALLFTITSFPATIMAR-RITMILYHLGARIQNELYHNSDIAMTLALT 278
 ::|||::|::|::|::|::|::|:
Db 245 --SRKATRMLAAVVLLFAVLMTPRTYLINSFVAOPFLDDEWL----FCRTCVYTMS 298
 ::|||::|::|::|::|::|::|:
279 AINFFLYCPISKPRMTMAATLK 301
 |||::|::|::|::|::|::|:
Db 299 AVNPVVYSIMSOKFR---AAPFK 318
 ::|||::|::|::|::|::|::|:

RESULT 7

JC7319
probable allatotetratin receptor-2 - fruit fly (*Drosophila melanogaster*)
CISpecies: Drosophila melanogaster
CDate: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
CAccession: JC7319
Rienz, C.; Williamson, M.; Grimmelikhuijsen, C.J.P.
Biochem. Biophys. Res. Commun. 273, 571-577, 2000
A>Title: Molecular cloning and genomic organization of a second probable allatotetratin re
A.Reference number: JC7319
A.Accession: JC7319
A.Molecule type: mRNA
A.Residues: 1-357 <LEN>
A.Cross-references: UNIPROT:Q9NBC8; UNIPARC:DPI000000BF41; GB:A25352
CComment: This receptor, belonging to the insect allatotetratin neuropeptide family, which
is a transmembrane glycoprotein.

C:Genetics:
A:Gene: dar-2
A:Map position: right arm of chromosome 3, 98D-E
A:introns: 180/3; 273/3; 326/3
C:Superfamily: endothelin receptor B
C:Keywords: extracellular protein; glycoprotein; neuropeptide; transmembrane protein

```
Query Match      11.4%; Score 225; DB 2; Length 357;  
Best Local Similarity 24.9%; Pred. No. 2,7e-11;  
Matches 87; Conservative 70; Mismatches 112; Indels 80; Gaps 18;
```

Dy 8 LAANSLSMWSPGACGLGFVPVYYSLLCLGPANILTVIIISQLVAROKSSNYTL 67
|||:::||::||::||::||::||::||::||::||::||::||::||::||
Db 31 LAINGTLPMT-----VGPF---FGVIATIGFNGMLYLIV--VENNNMSTINLMI 77

Qy 68 A-LAAADLVLFVFVDFFLEDFEL-----NMOPVDPKIEIYLEFSIHTS 115
|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 78 VNLAAADL-MFVLICPFTATDVMYWPYGRWCWSVOY-----LIIVTAFASITYT- 128

Qy 116 IWTIVPLTDRIYAIVCHPLKHVSYPARTRKOIVSYITCFELSDPY----- 163
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 129 --LVMISIDFLVAHVPIRSMRTENTILIAVTLMIVAVSVPAETHDVVDYDA 185

Qy 164 ----YMMPNIMVEDISTVSVHHLWIHCFTYLVNCGSFFLNLSIIVLKRRK----- 213
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 186 KKNITYGNCFTTNDDFGPRTYOVTPEI---SSLPLFMHSIGLYMRIMRLWRQGTCVR 242

Qy 214 -SNFRLGYSTGKTALILETITSIFATLMAP-RIMLHYLYGAPIORWLVAIMS-DI-A 270
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 243 MSKSQSGQRK-RTRLVVVVVYIAFSLMIPVOLILLKSL--DIVETNTLTGLGVQVTA 298

Qy 271 NMLALNTAINFELYFCISKRFRTMAATAIKAEFK--CKQPQVGYFN 316
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 299 QTLAYSSSCINPLLFAELENFR-----KAIFYAKVCSSR-YQNYS 339

RESULT 8
JC7677
allatostatin receptor - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: JC7677
R:Auerwald, J.; Birguet, N.; Gaede, G.; Kretenkamp, H.J.; Richner, D.
Biochem. Biophys. Res. Commun. 282, 904-909, 2001
A>Title: Structural, functional, and evolutionary characterization of novel members of t
A:Reference number: JC7677; PMID:21250673; PMID:11352636
A:Accession: JC7677
A:Molecule type: mRNA
A:Residues: 1-423 <AB>
A:Cross-references: UNIPROT:Q964D4; UNIPARC:UPI000017A507; GB:AF336364
C:Comment: This receptor, for the neuropeptide, is involved in the inhibition of juvenill
C:Genes:
A:Gene: Alshr
C:Keywords: neuropeptide; transmembrane protein
F:73-94/Domian: transmembrane #status predicted <TM1>
F:105-127/Domian: transmembrane #status predicted <TM2>
F:143-164/Domian: transmembrane #status predicted <TM3>
F:165-167/Region: active element DRF
F:187-207/Domian: transmembrane #status predicted <TM4>
F:243-264/Domian: transmembrane #status predicted <TM5>
F:290-312/Domian: transmembrane #status predicted <TM6>
F:327-350/Domian: transmembrane #status predicted <TM7>

```
Query Match      11.4%; Score 225; DB 2; Length 423;  
Best Local Similarity 23.5%; Pred. No. 3,2e-11;  
Matches 88; Conservative 75; Mismatches 126; Indels 86; Gaps 17;
```

Dy 28 VPVVVYSHLCAGPANILTIIISQLVAROKSSNYTLA-LAADLVLFV-F-VDF 85
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 71 VPL-LFGIIVLVGFGNALVVLVA--ANGQMSTNLLIINVLDL--FIVECPFP 124

Qy 86 LLEDPLNM-QMPVDPKIEIYLEFSIHSTIWITVPLTDRIYAIVCHPLKHTVSYTPAR 144
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 125 TATDYLPEPMPGDIWICKIYOYLIVTVAVASYTLVLSMDRFLAVHPITMSIRTEEN 184
Qy 145 TRKIVSVYTICFLTSPYPMNPMTEDYSTSVHYHLWIC----- 188
Db 185 AIAIAVWVWVILLASVYVILSHGEVITYT--SSAHTACVFLPADIPINRPOCVKPFQI 243
Qy 189 ---FTVYLPCSIFFILNSIIYVKLRKRSNFRLGYSTG-----KTALIFTI 233
Db 244 IFFATSVYTLPLALICGLYLMILLVRL-----WRGAAPGHVASAESRRGKRVTRMVVV 296
Qy 234 TSIPATLWAP-RITMILYHLGAPIQNRMLVHIMSDIANMLALNTAINFLYCFISGRF 292
Db 297 VAIFVAVCFPIQLILVLKSVDRKELTNTSV--MIDIVSHVAVYVNSCVNPILLYAFLSDFH 354
Qy 293 RTMAATLKAFFK---C-----OKOPVOFYTNHNSITSSPWISPNASHCIRKMLVYQYDKN 345
Db 355 R-----KARKVINCSSAGAPQPGPRY-----HRASTIQOQPOAN 389
Qy 346 GKPIKS---RNDKS 357
Db 390 GRALNNECCENDNKS 404
RESULT 9
JN0605
C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C.Accession: JN0605; JN0762; A47457
R.Xu, Y.; Song, J.; Bruno, J.F.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 193, 648-652, 1993
A.Title: Molecular cloning and sequencing of a human somatostatin receptor, hSSTR4.
A.Reference number: JN0605; MUID:93290656; PMID:5512564
A.Accession: JN0605
A.Molecule type: DNA
A.Residues: 1-388 <XU>
A.Cross-references: UNIPROT:P31391; UNIPARC:UPI0000135FP9; GB:L14856; NID:G292499; PIDN:R.Yamada, Y.; Kagimoto, S.; Kubota, A.; Yasuda, K.; Masuda, K.; Someya, Y.; Ihara, Y.; I
Biochem. Biophys. Res. Commun. 195, 844-852, 1993
A.Title: Cloning, functional expression and pharmacological characterization of a fourth
A.Reference number: JN0762; MUID:93384611; PMID:8373420
A.Accession: JN0762
A.Molecule type: DNA
A.Residues: 1-388 <YAM>
A.Cross-references: UNIPARC:UPI0000135FP9; GB:D16826; NID:G693907; PIDN:BA04106.1; PID:
R.Rohrer, L.; Raulf, F.; Bruns, C.; Buettner, R.; Hotstaedter, F.; Schule, R.
Proc. Natl. Acad. Sci. U.S.A. 90, 4196-4200, 1993
A.Title: Cloning and characterization of a fourth human somatostatin receptor.
A.Reference number: A47457; MUID:93248256; PMID:8483934
A.Accession: A47457
A.Molecule type: DNA
A.Residues: 1-82, 'T', '84-364, 'K', '366-388 <ROH>
A.Cross-references: UNIPARC:UPI000050436; GB:L07833; NID:G307429; PIDN:AAA60565.1; PID:
A.Note: sequence extracted from NCBI backbone (NCBIN:110856, NCBI:110856)
C.Comment: This protein mediates the diverse actions of the tetradecapeptide somatostatin.
C.Genetics:
A.Gene: GDB:SSTR4
A.Cross-references: GDB:202662; OMIM:182454
A.Map position: 20p11.2-20p11.2
A.Introns: #status absent
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; lipoprotein; pho
F:84-109/Domain: transmembrane #status predicted <TM1>
F:121-142/Domain: transmembrane #status predicted <TM2>
F:162-188/Domain: transmembrane #status predicted <TM3>
F:208-238/Domain: transmembrane #status predicted <TM4>
F:257-284/Domain: transmembrane #status predicted <TM5>
F:291-314/Domain: transmembrane #status predicted <TM6>
F:324/Binding site: carbonylate (Asn) (covalent) #status predicted
F:119-196/Disulfide bonds: #status predicted
F:161,253/Binding site: phosphate (Ser) (covalent) #status predicted
F:327/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 11.2%; Score 219.5; DB 2; Length 388;
Best Local Similarity 22.0%; Pred. No. 8.4e-11;
Matches 72; Conservative 75; Mismatches 130; Indels 51; Gaps 11;
Qy 19 PGSGAGLFVAV-VYSSLLCLGEPANLITYIISQVARROKSSYNTLLAAADIVL 77
Db 39 PGDRAAGMVAIQCIYALVCLVGNALVFLVILR-YAKKTAATNITLMLAAVDEL- 95
Qy 78 FFIVPVDLLEDFIL-NNQMPQVPDKITEVEFFSSIHFSIMTVPLTIDRYAVGPKY 136
Db 96 -FMISVFPVASSAALRHPFGSVLCRAVLSVDGLMFTSVCLTYLSDRYAAVHPLRA 154
Qy 137 HTVSYPARTRKIVSVYTICFLTSPY-----YMPN-IWTEDYIST 177
Db 155 ATYRRPSVAKLINIGVWLASLVTLPIAIFADTRPARGQAVALQPHPMASAVF-- 212
Qy 178 SVHVLWTHGFTV-YLVPCSIFFILNSIIYVKLR--KSNFRLRGYSTGKTALIFTI 233
Db 213 -----VYTFLLGFLPLVLAIGLCYLLIVGKRAVALRAGWQORRSEKKTITLVLMV 264
Qy 234 TSIPATLWAPRITMILYHLGAPIQNRMLVHIMSDIANMLALNTAINFLYCFISGRF 293
Db 265 VVVFVLCMPFPYVQQLNLVVTSLD-----ATVNHVSILTSYANSCANPILYGLSDNFR 319
Qy 294 -----TMAATLKAFFKQKOPVOFY 314
Db 320 RSPKRVLCRCCLLEGAGGAEPELDY 347
RESULT 10
A47249
brain-specific somatostatin receptor SSTR-4 - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A47249
R.Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 1151-1155, 1992
A.Title: Molecular cloning and functional expression of a brain-specific somatostatin re
A.Reference number: A47249; MUID:93087484; PMID:1360663
A.Accession: A47249
A.Status: preliminary
A.Molecule type: nucleic acid
A.Residues: 1-384 <BRU>
A.Cross-references: UNIPROT:P30937; UNIPARC:UPI0000135FPA; GB:M96544; NID:G207072; PIDN:
A.Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBI:119732)
C.Superfamily: vertebrate rhodopsin
C.Keywords: G protein-coupled receptor; transmembrane protein
Query Match 11.1%; Score 219; DB 2; Length 384;
Best Local Similarity 20.8%; Pred. No. 9.2e-11;
Matches 75; Conservative 80; Mismatches 133; Indels 66; Gaps 11;
Qy 3 HTHAHIANSSLSWSPG-----SACGLGFVAVV-----YSSLLCLGELPAN 44
Db 2 NTPATLPIGGEDETTTPIGINSWAPDEDEAVRSDGTGAGVNTIQCICVAVLCVGLVGN 61
Qy 45 ILTVIILSOLVARROKSSYNTLLAAADIVLFTVYVDLLEDFILANMQMPQVPDKI 104
Db 62 ALVIVFVILR-YAKMKTATNITLMLAAVDELFMLSVPPVASSAA--LRRHPGAVLCRAV 118
Qy 105 EYLSESSHTSHTWIVPLTIDRYAVGPKKHTVSYPARTRKIVSVYTICFLTSPY- 163
Db 119 LSVDELNMFTSVCLTYLSDRYAAVHPLRAITRRSSVAKLINIGVWLASLVTLPLA 178
Qy 164 -----YMPN-IWTEDYISTSVHVLWTHGFTV-YLVPCSIFFILNS 204
Db 179 VFADTRPARGGAVALNHPHMAVAVF-----ITFLLGFLPLVLAIGLCYL 228
Qy 205 IIVYVTLR--KSNFRLRGYSTGKTALIFTITSIFATLMPARITMILYHLGAPIQRM 261
Db 229 LIVGKRAVALRAGWQORRSEKKTITRLVLMVTVFVLCMPFPYVQQLNLVVTSLD--- 285

QY 262 LVHMSDIALNMLALNTAINTFLYCFISKRR-----TMAAATLKAFFKQKQKQVQFY 314
 Db 286 --ATVNVSLILSYANSCANPILYGLSDNFRSRQVRLCRLCULETTGGAEEBPLDY 343

RESULT 11

hypothetical protein B0334.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
 C:Accession: T18704

R:Swingburne, J.
 submitted to the EMBL Data Library, October 1995
 A:Reference number: Z19009
 A:Accession: T18704
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <NLI>
 A:Cross-references: UNIPROT:Q17478; UNIPARC:UPI0000179C62; EMBL:Z66519; NID:IG1044812; PI
 A:Experimental source: clone B0334
 C:Genetics:
 A:Gene: CESP:B0334.6
 A:Map position: 2
 A:Introns: 136/1; 160/3; 307/1

Query Match 11.1%; Score 217.5; DB 2; Length 340;
 Best Local Similarity 23.1%; Pred. No. 1.1e-10;
 Matches 84; Conservative 55; Mismatches 128; Indels 97; Gaps 13;

QY 5 HAHLAANSLSWSPGACGLFVPUVYVYSLLCGLPANITVYIISQLVARHROKSSYN 64
 Db 31 HEHDSQISISVWWS-----NVAVLPEVI-----ALIGLACNLNMAVLTSNKTARRIPSMN 80
 QY 65 YLALAAADILVLFPIVDFLEDFILNMQMPQVDPKIIIELEFSSIHITSIMIVPLTI 124
 Db 81 LLIATAVCDLSLFLIRAT-----LDVTPLSIPS-----LASTSNHYSIVLYI 125
 QY 125 -----DRIYAVCHPLKYHTVSYPARTRKVIYSVYTCELTISIPYWMFN 168
 Db 126 RLASTFYKSRNIPKSKFLANCOILE-----KIRHVNIHYR----- 164
 QY 169 IWTEDYISTSVHVLIMHCFVYVLPSCIFILNSIIVYKLRKRSNRLRGYS----- 222
 Db 165 --TMDYISLFAFNVL-----PIIGLLYMSRIIFTLRRVVDSDSRKYEBETKUSD 211
 QY 223 -----TGKTTAIFFTTSIFATLMAPRI-IMILYHLYGAPIQNRMLVHMSDIA 270
 Db 212 GLIQDANNRTRMRANMLFAVVPMLFCVCGQAPARILFDMYG-QYHFKAILVYC--LS 268
 QY 271 NMLALLNTAINPFLYCFISKRRPTMAAATLKAFF-KCOKQPVQFYTNHNSITSSPWISP 329
 Db 269 QQLVFLNLSINCLYCVVSKRYRTLMKQTLKKFLKLEGVDPHFQNLKQTKSSSAHYTS 328
 QY 330 ANSH 333
 Db 329 LEDH 332

RESULT 12

JC7209
 galanin receptor - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C:Accession: JC7209

R:Lenz, C.; Sondergaard, L.; Grimmelikhuisen, C.J.P.
 Biochem. Biophys. Res. Commun. 269, 91-96, 2000

A:Title: Molecular cloning and genomic organization of a novel receptor from *Drosophila*
 A:Reference number: JC7209; MUID:20160456; PMID:10694483
 A:Accession: JC7209
 A:Molecule type: mRNA
 A:Residues: 1-394 <LEN>
 A:Cross-references: UNIPROT:Q9U721; UNIPARC:UPI0000082510; GB:AF220216
 C:Comment: This receptor is a G-protein-coupled receptor and a transmembrane protein.

C:Genetics:
 A:Cross-references: FlyBase:FBgn0028961
 A:Map position: X distal end
 A:Introns: 98/1; 161/2; 193/2; 243/3; 283/2; 308/3; 360/3
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 11.1%; Score 217.5; DB 2; Length 394;
 Best Local Similarity 25.0%; Pred. No. 1.2e-10;
 Matches 99; Conservative 68; Mismatches 136; Indels 79; Gaps 22;

QY 2 EHT-HAHLAANSLSWSPGACG--LGFVPUVYVYSLLCGLPANITVYIISQLVAR 58
 Db 47 EHTHSDHNDASMEYDASVALERIVSTIYVFGIIGFGLGNGLVIV--VVAHQ 103
 QY 59 Q-KSSVNYLLA-LAADIIVLFPIV-FVDFLEDFILNMQMPQV-----DKIIELEFS 110
 Db 104 QMRSTNLLINLAVSOL---FVIFCVPTATDYVL---PEMPFGNWKCFQVYMIIV 156
 QY 111 SIHTSIMIVPLTIDRYIAVCHPLKYHTVSYPARTRKVIYSVYTCELTISIP----- 162
 Db 157 TCHGSVYTLVMSFDRFLAVVHPVTSMSLTERNATLAIMCAMWITVYTAIPVALSHSVR 216
 QY 163 -YVWMPNIMEDYISTSVHNLIM-----IHCF-TYVLPSCIFILNSIIVYKLR----- 210
 Db 217 IYQYHGNAGTACVFSTEBE--IWSLVGFQVSFPLSYVADLTICFLYMGMLRLMKSA 273
 QY 211 -----RRKSNRLNGYSTGKTTAIFFTTSIFATLMAP-RIIMIL--YHLYGAPIQN 259
 Db 274 PGCKPSAESRKQKGRV-----TRWVVVYVLAFAICMPRHIVILVKALNLVG----G 321
 QY 260 RMLVHMSDIALNMLALNTAINTFLYCFISKRRPTMAAATLKAFF--COKQVQRYTN 316
 Db 322 SHLSVITIIQISHVAVYVNSCINPILYAFSLNFR-----KARQVWVGSP-PLMTN 373
 QY 317 HNFSTSSPWISPANSHCIKML 338
 Db 374 QQVTKTKRTATGNGTSN-IEML 394

RESULT 13

JC8011
 G protein-coupled neuropeptide pyrokinin-2 receptor (CG8784) - fruit fly (*Drosophila mel*
 C:Species: *Drosophila melanogaster*
 C:Date: 04-Apr-2004 #sequence_revision 04-Apr-2004 #text_change 04-Apr-2004
 C:Accession: JC8011

R:Rozenkild, C.; Gazzanali, G.; Williamson, M.; Hauser, F.; Sondergaard, L.; Delotto, R
 Biochem. Biophys. Res. Commun. 309, 485-494, 2003
 A:Title: Molecular cloning, functional expression, and gene silencing of two *Drosophila*
 A:Reference number: JC8011; PMID: 12951076
 A:Accession: JC8011
 A:Molecule type: mRNA
 A:Residues: 1-658 <ROS>
 A:Cross-references: GB:AY277898
 C:Comment: This receptor is a G protein-coupled receptor and a transmembrane protein as
 development, diapause, feeding, and behavior.
 C:Genetics:
 A:Gene: CG8784
 A:Introns: 160/1; 215/2; 259/3; 326/1; 400/3
 C:Keywords: G protein-coupled receptor; neuropeptide pyrokinin; transmembrane protein

Query Match 11.1%; Score 217.5; DB 2; Length 658;
 Best Local Similarity 25.0%; Pred. No. 2.2e-10;
 Matches 82; Conservative 63; Mismatches 132; Indels 51; Gaps 14;

QY 31 VYYSLLCGLPANITVYIISQLVARQKSSNYLLAADIIVLFPIVDFLEDF 90
 Db 112 VCYALIFVAGVIGNITIVISRNPFMTATNF-YLFNLAVSDLLT-----VSGIQGE- 164
 QY 91 ILNMQMPQV---PDKII---EVLFEFSIHITSIMIVPLTIDRYIAVCHPLKYHTVSPAR 144
 Db 165 LYNLMYPMYPTDMCMGVSLSMAANAIVLTITATVERRYIAICHPFQHYMSKLSR 224

```

QY 145 TRKIVSVYITCFLTISIPYMPNII--WTEDYISIVHHVLIWICFTV-----YLVPQS 197
DB 225 AIKFIFAIWLAFLALPQAMQFQVYQEGYSCTEEND--FYAHFAVSGFIFGCGPWT 282
QY 198 IFFINLSIIVYTKRKSFRNL-----RGST--GKTTALIFTTISIFATLMAR 244
DB 283 AICVILVILGVGLKKS--RLQSLPRRTFDANRGLNAGRYIRMLVAVAAPFLCMAPF 339
QY 245 IMIIVYHLGAPIQRWL-----VHIMSDIANMLALNTAINPFLYCFISKPRPTWA 296
DB 340 HAQRLMAVYGLNLINIGIRDAFNDFRILDTSGVLVLTSCINPLNIMSHKREAF 399
QY 297 AATLKAFFKCKQ-----QPVQFYTNHNS 320
DB 400 KITLTROFGLARNHHQSQOH--QHNY 426

```

RESULT 14

JC2421

opioid receptor homolog, MOR-C - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: J02421; 149122

R:Niimi, M.; Takeshima, H.; Mori, M.; Nakagawara, K.; Takeuchi, T.

Biochem. Biophys. Res. Commun. 205, 1353-1357, 1994

A:Title: Structure and chromosomal mapping of genes for the mouse kappa-opioid receptor

A:Reference number: J02421; PMID:95100967; PMID:7802669

A:Accession: J02421

A:Molecule type: mRNA

A:Residues: 1-367 <NIS-

A:Cross-references: UNIPROT:P35377; UNIPARC:UPI000000400E; DDBJ:D31663

R:Halford, W.P.; Gebhardt, B.M.; Carr, D.J.

J. Neuroimmunol. 59, 91-101, 1995

A:Title: Functional role and sequence analysis of a lymphocyte orphan opioid receptor.

A:Reference number: 149122; PMID:95318231; PMID:7797625

A:Accession: 149122

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-357 <RES-

A:Cross-references: UNIPARC:UPI000016CAE4; EMBL:U14165; NID:G540092; PIDN:AAA87899.1; PI

C:Genetics:

A:Gene: MOR-C; MOR

A:Map position: 2H2-4

A:Introns: 75/2; 194/1

C:Superfamily: vertebrate rhodopsin

C:Keywords: receptor

Query Match 11.0%; Score 217; DB 2; Length 367;

Best Local Similarity 22.8%; Pred. No. 1.3e-10;

Matches 74; Conservative 65; Mismatches 117; Indels 68; Gaps 13;

```

QY 7 HLAANSLSWSPGACGIGF-VPVVYYSLLCL-GLPANILTVIILSQLVARROKSSYN 64
DB 32 HLLNASHAFLP-----LGLKVTIVGLYLVAVICIGLGNCLVMYVI--LRHTKMKKTATN 84
QY 65 -YLLAAADIVLFFIYF--VDPLEDFILNQMPQVDPDKIEVLEFSSIHSTIWTVP 121
DB 85 IYIFNLALADTLVLTLPFGTDILGFWPFGNAL-----CKTVIAIDYNNMFTSTFTLTA 140
QY 122 LTIIDRYIACHPKHTVSPARTKRVISVYITCFLTISIPY----- 163
DB 141 MSVDRYVAICHPIRALDVRTSKAQAVNVAIMALASVGVPAIMGSAQVDEDEICLVE 200
QY 164 -----YMPNITWEDYISTSVHVLIMHCFVTVLPCSFIFILNSIIVYKLR----- 211
DB 201 IPAPODYWGP-----VFALCIFLFSF--IIPVLIIISVCYSIMIRLRGVRLLS 246
QY 212 --RKSNFRLRGYSTGKTTALIFTTISIFATLMAPRIIMILYHLYGAPIONRMLVHIMSDI 269
DB 247 GSRKRDNRIR-----RITRLVLVVAVFVGCVTPVQVFLVQGLGVQPSSETRAVAILR-F 300
QY 270 ANMLALNTAINPFLYCFISKRR 293

```

DB 301 CTALGYVNSCLNPLIYAFDENFK 324

RESULT 15

149022

kappa opioid receptor 3 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: 149022

R:Pan, Y.X.; Cheng, J.; Xu, J.; Rosel, G.; Jacobson, E.; Ryan-Moro, J.; Brooks, A.I.; De

Mol. Pharmacol. 47, 1180-1188, 1995

A:Title: Cloning and functional characterization through antisense mapping of a kappa 3-

A:Reference number: 149022; PMID:95327076; PMID:7603458

A:Accession: 149022

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-367 <RES-

A:Cross-references: UNIPROT:P35377; UNIPARC:UPI000016CAC8; EMBL:U09421; NID:G551484; PID

C:Superfamily: vertebrate rhodopsin

Query Match 11.0%; Score 217; DB 2; Length 367;

Best Local Similarity 22.8%; Pred. No. 1.3e-10;

Matches 74; Conservative 65; Mismatches 117; Indels 68; Gaps 13;

```

QY 7 HLAANSLSWSPGACGIGF-VPVVYYSLLCL-GLPANILTVIILSQLVARROKSSYN 64
DB 32 HLLNASHAFLP-----LGLKVTIVGLYLVAVICIGLGNCLVMYVI--LRHTKMKKTATN 84
QY 65 -YLLAAADIVLFFIYF--VDPLEDFILNQMPQVDPDKIEVLEFSSIHSTIWTVP 121
DB 85 IYIFNLALADTLVLTLPFGTDILGFWPFGNAL-----CKTVIAIDYNNMFTSTFTLTA 140
QY 122 LTIIDRYIACHPKHTVSPARTKRVISVYITCFLTISIPY----- 163
DB 141 MSVDRYVAICHPIRALDVRTSKAQAVNVAIMALASVGVPAIMGSAQVDEDEICLVE 200
QY 164 -----YMPNITWEDYISTSVHVLIMHCFVTVLPCSFIFILNSIIVYKLR----- 211
DB 201 IPAPODYWGP-----VFALCIFLFSF--IIPVLIIISVCYSIMIRLRGVRLLS 246
QY 212 --RKSNFRLRGYSTGKTTALIFTTISIFATLMAPRIIMILYHLYGAPIONRMLVHIMSDI 269
DB 247 GSRKRDNRIR-----RITRLVLVVAVFVGCVTPVQVFLVQGLGVQPSSETRAVAILR-F 300
QY 270 ANMLALNTAINPFLYCFISKRR 293
DB 301 CTALGYVNSCLNPLIYAFDENFK 324

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Search completed: December 3, 2005, 06:31:40

Job time : 23.1364 secs

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QY 241 WAPRIMILYLYGAPIONRMLVHMSDIANMLALNTAINFLYCFISKRRFMAATL 300
DB 241 WAPRIMILYLYGAPIONRMLVHMSDIANMLALNTAINFLYCFISKRRFMAATL 300
QY 301 KAFKFCQKQPOVQFYTNHNFSTSSPWISPAISHCCKMLVYQDKXGKPIK 350
DB 301 KAFKFCQKQPOVQFYTNHNFSTSSPWISPAISHCCKMLVYQDKXGKPIK 350

RESULT 2

Q8TDU8_HUMAN PRELIMINARY; PRT; 388 AA.
ID Q8TDU8_HUMAN PRELIMINARY; PRT; 388 AA.
AC Q8TDU8;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative G-protein coupled receptor.
GN Name=GPCR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.,
RA Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
DR EMBL; AB093599; BAB9307.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 388 AA; 44893 MW; D8DF1CF0CC95D98 CRC64;

Query Match 82.5%; Score 1623; DB 2; Length 388;
Best Local Similarity 100.0%; Pred. No. 6.5e-105;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ANILTVIILSQLVARROKSSNYVLLAAADILVLFPIVDFLEDFILNQMPQVDPK 102
DB 78 ANILTVIILSQLVARROKSSNYVLLAAADILVLFPIVDFLEDFILNQMPQVDPK 137
QY 103 IIEVLEFSSIHSTIWTYPLTIDRYIANGCHPLKHTVSYPARTKRVISVYTCTLTSP 162
DB 138 IIEVLEFSSIHSTIWTYPLTIDRYIANGCHPLKHTVSYPARTKRVISVYTCTLTSP 197
QY 163 YVWMPNMTEDYISTSVHVLVIMHCFYVLPVPCSIFFILNSIYYKLRKSNFRLGYS 222
DB 198 YVWMPNMTEDYISTSVHVLVIMHCFYVLPVPCSIFFILNSIYYKLRKSNFRLGYS 257
QY 223 TGTCTAILFTTISFATLMAPRIIMILVLYGAPIONRMLVHMSDIANMLALNTAINF 282
DB 258 TGTCTAILFTTISFATLMAPRIIMILVLYGAPIONRMLVHMSDIANMLALNTAINF 317
QY 283 FLYCFISKRFRMAATLKAFKCOQPOVQFYTNHNFSTSSPWISPAISHCCKMLVYQ 342
DB 318 FLYCFISKRFRMAATLKAFKCOQPOVQFYTNHNFSTSSPWISPAISHCCKMLVYQ 377
QY 343 DKXGKPIK 350
DB 378 DKXGKPIK 385

RESULT 3

Q9BTY4_HUMAN PRELIMINARY; PRT; 265 AA.
ID Q9BTY4_HUMAN PRELIMINARY; PRT; 265 AA.

AC Q9BTY4;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative transmembrane receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RL MEDLINE=21853304; PubMed=11863363; DOI=10.1006/geno.2002.6711;
RA Otolenghi C., Barbieri M., McElwee K., Fellous M.,
RT "Novel paralogy relations among human chromosomes support a link
RT between the phylogeny of doublesex-related genes and the evolution of
RT sex determination." (2002).
RL Genomics 79:333-343(2002).
DR EMBL; AJ303165; CAC33085.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 265 AA; 30999 MW; 8F1A368A9A923958 CRC64;
Query Match 67.0%; Score 1317; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 8.7e-84;
Matches 252; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 ANILTVIILSQLVARROKSSNYVLLAAADILVLFPIVDFLEDFILNQMPQVDPK 102
DB 14 ANILTVIILSQLVARROKSSNYVLLAAADILVLFPIVDFLEDFILNQMPQVDPK 73
QY 103 IIEVLEFSSIHSTIWTYPLTIDRYIANGCHPLKHTVSYPARTKRVISVYTCTLTSP 162
DB 74 IIEVLEFSSIHSTIWTYPLTIDRYIANGCHPLKHTVSYPARTKRVISVYTCTLTSP 133
QY 163 YVWMPNMTEDYISTSVHVLVIMHCFYVLPVPCSIFFILNSIYYKLRKSNFRLGYS 222
DB 134 YVWMPNMTEDYISTSVHVLVIMHCFYVLPVPCSIFFILNSIYYKLRKSNFRLGYS 193
QY 223 TGTCTAILFTTISFATLMAPRIIMILVLYGAPIONRMLVHMSDIANMLALNTAINF 282
DB 194 TGTCTAILFTTISFATLMAPRIIMILVLYGAPIONRMLVHMSDIANMLALNTAINF 253
QY 283 FLYCFISKRFR 294
DB 254 FLYCFISKRFR 265

RESULT 4

Q7T2L1_FUGRU PRELIMINARY; PRT; 383 AA.
ID Q7T2L1_FUGRU PRELIMINARY; PRT; 383 AA.
AC Q7T2L1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE G-protein-coupled receptor 142b (Fragment).
GN Name=GPR142b;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphae; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxId=31033;

```

RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoeglund P.J., Giorlam D.E.I., Lagerstroem M.C.,
RA Schioeth H.B.;
RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives."
RL FEBS Lett. 554:381-388(2003).
DR EMBL, AY88414; AAP7123.1; -; mRNA.
DR Ensembl: SINFUG0000127396; Fugu rubripes.
DR GO, GO:0016021; C:integral to membrane; IEA.
DR GO, GO:0004872; F:receptor activity; IEA.
DR GO, GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO, GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO, GO:0007165; P:signal transduction; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1. 1.
DR PRINTS, PR00237; GPCR_RHODOPSIN.
DR PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 383
SQ SEQUENCE 383 AA; 42610 MW; 761B0AA3B97ECED1 CRC64;

Query Match 64.7%; Score 1273.5; DB 2; Length 383;
Best Local Similarity 66.6%; Pred. No. 1.3e-80;
Matches 249; Conservative 34; Mismatches 66; Indels 25; Gaps 5;

QY 1 MHTTAHLAANSLSWSG-----SACGAGFVVVVVYLLCLGLP-ANILVYIIIS 52
DB 6 MEHSHIFSLALPNESSTGCHPSEATGCGPLGLPLVIVYSALLCLGLVNAVILVYIIIS 65
QY 53 QLVARROKSSNYVLLALAAADILVLFYIFVDFLEDFILNMQMPQVPRKIIIEVEFSS 112
DB 66 QLVARROKSSNYVLLALAAADILVLLIFVDFLEDFILNPPLPSLSANVOLEFSS 125
QY 113 HTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYTICPLTSIPYWPMPINWE 172
DB 126 HTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYTICPLTSIPYWPMPINWE 185
QY 173 -----DYISTSVHVLIVHCTVYLVPCSIFFIINSLIYVKL-RRKSNPL 218
DB 186 LPTGEGGGAGGAGGNRTVAQOILVWNAHCITVFLPCTVFFSLNAVIVHKLRRRSRCP 245
QY 219 RGVSTGKTALIFTISIFATLWAPRIIMLVHLYGAPIQNRW---LVHIMSIAIML 275
DB 246 RGVSTGKTALIFTISIFATLWAPRIIMLVHLYGAPIQNRW---LVHIMSIAIML 305
QY 276 LNTAINFPLVCFISKRFRTMAATLKAFFKQKQPOVQFYTNHNFSTSSPWSIPANS 335
DB 306 LNTGVNFFLYCFISKRFRTMAATLKAFFKQKQPOVQFYTNHNFSTSSPWSIPANS 365
QY 336 KMLVYQYDKNGKPI 349
DB 366 KMLVYQYDKNGKPI 379

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomas N.,
RA Mauceli E., Bouneau L., Fischer C., Okou-Costaz C., Bernot A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Caselli G.,
RA Anthouard V., Jubin C., Caselli V., Katinka M., Vachet B.,
RA Biemont C., Skaili Z., Catolico L., Poulain J., De Berardinis V.,
RA Cruad C., Duprat S., Broctier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volf J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Sautin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Croillien H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CA601015037; CAG11412.1; -; Genomic DNA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm 1. 1.
DR PRINTS, PR00237; GPCR_RHODOPSIN.
DR PROSITE, PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT NON_TER 1
FT NON_TER 327
SQ SEQUENCE 327 AA; 36754 MW; 529EDB93E8C22295 CRC64;

Query Match 59.5%; Score 1171; DB 2; Length 327;
Best Local Similarity 68.7%; Pred. No. 1.5e-73;
Matches 222; Conservative 34; Mismatches 51; Indels 16; Gaps 3;

QY 43 ANILVYIIISQVARROKSSNYVLLALAAADILVLFYIFVDFLEDFILNMQMPQVPRK 102
DB 1 ANILVYIIISQVARROKSSNYVLLALAAADILVLLIFVDFLEDFILNPPLPSLS 60
QY 103 IIEVEFSSHTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYTICPLTSIP 162
DB 61 AVQVLEFSSHTSITVPLTIDRYAVCHPLKHTVSPARTKRVIVSVYTICPLTSIP 120
QY 163 YVWPMPINW-----TEDYISTSVHVLIVHCTVYLVPCSIFFIINSLIYVKL 210
DB 121 YVWPMPINW-----TEDYISTSVHVLIVHCTVYLVPCSIFFIINSLIYVKL 180
QY 211 -RRKSNPLRGVSTGKTALIFTISIFATLWAPRIIMLVHLYGAPIQNRW---LVH 266
DB 181 RRRKSNPLRGVSTGKTALIFTISIFATLWAPRIIMLVHLYGAPIQNRW---LVH 240
QY 267 SDIANMLALNTAINFPLVCFISKRFRTMAATLKAFFKQKQPOVQFYTNHNFSTSS 326
DB 241 TDLANMLALNTGVNFFLYCFISKRFRTMAATLKAFFKQKQPOVQFYTNHNFSTSS 300
QY 327 ISPANSHCIKMLVYQYDKNGKPI 349
DB 301 ISPANSHCIKMLVYQYDKNGKPI 323

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RESULT 5
Q4RJM0_TETNG
ID Q4RJM0_TETNG PRELIMINARY; PRT; 327 AA.
AC Q4RJM0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 3 SCAP15037, whole genome shotgun sequence.
DE (Fragment).
DE ORFNames=GSTENG0003377001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxId=99883;

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RESULT 6
Q86SP2_HUMAN
ID Q86SP2_HUMAN PRELIMINARY; PRT; 186 AA.
AC Q86SP2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G-protein-coupled receptor FGR3 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
 RA Vasiliadis D.K., Hohmann J.G., Zeng H., Li F., Rantchalis J.E.,
 Mortrud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
 Bergman J.E., Galtanaris G.A.;
 RT "The G protein-coupled receptor repertoire of human and mouse."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).
 DR EMBL: AY255545; AAC85057.1; -; mRNA.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signaln. .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR Receptor.
 KM Receptor.
 FT NON_TER 1 186
 FT TER 186
 SQ SEQUENCE 166 AA; 21687 MW; E402AE947EC080AF CRC64;

Query Match 49.8%; Score 979; DB 2; Length 186;
 Best Local Similarity 100.0%; Pred. No. 2e-60;
 Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 168 NIMWEDYSTSVHNLWIMHCTVYLVPCISFIILNSIIVYLRKRSNRLRGSTGKT 227
 DB 1 NIMWEDYSTSVHNLWIMHCTVYLVPCISFIILNSIIVYLRKRSNRLRGSTGKT 60
 OY 228 AILFTTISIPATLMAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFLYCF 287
 DB 61 AILFTTISIPATLMAPRIIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFLYCF 120
 OY 268 ISKRRTMAATLTKAFKCKQKQVQFYNNANSTSSPISPAHSHCIKMLVQYDKXGK 347
 DB 121 ISKRRTMAATLTKAFKCKQKQVQFYNNANSTSSPISPAHSHCIKMLVQYDKXGK 180
 OY 348 PIK 350
 DB 181 PIK 183

RESULT 7

QAS813_TETNG PRELIMINARY; PRT; 309 AA.
 ID QAS813_TETNG
 AC QAS813
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAP14705, whole genome shotgun sequence.
 DE (Fragment)
 GN ORName=GSTENG00022326001;
 OS Tetradon nigriviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Tetradon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 Maucell E., Bonnaud L., Fischer C., Ozouf-Costaz C., Bernot A.,
 Nicoud S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segutens B.,
 Daebliva C., Sallanoubat M., Levy M., Boudet N., Castellano S.,
 Auerhard V., Jubin C., Castel V., Katinka M., Vacherie B.,
 Bismont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,
 Cruaud C., Duprat S., Broctier P., Coulanceau J.P., Guzy J.,
 Parra G., Lardier G., Chappe C., McKernan K.J., McEwan P., Bosak S.,
 Kellis M., Volff J.N., Guiso R., Zody M.C., Medilov J.,
 Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

RA Laudet V., Schachter V., Quetier F., Saurin M., Scarpelli C.,
 Wincker P., Lander B.S., Weissbach J., Roest Crolius H.,
 RT "Genome duplication in the teleost fish Tetradon nigriviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.

CC EMBL: CA601014705; CAG03049.1; -; Genomic DNA.
 DR InterPro: IPR00276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7cm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSN.
 DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 KM Non-ter 309 309
 FT NON_TER 309
 SQ SEQUENCE 309 AA; 34931 MW; AB2P9FE95211EF6 CRC64;

Query Match 39.8%; Score 782; DB 2; Length 309;
 Best Local Similarity 48.5%; Pred. No. 1.6e-46;
 Matches 141; Conservative 62; Mismatches 76; Indels 12; Gaps 4;

OY 15 SWSBPG--SACGLFVPVYVYLLCGLPANLITVILISQLVARRKSSYNLLALAA 72
 DB 11 SRWEDLKSACVLGIPVYVYVLLCVGPVNIITAVLTLRLSRTKALYYLLAVGS 70
 OY 73 DILVLFVFPVDFLEPDIAMQMPQVDPKIEVLFSSITSTWITPLTIDYIANCH 132
 DB 71 DILQFLIFVGFLETVAFHREVPALLHSVAEEFANASITWITPLTVDRVALCH 130
 OY 133 PLKYHTVSVPARTKVIYSVITCFLTSPYVMPNITWEDYSTSVHNLWIMHCTVY 192
 DB 131 PLHRQISIPARTRIIVLVLSASGLPFVMSDMWRNSHPALDAVIMHVTIY 190
 OY 193 LVPCISFIILNSIIVYKLR-RKSNRLG---YST---GKTAIFTTISIPATLMA 242
 DB 191 FLPCISFIILNSIILHTRLRQRORSRGEGPKSTPRRLGKSTAMLATTSVFSVLA 250
 OY 243 PRIMILYHLYGAPIQNRWLVIHMSDIANMLALNTAINFLYCFISKRF 293
 DB 251 PRIVVIVLYHLYSVHRDVRVLAIVLSNMALNTAVNFFLYCFVSKPR 301

RESULT 8

Q772L2_FUGRU PRELIMINARY; PRT; 371 AA.
 ID Q772L2_FUGRU
 AC Q772L2
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE G protein-coupled receptor 142a (Fragment).
 GN Name=GPR142a;
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Takifugu.
 OX NCBI_TaxID=31033;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
 RA Fredriksson R., Hoeglund P.J., Gloriam D.E.I., Lagerstrom M.C.,
 Schioeth H.B.;
 RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
 receptors lacking close relatives."
 RL FEBS Lett. 554:381-388(2003).
 DR EMBL: AY286413; AAP72122.1; -; mRNA.
 DR Ensembl: SINFRUG00000154383; Fugu rubripes.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.

DR GO; GO:0001584; F-rodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; G-protein coupled receptor protein signalin...; IEA.
 DR GO; GO:0007165; P-igial transduction; IEA.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7cm 1; 1.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT NON_TER 1
 FT NON_TER 371
 SQ SEQUENCE 371 AA; 42000 MW; C1A95B619681AB3 CRC64;
 Query Match 39.2%; Score 771; DB 2; Length 371;
 Best Local Similarity 47.0%; Pred. No. 1.1e-45;
 Matches 133; Conservative 65; Mismatches 75; Indels 10; Gaps 2;
 QY 21 SACGIGFVPVYVYLLCLGLPANITVTIISQVARRKSSVNYLLAADIIVLPFI 80
 DB 32 SACVIGFIVYVYVLLCGVDPVNTITVAVALTRLSRTKALYYVLLAVTGSIDLSQLEI 91
 QY 81 VFVDFLEDFIIMQMPOVPDKIEVLEESSIHSTSWIVPLTIDRYIVACHPKYHTVS 140
 DB 92 IFVGFLETAVFHREVPALLLSVSAAEPAANASISWAVPLVDYVVALCHPLHRQIS 151
 QY 141 YPARTRKIVSVYITCFITSIPIYVWMPNITWEDYISTSVHNVLIWICFTVYLVPCISIF 200
 DB 152 YPARTRRIAMVVLVSLASGLPEFWMDWRNSHPRTADALIMVHTVITITFLPESITL 211
 QY 201 IINSIIVYKLRRKSNFRL---RGYST---GKTTAILFITTSIFATLWAPRIIMIDY 250
 DB 212 VLSNLIHTLRARORQCSQDERGPGSAPPRLRGKTTAMLAITSVFSVLAAPRTVVIY 271
 QY 251 HIYGAPIQNRVLVHIMSDIANMLALINTAINPFLYCFISKRR 293
 DB 272 HLIVSSVHRDMRWHLAYDLISNMLAMLTAVNPFLYCFVSKPR 314
 RESULT 9
 GP142_HUMAN
 ID GP142_HUMAN STANDARD; PRT; 462 AA.
 AC Q72601; Q86SL3;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Probable G-protein coupled receptor 142 (G-protein coupled receptor
 DE PGR2).
 GN Name=GPRI42; Synonyms=PGR2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxId=9606;
 OC (1)
 RN NUCLEOTIDE SEQUENCE [MRNA].
 RP MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
 RA Fredriksson R., Hoeglund P.J., Gloriam D.E.I., Lagerstrom M.C.,
 RA Schioeth H.B.;
 RT "Seven evolutionarily conserved human rhodopsin G protein-coupled
 RT receptors lacking close relatives.";
 RL FEBS Lett. 554:381-388 (2003).
 RN [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 123-436.
 RX MEDLINE=22584407; PubMed=12679517; DOI=10.1073/pnas.0230374100;
 RA Vassiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,
 RA Mottud M.T., Brown A., Rodriguez S.S., Weller J.R., Wright A.C.,
 RA Bergmann J.B., Galtanaris G.A.;
 RT "The G protein-coupled receptor repertoires of human and mouse.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908 (2003).
 RL
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AY288421; AAP72130.1; -; mRNA.
 CC EMBL; AY255622; AAO85134.1; -; mRNA.
 CC Ensembl; ENSG00000197344; Homo sapiens.
 CC HGNC; HGNC:20088; GPR142.
 CC MIM; 609046; -; GPCR_Rhodpsn.
 CC InterPro; IPR000276; GPCR_Rhodpsn.
 CC Pfam; PF00001; 7cm 1; 1.
 CC PRINTS; PR00237; GPCR_RHODPSN.
 CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
 FT TOPO_DOM 1
 FT TOPO_DOM 152
 FT TRANSMEM 153
 FT TRANSMEM 173
 FT TOPO_DOM 174
 FT TOPO_DOM 195
 FT TRANSMEM 196
 FT TOPO_DOM 217
 FT TRANSMEM 216
 FT TOPO_DOM 224
 FT TRANSMEM 223
 FT TOPO_DOM 234
 FT TRANSMEM 233
 FT TOPO_DOM 255
 FT TRANSMEM 254
 FT TOPO_DOM 278
 FT TRANSMEM 278
 FT TOPO_DOM 299
 FT TRANSMEM 300
 FT TOPO_DOM 316
 FT TOPO_DOM 317
 FT TOPO_DOM 337
 FT TRANSMEM 338
 FT TOPO_DOM 357
 FT TRANSMEM 358
 FT TOPO_DOM 378
 FT TRANSMEM 379
 FT TOPO_DOM 397
 FT TRANSMEM 398
 FT TOPO_DOM 418
 FT TOPO_DOM 419
 FT TOPO_DOM 462
 FT CONFLICT 132
 FT CONFLICT 132
 SQ SEQUENCE 462 AA; 51106 MW; E9120B52372C75CA CRC64;
 Query Match 37.5%; Score 737; DB 1; Length 462;
 Best Local Similarity 46.3%; Pred. No. 3.1e-43;
 Matches 133; Conservative 57; Mismatches 95; Indels 2; Gaps 2;
 QY 21 SACGIGFVPVYVYLLCLGLPANITVTIISQVARRKSSVNYLLAADIIVLPFI 80
 DB 151 SPVAGVIVPIYVYVLLGLGLVSLTAVALARLTRRPSYVYLLATADIIIVQVI 210
 QY 81 VFVDFLEDFIIMQMPOVPDKIEVLEESSIHSTSWIVPLTIDRYIVACHPKYHTVS 140
 DB 211 VPSGFLGCAVLAHQVPAVAVRTANILERPANAASVMIILITVDRTYLCPLHNRAS 270
 QY 141 YPARTRKIVSVYITCFITSIPIYVWMPNITWEDYISTSVHNVLIWICFTVYLVPCISIF 200
 DB 271 SPGRTRRIAMVVLVSLASGLPEFWMDWRNSHPRTLDEVLKNAHCLTVYFICGVPL 330
 QY 201 IINSIIVYKLRRKSNFRLRGYSTGKTTAILFITTSIFATLWAPRIIMIDY 260
 DB 331 VTNSAIHHRRLRRGRSGLOP-RVKGSTAILGITTLFTLLMAPRVVMLYHNVAVRH 389
 QY 261 WIVHIMSIDIANMLALINTAINPFLYCFISKRR-TMAAATLAFKFC 306
 DB 390 WRVHIALDVANVAMLTANFGLYCFVSKTRFATVROVITDAYAPLC 436
 RESULT 10
 O8NG80_HUMAN
 ID O8NG80_HUMAN PRELIMINARY; PRT; 1464 AA.
 AC Q8NG80;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Seven transmembrane helix receptor.
 GN Name=GPRI42;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.

```

OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
DR EMBL; AB065914; BAC06129.1; -; Genomic_DNA.
DR HGNC; HGNC:2008; GPR142.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR002767; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 1464 AA; 156508 MW; FF8C63F8353ACF7E CRC64;

Query Match 37.5%; Score 737; DB 2; Length 1464;
Beet Local Similarity 46.3%; Pred. No. 8.7e-43;
Matches 133; Conservative 57; Mismatches 95; Indels 2; Gaps 2;

QY 21 SAGGIFVPPVYVYLLCLGLPANIIVYILSQLVARCKSSYNVLLAAADILVLFPI 80
DB 1113 SPCVAGVIVPIYVYVLLGLFVSLITVAALRLATRRPSYVYLLATASDIIIVYI 1172
QY 81 VFVDLLEDFILNMQPVPDKIEVLEFSSIHSTIVTPTLTDRIYAVCHPLKYHTVS 140
DB 1173 VFAGFLLOGAVILARQVPAVVNTANILEFANHAWSVAIVLITVDRYVALCHPLHRAAS 1232
QY 141 YPARTRKYIVSYITCPLTISIPYWMPPNWTEDYISTSVHVLIVIHCTVYLVPCSIFF 200
DB 1223 SPGRTRRLAAVLAVALTGLTFYMWLDWMDRDTSEPTIDEVLEKNAHCLIVYFICGVFL 1292
QY 201 ILNSIIYVKLRKRSNFRLGYSTGKTTALIFTITSIFATLWAPRIIMILYHLYGAPICNR 260
DB 1293 VTNSAIIHRLRRRSGSLQRP-RVGSSTAILLGLITTLFTLWAPRYFVWLHYHVAVPVARD 1351
QY 261 WLVHMSDIANMLALNTAINFPLYCFISKRR-TMAAATLKAFKRC 306
DB 1352 WRVHLADLVANNVAMVMTAANFGLYCFVSKTFRAIVRQVIDYALPC 1398

RESULT 11
GPI42_MOUSE STANDARD; PRT; 365 AA.
AC Q7TON9;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Probable G-protein coupled receptor 142.
GN Name=Gpr142;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN NUCLEOTIDE SEQUENCE [MRNA].
RA MEDLINE=22985413; PubMed=14623098; DOI=10.1016/S0014-5793(03)01196-7;
RA Fredriksson R., Hoeglund P.J., Gloriam D.E.I., Lagerstrom M.C.,
RA Schioeth H.B.;
DE Seven evolutionarily conserved human rhodopsin G protein-coupled
RT receptors lacking close relatives."
RL FEBS Lett. 554:381-388(2003).
CC -1- FUNCTION: Orphan receptor.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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CC -----
DR EMBL; AY288428; AAP72137.1; -; mRNA.
DR EMBL; ENSMUSG0000034677; Mus musculus.
DR MGI; MGI:266437; Gpr142.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
DR Transmembrane.
FT TOPO_DOM 1 66 Extracellular (Potential).
FT TRANSMEM 67 87 1 (Potential).
FT TOPO_DOM 88 102 Cytoplasmic (Potential).
FT TRANSMEM 103 123 2 (Potential).
FT TOPO_DOM 124 140 Extracellular (Potential).
FT TRANSMEM 141 161 3 (Potential).
FT TOPO_DOM 162 185 Cytoplasmic (Potential).
FT TRANSMEM 186 206 4 (Potential).
FT TOPO_DOM 207 224 Extracellular (Potential).
FT TRANSMEM 225 245 5 (Potential).
FT TOPO_DOM 246 264 Cytoplasmic (Potential).
FT TRANSMEM 265 285 6 (Potential).
FT TOPO_DOM 286 304 Extracellular (Potential).
FT TRANSMEM 305 325 7 Potential.
FT TOPO_DOM 326 365 Cytoplasmic (Potential).
FT CAROXYD 44 44 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 365 AA; 40758 MW; ACA8649245CDAB47 CRC64;

Query Match 36.2%; Score 713; DB 1; Length 365;
Beet Local Similarity 46.8%; Pred. No. 1.2e-41;
Matches 138; Conservative 51; Mismatches 96; Indels 10; Gaps 4;

QY 21 SAGGIFVPPVYVYLLCLGLPANIIVYILSQLVARCKSSYNVLLAAADILVLFPI 80
DB 64 SPCVAGVIVPIYVYVLLGLFVSLITVAALRLATRRPSYVYLLATASDIIIVYI 117
QY 81 VFVDLLEDFILNMQPVPDKIEVLEFSSIHSTIVTPTLTDRIYAVCHPLKYHTVS 140
DB 118 VFAGFLLOGAVILARQVPAVVNTANILEFANHAWSVAIVLITVDRYVALCHPLHRAAS 177
QY 141 YPARTRKYIVSYITCPLTISIPYWMPPNWTEDYISTSVHVLIVIHCTVYLVPCSIFF 200
DB 178 SPGRTRRLAAVLAVALTGLTFYMWLDWMDRDTSEPTIDEVLEKNAHCLIVYFICGVFL 237
QY 201 ILNSIIYVKLRKRSNFRLGYSTGKTTALIFTITSIFATLWAPRIIMILYHLYGAPICNR 260
DB 238 VTNSAIIHRLRRRSGSLQRP-VSKSTAILLGLITTLFTLWAPRIIVLWLVYVAVPARD 296
QY 261 WLVHMSDIANMLALNTAINFPLYCFISKRR-TMAAATLKAFKRC--QKQPV 312
DB 297 WRVHLADLVANNVAMVMTAANFGLYCFVSKTFRAIVRQVIDYVMAKLSQPKQ 351

RESULT 12
Q4RX3_TETNG
ID Q4RX3_TETNG PRELIMINARY; PRT; 358 AA.
AC Q4RX3;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Chromosome 9 SCAR15033, whole genome shotgun sequence.
GN ORFNames=GSTENG00032328001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
OC Tetradontidae; Tetradontidae; Tetradon.

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QY	DB	Query Match	Best Local Match	Similarity	Score 262;	DB 2;	Length 54;	Mismatches	Indels	Gaps
226	1	TTAATTTTATATMARIIMIIYHAKGAPIONRWYHIMSDINMALLANTA	51; Conservative	13.3%;	94.4%;	Pred. No. 4.7e-11;	54	2;	0;	0;
SO		SEQUENCE	54 AA;	6082 MW;	587B44A140EF8FDD	CRC64;				
FT		NON_TER	1	1						
DR		GO: GO:0004872; F:receptor activity; IEA.								
DR		MG1: MG1:2685341; Gp1139.								
DR		EMBL: AY255548; AA085060.1; -; mRNA.								
DR		Proc. Natl. Acad. Sci. U.S.A. 100:4903-4908(2003).								
RT		"The G protein-coupled receptor repertoires of human and mouse."								
RA		Bergmann U.E., Galtanaris G.A., Rodriguez S.S., Weller J.R., Wright A.C.,								
RA		Mottrund M.T., Brown A.,								
RA		Medline=22584407; Pubmed=12679517; DOI=10.1073/pnas.0230374100;								
RA		Vasiliadis D.K., Hohmann J.G., Zeng H., Li F., Ranchalis J.E.,								

[illegible]

Search completed: December 3, 2005, 06:36:46
Job time : 128.127 secs

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RESULT 15
ID 017478_CAEEL.
AC 017478_CAEEL PRELIMINARY; PRT; 394 AA.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein B0334.6.
GN ORFNames=B0334.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG "The C. elegans sequencing consortium."
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018 (1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; Z66519; CA91374.3; -; Genomic_DNA.
DR PIR; T18704; T18704
DR Ensembl; B0334.6; Caenorhabditis elegans.
DR WormBase; WBGene00007146; B0334.6.
DR WormPeP; B0334.6; CE30473.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . ; IEA
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GFCCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS02622; G_PROTEIN_RECP_F1_2; 1.
KW Complete proteome; G-protein coupled receptor; Hypothetical protein;
KW Receptor; Transducer; Transmembrane
SQ SEQUENCE 394 AA; 45121 MW; E0EC6180653B8627 CRC64;

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Query Match	13.2%	Score 260.5;	DB 2;	Length 394;
Best Local Similarity	23.6%;	Pred. No. 3.6e-10;		
Matches 90;	Conservative 62;	Mismatches 151;	Indels 79;	Gaps 12

```

QY      5  HAHLAANSLJMSPPSAGCLGFVPVYVYSLLCGLPNLITVILISQVARRQKSSYN  64
      | | | | | : | | | | | : | | | | | : | | | | |
Db     31  HEHDEQGISLVMMS-----NVAVLPIY-----ALIGLAONLMAVLSNKTARIPBMN  80
      | | | | | : | | | | | : | | | | | : | | | | |
QY     65  YLLALAAADILVLFYIVFDLFLEEDFLINQMOPQVD-----KIIEVLEF  105
      | | | | | : | | | | | : | | | | | : | | | | |

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